GP 35730 (11)

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
19 May 2005 (19.05.2005)

PCT

(10) International Publication Number
WO 2005/044990 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number:
PCT/US2004/036404

(22) International Filing Date:
1 November 2004 (01.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
10/700,439 4 November 2003 (04.11.2003) US

(71) Applicants *(for all designated States except US)*: **BAYER HEALTHCARE LLC** [US/US]; 511 Benedict Avenue, Tarrytown, NY 10591 (US). **MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH** [US/US]; 200 First Street SW, Rochester, MN 55905 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BURGESS, Christopher** [US/US]; 97 Canton Terrace, Westwood, MA 02090 (US). **MYEROW, Susan** [US/US]; 5 Ellison Road, Lexington, MA 02421 (US). **THIAGALINGAM, Arunthathi** [US/US]; 26 Winchester Drive, Lexington, MA 02420 (US). **MAIMONIS, Peter** [US/US]; 83 Fensview Drive, Westwood, MA 02090 (US). **MOLINO, Gary** [US/US]; 3 Essex Street, Norfolk, MA 02056 (US). **BURGART, Lawrence** [US/US]; 5685 Chateau Road NW, Rochester, MN 55901 (US). **BOARDMAN, Lisa, Allyn** [US/US]; 3831 Halling Place SW, Rochester, MN 55902 (US). **THIBODEAU, Stephen** [US/US]; 1610 21st Avenue NE, Rochester, MN 55906 (US). **LEWIS, Marcia** [US/US]; 67 Wheelwright Farm, Cohasset, MA 02025 (US).

(74) Agent: **CAMPBELL EVANS, Paula**; Palmer & Dodge LLP, 111 Huntington Avenue, Boston, MA 02199-7613 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2005/044990 A2

(54) Title: USE OF DIFFERENTIALLY EXPRESSED NUCLEIC ACID SEQUENCES AS BIOMARKERS FOR CANCER

(57) Abstract: The present invention relates to novel marker sequences that are differentially expressed in cancer cells or tissue of a subject with cancerous conditions. The present invention also relates to assays for diagnosis, prognosis, staging, monitoring, therapeutic treatment, and marker sequence related agents including probes, primers, antibodies, and therapeutic compositions.

USE OF DIFFERENTIALLY EXPRESSED NUCLEIC ACID SEQUENCES AS BIOMARKERS FOR CANCER

Field of the Invention

The present invention relates to methods for diagnosis, prognosis, characterization, management, and therapy of cancer including colon cancer, based on the identification of certain colon cancer-associated differentially expressed marker sequences.

Background of the Invention

Cancers are the second leading cause of death, next to cardiovascular disease, in the United States. The pathological and molecular mechanisms for cancer initiation and promotion have been revealed after decades of researches. Many genes are involved in the initiation and progression of cancers, including oncogenic and tumor suppressive genes. Multiple factors including genetic, endocrinologic, immunologic, and environmental factors, intertwine in the process of transformation and progression of cancers. The control and cure of cancers remain to be one of the most challenging health care tasks. Particularly, one of the most pressing health issues today is diagnosing, monitoring, and treating cancer.

Colorectal carcinoma is a malignant neoplastic disease. There is a high incidence of colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type often metastasize through lymphatic and vascular channels. Many patients with colorectal carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the United States alone die of colorectal carcinoma annually.

However, if diagnosed early, colon cancer may be treated effectively by surgical removal of the cancerous tissue. Colorectal cancers originate in the colorectal epithelium and typically are not extensively vascularized (and therefore not invasive) during the early stages of development. Colorectal cancer is thought to result from the clonal expansion of a single mutant cell in the epithelial lining of the colon or rectum. The transition to a highly vascularized, invasive and ultimately metastatic cancer which spreads throughout the body commonly takes ten years or longer. If the cancer is detected prior to invasion, surgical removal of the cancerous tissue is an effective cure. However, colorectal cancer is often detected only upon manifestation of clinical symptoms, such as pain and black tarry stool. Generally, such symptoms are present only when the disease is well established, often after metastasis has occurred, and the prognosis

for the patient is poor, even after surgical resection of the cancerous tissue. Early detection of colorectal cancer therefore is important in that detection may significantly reduce its morbidity.

Invasive diagnostic methods such as endoscopic examination allow for direct visual identification, removal, and biopsy of potentially cancerous growths such as polyps. Endoscopy is expensive, uncomfortable, inherently risky, and therefore not a practical tool for screening populations to identify those with colorectal cancer. Non-invasive analysis of stool samples for characteristics indicative of the presence of colorectal cancer or precancer is a preferred alternative for early diagnosis, but no known diagnostic methods are available which reliably achieve this goal.

Summary of the Invention

The present invention relates to nucleic acid sequences that are differentially expressed in cancer tissue compared to normal tissue, and various methods, reagents and kits for diagnosis, staging, prognosis, monitoring and treatment of cancer, including colon cancer.

In one aspect, the present invention provides methods for determining the expression levels of individual and/or combinations of the differentially expressed marker sequences in a biological sample that are indicative of the presence, or stage of the disease, or the efficacy of therapy. The method comprises contacting said sample with a polynucleotide probe or a polypeptide ligand under conditions effective for said probe or ligand to hybridize specifically to a nucleic acid or a polypeptide in said sample, and detecting the presence or absence of marker sequences. In one embodiment, methods are provided to determine the amounts and/or the differentially expressed levels at which the marker sequences of the present invention are expressed in samples. Such methods can comprise contacting said sample with a polynucleotide probe or a polypeptide ligand under conditions effective for said probe to hybridize specifically to the nucleic acids in said sample, and detecting the amounts or differentially expressed level of the marker sequences. In one preferred embodiment, said polynucleotide probe is a polynucleotide designed to identify one of the marker sequences in Tables 1 and 2. In another preferred embodiment, said polypeptide ligand is an antibody.

In another aspect, the present invention provides probes and primers designed to detect transcripts or genomic sequences corresponding to one or more marker sequences of the present

invention. The probes and primers may comprise a portion or all of the sequences listed in SEQ ID NOs: 1-93, or sequences complementary thereto, or sequences which hybridize under stringent conditions to a portion or all of SEQ ID NOs: 1-93.

In another aspect, the present invention provides polypetides encoded by the marker sequences, biologically active portions thereof, and polypetide fragments suitable for use as immunogens to raise antibodies directed against polypeptides of the marker sequences of the present invention.

In another aspect, the present invention provides ligands directed to polypeptides and fragments thereof of the marker sequences of the present invention. Preferably, said polypeptide ligands are antibodies. Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized, or chimeric antibodies, single chain antibodies, Fab fragments, Fv fragments F(ab') fragments, fragments produced by a Fab expression library, anti-iodiotypic antibodies, or other epitope binding polypeptide. Preferably, an antibody, useful in the present invention for the detection of the individual marker sequences (and optionally at least one additional colon cancer-specific marker), is a human antibody or fragment thereof, including scFv, Fab, Fab', F(ab'), Fd, single chain antibody, of Fv. Antibodies, useful in the invention may include a complete heavy or light chain constant region, or a portion thereof, or an absence thereof.

Another aspect of the present invention provides a method of assessing whether a subject is suffering from or at risk of developing cancer including colon cancer by detecting the differential expression of the marker sequences of the present invention. In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA or cDNA and/or protein level of the marker sequences. The method comprises detecting the expression level of the individual and/or the combinations of the marker sequences in a biological sample obtained from a patient. Specifically, the method comprises:

(1). Providing a nucleic acid probe comprising a nucleotide sequence at least about 8 nucleotides in length, at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a

portion of the coding sequence of a nucleic acid sequence represented by SEQ ID NOs:1-93, or a sequence complementary thereto;

(2). Obtaining a clinical sample from a patient potentially comprising one or more nucleic acid marker sequences;

(3). Providing a second clinical sample from an individual known to not have colon cancer, or a cancer-free tissue of the same patient;

(4). Contacting the nucleic acid probe under stringent conditions with RNA of each of said first and second clinical samples (e.g., in a Northern blot or in situ hybridization assay); and

(5). Comparing (a) the amount of hybridization of the probe with RNA of the first serum sample, with (b) the amount of hybridization of the probe with RNA of the second clinical sample; wherein a statistically change (e.g., either an increase or a decrease) in the amount of hybridization with the RNA of the first clinical sample as compared to the amount of hybridization with the RNA of the second clinical sample is indicative of the presence of one or more marker sequences in the first clinical sample.

In another embodiment, the diagnostic methods comprise detecting the polypeptides encoded by the marker sequences of the present invention. The assay would include contacting the polypeptides of the test cell or tissue with one or more polypeptide ligands specific for the polypeptides represented by SEQ ID NOs: 94-186, and determining the approximate amount of complex formation by the ligands and polypeptides of the test cell or tissue, wherein a statistically significant difference (either an increase or a decrease) in the amount of the complex formed with the polypeptides of a test cell or tissue as compared to a normal cell or tissue is an indication that the test cell is cancerous or pre-cancerous. In particular, the assay evaluates the level of marker polypeptide in the test cells, and preferably, compares the measured level with marker polypeptide detected in at least one control cell, e.g., a normal cell and/or a transformed cell of known phenotype.

In another aspect, the present invention provides DNA and protein microarrays for detecting the differential expression levels of the marker sequences. In some embodiments, the microarrays comprise at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15, or more nucleic acids that are complimentary to at least a portion of the coding sequences of the marker sequences

represented by SEQ ID NOs: 1-93. In some embodiments, the microarrays comprise antibodies or antigen-binding fragments thereof, that specifically bind to at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 different marker polypeptides encoded by nucleic acids comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-93. In one embodiment, the probe/primer can comprise a sequence that hybridizes under stringent conditions to at least about 7, preferably 12, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400, or more consecutive nucleotides of SEQ ID NOs: 1-93 of the present invention. In another embodiment, the probe/primer can comprise a sequence that hybridizes under moderately stringent conditions to at least about 7, preferably 12, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400, or more consecutive nucleotides of SEQ ID NOs: 1-93 of the present invention.

In another aspect, the present invention provides methods for determining cancer prognosis and stage based on examining the expression levels of the nucleic acid marker sequences and polypeptides using the methods described in the present invention.

In one embodiment, the methods comprise:

(1). detecting in a biological sample of the subject at a first point in time, the expression of one or more nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93;

(2). repeating step (a) at a subsequent point in time; and

(3). comparing the expression level detected in steps (a) and (b), wherein a change in the expression level is indicative of progression of cancer or a pre-malignant condition thereof in the subject.

In another embodiment, the methods comprise:

(1). detecting in a biological sample of the subject at a first point in time, the expression of one or more polypeptides comprising one or more polypeptide sequences selected from the group consisting of SEQ ID NOs: 94-186;

(2). repeating step (a) at a subsequent point in time; and

(3). comparing the expression level detected in steps (a) and (b), wherein a change in the expression level is indicative of progression of cancer or a pre-malignant condition thereof in the subject.

In another aspect, the present invention also provides methods that permit the assessment and/or monitoring of patients who will be likely to benefit from both traditional and non-traditional treatments and therapies for cancers, particularly colon cancer. The methods include assessing the levels of one or more of the marker sequences in a biological sample for the purposes of determining the status of a patient's disease an/or the efficacy, reaction, and response to cancer or neoplastic disease treatments or therapies that the patient is undergoing.

The present invention also includes methods of assessing the efficacy of a test composition for inhibiting cancer including colon cancer. The methods comprise comparing expression levels of one or more marker sequences in a first biological sample maintained in the presence of a test composition with the expression levels of the same marker sequences in a second biological sample maintained in the absence of the test composition.

In another aspect, the present invention provides assays for determining compounds that modulate the biological activity of the nucleic acids or the polypeptides encoded by the marker sequences. Methods of identifying compounds generally comprise steps in which a compound is placed in contact with a marker sequence, its transcription product, its translation product, or other target, and determination of whether the compound modulates the marker sequence.

In another aspect, the present invention also provides methods for screening drugs that inhibit cancer including colon cancer. Drug screening is performed by adding a test compound to a sample of cells and monitoring the effect. The screening methods may include both *in vitro* and *in vivo* screening of a cell or tissue.

In another aspect, the present invention also provides kits for determining the differential expression levels of the marker sequences of the present invention in a biological sample. Such kits can be used to determine (1) presence or absence of cancer, (2) prognosis and stage of cancer, (3) drugs that inhibit cancer, and (4) treatment for cancer.

Detailed Description of the Invention

I General

The present invention is based, in part, on the identification of marker sequences that are differentially expressed (including both over- and under-expression of the sequences) in various types of humans cells (i.e., cells obtained from a human, cultured human cells, archived or preserved human cells, and *in vivo* cells) relative to normal (i.e., non-cancerous) human cells. It has been discovered that the level of expression of individual marker sequences and combinations of marker sequences described in the present invention correlates with the presence of cancer or pre-malignant condition in a patient. The expression of one or more marker sequences in human cells can be assessed by detecting the RNA transcripts and/or proteins encoded by the marker sequences. Accordingly, the present invention provides methods for identifying cancer, particularly colon cancer, in an individual by screening for sequences which are over- or under-expressed in cancerous cells relative to the level of expression in normal cells, such as cells from colon tissue. Particularly, the present invention provides a method for the identifying colon cancer in an individual by detecting individual marker sequences and/or combinations of marker sequences in the individual relative to a control expression level of the marker sequences in an individual without cancer. The present invention further provides methods for monitoring the onset, progression, or regression of cancer, particularly colon cancer, in an individual by monitoring the expression level of individual marker sequences and/or combinations of marker sequences in the individual at different points in time. The present invention further provides methods for assessing the efficacy of a therapy for inhibiting cancer, particularly colon cancer in a patient by comparing the expression level of individual marker sequences and/or combinations of marker sequences in the individual prior to and after the therapeutic treatment. The present invention further provides methods for selecting a composition for inhibiting cancer, particularly colon cancer, in a patient by comparing the expression level of individual marker sequences and/or combinations of marker sequences in the presence and absence of the composition. The present invention further provides methods for inhibiting cancer, particularly colon cancer, in a patient by administering to the patient a therapeutic composition, wherein the efficacy of the therapeutic composition is indicated by the change in the expression level of individual marker sequences and/or combinations of marker sequences.

In addition to the above methods, the present invention also provides compositions and various kits for the use in the above methods.

II Definitions

As used herein, the term "differentially expressed" refers to expression levels in a test cell that differ significantly from levels in a reference cell, e.g., mRNA is found at levels at least about 25%, at least about 50% to about 75%, at least about 90% increased or decreased, generally at least about 1.2-fold, at least about 1.5-fold, at least about 2-fold, at least about 5-fold, at least about 10-fold, or at least about 50-fold or more increased or decreased in a cancerous cell when compared with a cell of the same type that is not cancerous. The comparison can be made between two tissues, for example, if one is using in situ hybridization or another assay method that allows some degree of discrimination among cell types in the tissue. The comparison may also be made between cells removed from their tissue source. "Differential expression" refers to both quantitative, as well as qualitative, differences in the genes' temporal and/or cellular expression patterns among, for example, normal and neoplastic tumor cells, and/or among tumor cells which have undergone different tumor progression events.

As used herein, the term "a biological sample" refers to a whole organism or a subset of its tissues, cells or component parts (e.g. body fluids, including but not limited to blood, mucus, lymphatic fluid, synovial fluid, cerebrospinal fluid, saliva, amniotic fluid, amniotic cord blood, urine, vaginal fluid and semen). "A biological sample" further refers to a homogenate, lysate or extract prepared from a whole organism or a subset of its tissues, cells or component parts, or a fraction or portion thereof, including but not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, blood cells, tumors, organs. Most often, the sample has been removed from an animal, but the term "biological sample" can also refer to cells or tissue analyzed *in vivo*, i.e., without removal from animal. Typically, a "biological sample" will contain cells from the animal, but the term can also refer to non-cellular biological material, such as non-cellular fractions of blood, saliva, or urine, that can be used to measure the cancer-associated polynucleotide or polypeptides levels. "A biological sample" further refers to a medium, such as a nutrient broth or gel in which an organism has been propagated, which contains cellular components, such as proteins or nucleic acid molecules.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides. ESTs, chromosomes, cDNAs, mRNAs, and rRNAs are representative examples of molecules that may be referred to as nucleic acids.

As used herein, the term "change in the expression level" refers to either an increase or a decrease of the expression level in a test sample from the control level by an amount greater than the standard error of the assay employed to assess expression. Preferably, the change is by at least about twice, and more preferably three, four, five or ten times that amount. For increase, the change is determined by comparing the expression level in the test sample to the control level. For decrease, the change is determined by comparing the control level to the expression level in the test sample. Alternatively, the decrease is determined by comparing the expression level in the test sample to the control level and the decrease in the expression level is by at least about 15%, 25%, 30%, 40%, 50%, 65%, 80%, or greater. The term "significant change in the specific binding" refers to either an increase or a decrease from the specific binding in the cancer-free sample by at least about 10%, 20%, 25%, 30%, preferably at least about 40%, 50%, more preferably at least about 60%, 70%, or 90%.

As used herein, the term "expression level of one or more nucleic acid sequences" refers to the amount of mRNA transcribed from the corresponding genes that are present in a biological sample. The expression level can be detected with or without comparison to a level from a control sample or a level expected of a control sample.

As used herein, the term "control expression level of one or more nucleic acid sequences" refers to the amount of mRNA transcribed from the corresponding genes that are present in a biological sample representative of healthy, cancer-free subjects. The term "control expression level" can also refer to an established level of mRNA representative of the cancer-free population, that has been previously established based on measurement from healthy, cancer-free subjects.

As used herein, the term "cancerous cell" or "cancer cell", used either in the singular or plural form, refers to cells that have undergone a malignant transformation that makes them

pathological to the host organism. Malignant transformation is a single- or multi-step process, which involves in part an alteration in the genetic makeup of the cell and/or the gene expression profile. Malignant transformation may occur either spontaneously, or via an event or combination of events such as drug or chemical treatment, radiation, fusion with other cells, viral infection, or activation or inactivation of particular genes. Malignant transformation may occur in vivo or in vitro, and can if necessary be experimentally induced. Malignant cells may be found within the well-defined tumor mass or may have metastasized to other physical locations. A feature of cancer cells is the tendency to grow in a manner that is uncontrollable by the host, but the pathology associated with a particular cancer cell may take any form. Primary cancer cells (that is, cells obtained from near the site of malignant transformation) can be readily distinguished from non-cancerous cells by well-established pathology techniques, particularly histological examination. The definition of a cancer cell, as used herein, includes not only a primary cancer cell, but any cell derived from a cancer cell ancestor. This includes metastasized cancer cells, and in vitro cultures and cell lines derived from cancer cells.

As used herein, the term "efficacy" refers to either inhibition to some extent, of cell growth causing or contributing to a cell proliferative disorder, or the inhibition, to some extent, of the production of factors (e.g., growth factors) causing or contributing to a cell proliferative disorder. "A therapeutic efficacy" refers to relief of one or more of the symptoms of a cell proliferative disorder. In reference to the treatment of a cancer, a therapeutic efficacy refers to one or more of the following: 1) reduction in the number of cancer cells; 2) reduction in tumor size; 3) inhibition (i.e., slowing to some extent, preferably stopping) of cancer cell infiltration into peripheral organs; 3) inhibition (i.e., slowing to some extent, preferably stopping) of tumor metastasis; 4) inhibition, to some extent, of tumor growth; and/or 5) relieving to some extent one or more of the symptoms associated with the disorder. In reference to the treatment of a cell proliferative disorder other than a cancer, a therapeutic efficacy refers to 1) either inhibition to some extent, of the growth of cells causing the disorder; 2) the inhibition, to some extent, of the production of factors (e.g., growth factors) causing the disorder; and/or 3) relieving to some extent one or more of the symptoms associated with the disorder.

As used herein, the term "detectable label" refers to a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means.

As used herein, the term "a polynucleotide probe" refers to a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified on bases (7-deazaguanosine, inosine, etc.) or on sugar moiety. In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

As used herein, the term "hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

As used herein, the term "subject" refers to any human or non-human organism.

As used herein, "individual" refers to a mammal, preferably a human.

As used herein, "detecting" refers to the identification of the presence or absence of a molecule in a sample. Where the molecule to be detected is a polypeptide, the step of detecting can be performed by binding the polypeptide with an antibody that is detectably labeled. A detectable label is a molecule which is capable of generating, either independently, or in response to a stimulus, an observable signal. A detectable label can be, but is not limited to a fluorescent label, a chromogenic label, a luminescent label, or a radioactive label. Methods for "detecting" a label include quantitative and qualitative methods adapted for standard or confocal microscopy, FACS analysis, and those adapted for high throughput methods involving multi-well plates, arrays or microarrays. One of skill in the art can select appropriate filter sets and excitation energy sources for the detection of fluorescent emission from a given fluorescent polypeptide or dye. "Detecting" as used herein can also include the use of multiple antibodies to a polypeptide to be detected, wherein the multiple antibodies bind to different epitopes on the

polypeptide to be detected. Antibodies used in this manner can employ two or more detectable labels, and can include, for example a FRET pair. A polypeptide molecule is "detected" according to the present invention when the level of detectable signal is at all greater than the background level of the detectable label, or where the level of measured nucleic acid is at all greater than the level measured in a control sample.

As used herein, "detecting" also refers to detecting the presence of a target nucleic acid molecule (e.g., a nucleic acid molecule encoding the marker sequence) refers to a process wherein the signal generated by a directly or indirectly labeled probe nucleic acid molecule (capable of hybridizing to a target, e.g., a sequence encoding Reg1α, in a serum sample) is measured or observed. Thus, detection of the probe nucleic acid is directly indicative of the presence, and thus the detection, of a target nucleic acid, such as a sequence encoding a marker sequence. For example, if the detectable label is a fluorescent label, the target nucleic acid is "detected" by observing or measuring the light emitted by the fluorescent label on the probe nucleic acid when it is excited by the appropriate wavelength, or if the detectable label is a fluorescence/quencher pair, the target nucleic acid is "detected" by observing or measuring the light emitted upon association or dissociation of the fluorescence/quencher pair present on the probe nucleic acid, wherein detection of the probe nucleic acid indicates detection of the target nucleic acid. If the detectable label is a radioactive label, the target nucleic acid, following hybridization with a radioactively labeled probe is "detected" by, for example, autoradiography. Methods and techniques for "detecting" fluorescent, radioactive, and other chemical labels may be found in Ausubel et al. (1995, *Short Protocols in Molecular Biology*, 3rd Ed. John Wiley and Sons, Inc.). Alternatively, a nucleic acid may be "indirectly detected" wherein a moiety is attached to a probe nucleic acid which will hybridize with the target, such as an enzyme activity, allowing detection in the presence of an appropriate substrate, or a specific antigen or other marker allowing detection by addition of an antibody or other specific indicator. Alternatively, a target nucleic acid molecule can be detected by amplifying a nucleic acid sample prepared from a patient clinical sample, using oligonucleotide primers which are specifically designed to hybridize with a portion of the target nucleic acid sequence. Quantitative amplification methods, such as, but not limited to TaqMan, may also be used to "detect" a target nucleic acid according to the invention. A nucleic acid molecule is "detected" as used herein where the level of nucleic acid measured (such as by quantitative PCR), or the level of detectable signal provided by the detectable label is at all above the background level.

As used herein, "detecting" refers further to the early detection of colorectal cancer in a patient, wherein "early" detection refers to the detection of colorectal cancer at Dukes stage A or preferably, prior to a time when the colorectal cancer is morphologically able to be classified in a particular Dukes stage. "Detecting" as used herein further refers to the detection of colorectal cancer recurrence in an individual, using the same detection criteria as indicated above. "Detecting" as used herein still further refers to the measuring of a change in the degree of colorectal cancer before and/or after treatment with a therapeutic compound. In this case, a change in the degree of colorectal cancer in response to a therapeutic compound refers to an increase or decrease in the expression of the marker sequences including one or more colorectal cancer associated markers, or alternatively, in the amount of the marker polypeptide including one or more colorectal cancer associated markers presented in a clinical sample by at least 10% in response to the presence of a therapeutic compound relative to the expression level in the absence of the therapeutic compound.

As used herein, the term "polypeptide" refers to a polymer in which the monomers are amino acids and are joined together through peptide or disulfide bonds. It also refers to either a full-length naturally-occurring amino acid sequence or a fragment thereof between about 8 and about 500 amino acids in length. Additionally, unnatural amino acids, for example, β-alanine, phenyl glycine and homoarginine may be included. Commonly-encountered amino acids which are not gene-encoded may also be used in the present invention. All of the amino acids used in the present invention may be either the D- or L- optical isomer. The L-isomers are preferred.

As used herein, the term "ligand" refers to any compound that interacts with the ligand binding domain of a receptor and modulate its activity. The term "ligand" also refers to a molecule, such as a peptide or variable segment sequence, that is recognized by a particular receptor. As one of ordinary skill in the art will recognize, a molecule (or macromolecular complex) can be both a receptor and a ligand. In general, the binding partner having a smaller molecular weight is referred to as the ligand and the binding partner having a greater molecular weight is referred to as a receptor. Representative ligands include but are not limited to drugs, drug derivatives, isomers thereof, hormones, polypeptides, nucleotides, and the like.

The term "antibody" refers to the conventional immunoglobulin molecule, as well as fragments thereof which are also specifically reactive with one of the subject polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for

utility in the same manner as described herein below for whole antibodies. For example, $F(ab)_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab)_2$ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific, single-chain, and chimeric and humanized molecules having affinity for a polypeptide conferred by at least one CDR region of the antibody. In preferred embodiments, the antibodies, the antibody further comprises a label attached thereto and able to be detected, (e.g., the label can be a radioisotope, fluorescent compound, chemiluminescent compound, enzyme, or enzyme co-factor).

The term "monoclonal antibody" refers to an antibody that recognizes only one type of antigen. This type of antibodies is produced by the daughter cells of a single antibody-producing hybridoma.

As used herein, the terms specific "binding" or "specifically binding", refers to the interaction of an antibody and a protein or peptide. The interaction is dependent upon the presence of a particular structure (*i.e.*, the antigenic determinant or epitope) on the protein; in other words, the antibody is recognizing and binding to a specific protein structure rather than to proteins in general. For example, if an antibody is specific for epitope A, the presence of a protein containing epitope A (or free, unlabeled A) in a reaction containing labeled "A" and the antibody will reduce the amount of labeled A bound to the antibody.

III Identification of marker sequences

One aspect of the present invention pertains to identification of differentially expressed marker sequences (either over- or under-expressed) in a biological sample from a patient with cancerous or pre-malignant conditions. In general, the method of identifying the marker sequences involves providing a pool of target nucleic acids (derived from both tumor and normal cells and/or tissue) comprising RNA transcripts of one or more target genes, or nucleic acids derived from the RNA transcripts, hybridizing the nucleic acid sample to one or more probes, and detecting the hybridized nucleic acids and calculating a relative expression level relative to the control expression level of the same nucleic acids. A variety of methods have been employed to achieve this end. They include differential screening of cDNA libraries with selective probes, subtractive hybridization utilizing DNA/DNA hybrids or DNA/RNA hybrids, RNA fingerprinting and differential display (Mather, et al. (1981) *Cell* 23:369-378; Hedrick et al.

(1984) *Nature* 308:149-153; Davis et al. (1992) *Cell* 51:987-1000; Welsh et al. (1992) *Nucleic Acids Res.* 20:4965-4970; and Liang and Pardee (1992) *Science* 257:967-971). Recently, PCR-coupled subtractive processes have also been reported (Straus and Ausubel (1990) *Proc. Natl. Sci. USA* 87:1889-1893; Sive and John (1988) *Nucleic Acids Res.* 16:10937; Wieland et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:2720-2724; Wang and Brown (1991) *Proc. Natl. Acad. Sci. USA* 88:11505-11509; Lisitsyn et al. (1993) *Science* 259:946-951; Zeng et al. (1994) *Nucleic Acids Res.* 22:4381-4385; Hubank and Schatz (1994) *Nucleic Acids Res.* 22:5640-5648). Also recently, a microarray technology (DNA chips) developed by Affymetrix (Santa Clara, CA) has been used as a powerful tool to simultaneously identify a large number of differentially expressed genes in a biological sample. Each of these methods can be employed in the present invention and is hereby incorporated by reference in entirety.

By using the Affymetrix chips (GeneChip Human Genome U133 Set), the inventors of the present invention identified two clusters of differentially expressed marker sequences that have shown at least a two-fold change (either increase or decrease) in expression level in biological samples from tumor cells and/or tissue, e.g., colon cancer-derived cells and/or tissue, relative to the expression level in samples from normal cells and/or tissue, e.g., normal colon tissue and/or normal non-colon tissue. Table 1 describes 47 marker sequences that are over-expressed (up-regulated) in tumor cells and/or tissue, e.g., colon cancer-derived cells and/or tissue.

Table 1. Over-expressed Marker sequences

SEQ ID NO	Gene Symbol & Locus ID	Accession Number	Type	Corresponding Protein Accession Number	Protein SEQ ID NO
1	KRT23, 25984	NM_015515	RNA	NP_056330	94
2	REG1A, 5967	NM_002909	RNA	NP_002900	95
3	REG1B, 5968	NM_006507	RNA	NP_006498	96
4	DPEP1, 1800	NM_004413	RNA	NP_004404	97

5	IL8, 3576	NM_000584	RNA	NP_00575	98
6	MMP1, 4312	NM_002421	RNA	NP_002412	99
7	MMP7, 4316	NM_002423	RNA	NP_002414	100
8	SSP1, 6696	NM_000582	RNA	NP_000573	101
9	CXCL10, 3627	NM_001565	RNA	NP_001556	102
10	SULF1, 23213	NM_015170	RNA	NP_055985	103
11	COL5A2, 1290	NM_000393	RNA	NP_000384	104
12	CXCL1, 2919	NM_001511	RNA	NP_001502	105
13	CCL18, 6362	NM_002988	RNA	NP_002979	106
14	CDH11, 1009	NM_001797	RNA	NP_001788	107
15	BST2, 684	NM_004335	RNA	NP_004326	108
16	C20orf97, 57761	NM_021158	RNA	NP_066981	109
17	THBS2, 7058	NM_003247	RNA	NP_003238	110
18	G1P3, 2537	NM_022873	RNA	NP_075011	111
19	CKTSF1B1, 26585	NM_013372	RNA	NP_037504	112
20	MMP9, 4318	NM_004994	RNA	NP_004985	113
21	RAB31, 11031	NM_006868	RNA	NP_006859	114
22	DD96, 10158	NM_005764	RNA	NP_005755	115

23	SUPT4H1, 6827	NM_003168	RNA	NP_003159	116
24	FXYD5, 53827	NM_014164	RNA	NP_054883	117
25	CSPG2, 1462	NM_004385	RNA	NP_004376	118
26	LAPTM4B, 55353	NM_018407	RNA	NP_060877	119
27	SOX4, 6659	NM_003107	RNA	NP_003098	120
28	SORD, 6652	NM_003104	RNA	NP_003095	121
29	MMP12, 4321	NM_002426	RNA	NP_002417	122
30	UBD, 10537	NM_006398	RNA	NP_006389	123
31	DKFZp564I1922, 25878	NM_015419	RNA	NP_056234	124
32	COL1A1, 1277	NM_000088	RNA	NP_000079	125
33	PLAB, 9518	NM_004864	RNA	NP_004855	126
34	SCD, 6319	NM_005063	RNA	NP_005054	127
35	CCL20, 6364	NM_004591	RNA	NP_004582	128
36	BACE2, 25825	NM_012105	RNA	NP_036237	129
37	GTF3A, 2971	NM_002097	RNA	NP_002088	130
38	C20orf42, 55612	NM_017671	RNA	NP_060141	131
39	OSF-2, 10631	NM_006475	RNA	NP_006466	132
40	SPARC, 6678	NM_003118	RNA	NP_003109	133

41	TGFBI, 7045	NM_000358	RNA	NP_000349	134
42	FN1, 2335	NM_002026	RNA	NP_002017	135
43	COL1A2, 1278	NM_000089	RNA	NP_000080	136
44	S100A11, 6282	NM_005620	RNA	NP_005611	137
45	IFITM1, 8519	NM_003641	RNA	NP_003632	138
46		AF130095	RNA	AAG35520	139
47	COL3A1, 1281	NM_000090	RNA	NP_000081	140

Accordingly, the present invention provides marker sequences in Table 1 that are over-expressed by at least about 2 fold, at least about 5 fold, at least about 10 fold, at least about 20 fold, or at least about 50 fold. In one embodiment, the present invention encompasses marker sequences that are over-expressed (up-regulated) in tumor cells and/or tissue, especially in colon cancer cells and/or tissue and/or colon cancer-derived cell lines. In a preferred embodiment, the marker sequences are over-expressed (up-regulated) by at least about 2 fold, at least about 5 fold, at least about 10 fold, at least about 20 fold, or at least about 50 fold.

Table 2 describes 46 marker sequences that are under-expressed (down-regulated) in tumor cells and/or tissue, e.g., colon cancer-derived cells and/or tissue.

Table 2 Under-expressed Marker sequences

SEQ ID NO	Gene Symbol & Locus ID	Accession Number	Type	Corresponding Protein Accession Number	Protein SEQ ID NO
48	GCG, 2641	NM_002054	RNA	NP_002045	141
49	SPINK5, 11005	NM_006846	RNA	NP_006837	142
50	ANPEP, 290	NM_001150	RNA	NP_001141	143

51	AQP8, 343	NM_001169	RNA	NP_001160	144
52	GUCA2B, 2981	NM_007102	RNA	NP_009033	145
53	CLCA4, 22802	NM_012128	RNA	NP_036260	146
54	PRV1, 57126	NM_020406	RNA	NP_065139	147
55	EKI1, 55500	NM_018638	RNA	NP_061108	148
56	FLJ22595, 80117	NM_025047	RNA	NP_079323	149
57	UGT2B15	NM_001076	RNA	NP_001067	150
58	CEACAM7, 1087	NM_006890	RNA	NP_008821	151
59	CHGA, 1113	NM_001275	RNA	NP_001266	152
60	HPGD, 3248	NM_000860	RNA	NP_000851	153
61	MGC4172, 79154	NM_024308	RNA	NP_077284	154
62	CA4, 762	NM_000717	RNA	NP_000708	155
63	IL1R2, 7850	NM_004633	RNA	NP_004624	156
64	FLJ20127, 54827	NM_017678	RNA	NP_060148	157
65	MS4A12, 54860	NM_017716	RNA	NP_060186	158
66	EMP1, 2012	NM_001423	RNA	NP_001414	159
67	SLC4A4, 8671	NM_003759	RNA	NP_003750	160

68	ADH1C, 126	NM_000669	RNA	NP_000660	161
69	CEACAM1, 634	NM_001712	RNA	NP_001703	162
70	MAWBP, 64081	NM_022129	RNA	NP_071412	163
71	PCK1, 5105	NM_002591	RNA	NP_002582	164
72	UGT2B17, 7367	NM_001077	RNA	NP_001068	165
73	HSD17B2	NM_002153	RNA	NP_002144	166
74	LOC63928, 63928	NM_022097	RNA	NP_071380	167
75	RDHL, 10170	NM_005771	RNA	NP_005762	168
76	GUCA1B, 2979	NM_002098	RNA	NP_002089	169
77	FHL1, 2273	NM_001449	RNA	NP_001440	170
78	ADAMDEC1, 27299	NM_014479	RNA	NP_055294	171
79	SPINK4, 27290	NM_014471	RNA	NP_055286	172
80	CA1, 759	NM_001738	RNA	NP_001729	173
81	SGK, 6446	NM_005627	RNA	NP_005618	174
82	CKB, 1152	NM_001823	RNA	NP_001814	175
83	SLC26A2, 1836	NM_000112	RNA	NP_000103	176
84	RNAHP, 11325	NM_007372	RNA	NP_031398	177
85	MUC2, 4583	NM_002457	RNA	NP_002448	178

86	HMGCS2, 3258	NM_005518	RNA	NP_005509	179
87	CLCA1, 1179	NM_001285	RNA	NP_001276	180
88	MT1F, 4494	NM_005949	RNA	NP_005940	181
89	CA2, 760	NM_000067	RNA	NP_000058	182
90	MT1H, 4496	NM_005951	RNA	NP_005942	183
91	MT1G, 4495	NM_005950	RNA	NP_005941	184
92	ZG16, 123887	NM_152338	RNA	NP_689551	185
93	MT1X, 4501	NM_005952	RNA	NP_005943	186

Accordingly, the present invention provides marker sequences in Table 2 that are under-expressed (down-regulated) by at least about 2 fold, at least about 5 fold, at least about 10 fold, at least about 20 fold, or at least about 50 fold. In one embodiment, the present invention encompasses marker sequences that are over-expressed (down-regulated) in tumor cells and/or tissue, especially in colon cancer cells and/or tissue and/or colon cancer-derived cell lines. In a preferred embodiment, the marker sequences are under-expressed (down-regulated) by at least about 2 fold, at least about 5 fold, at least about 10 fold, at least about 20 fold, or at least about 50 fold.

The present invention also encompasses sequences which differ from the marker sequences identified in Tables 1 and 2, but which produce the same phenotypic effect, for example, an allelic variant.

The present invention further encompasses polynucleotides which are at least about 85%, or at least about 90%, or more preferably equal to or greater than about 95% identical to the sequences of the RNA transcripts or cDNAs of the marker sequences. Sequence identity as used herein refers to the proportion of base matches between two nucleic acid sequences or the proportion amino acid matches between two amino acid sequences. When sequence homology is

expressed as a percentage, e.g., 50%, the percentage denotes the proportion of matches over the length of sequence from one sequence that is compared to some other sequence.

The identification of marker sequences that are differentially expressed in tumor cells and/or tissue as compared to normal cells and/or tissue, has applications in a number of ways. For example, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Similarly, a particular treatment may be evaluated, such evaluation including whether a therapeutic treatment improves the long-term prognosis in a particular patient. Furthermore, the gene expression profiles or individual genes allow screening drug candidates. These methods can also be done at protein level. That is, protein expression levels of the marker sequences associated with the tumor or pre-malignant conditions can be evaluated for diagnostic and prognostic purposes or for screening candidate composition for inhibiting tumors or pre-malignant conditions.

IV Primers and probes

The nucleic acid sequences of the identified marker sequences that are differentially expressed in tumor cells and/or tissue will further allow for the generation of probes and primers designed to detect transcripts or genomic sequences corresponding to one or more marker sequences of the present invention. The probe/primer is typically used as one or more substantially purified oligonucleotides. The primer/probe may comprise a portion or all of the sequences listed in SEQ ID NOs: 1-93, or sequences complementary thereto, or sequences which hybridize under stringent conditions to a portion or all of SEQ ID NOs: 1-93. In one embodiment, the probe/primer can comprise a sequence that hybridizes under stringent conditions to at least about 7, preferably about 12, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400, or more consecutive nucleotides of SEQ ID NOs: 1-93 of the present invention. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least about 75% (about 80%, 85%, preferably about 90%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions for annealing two single-stranded DNA each of which is at least about 100 bases in length and/or for annealing a single-stranded DNA and a single-stranded

RNA each of which is at least about 100 bases in length, are hybridization in 6 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 x SSC, 0.1% SDS at 50-65°C. Further preferred hybridization conditions are taught in Lockhart, et al., *Nature Biotechnology*, 14:1675-1680 (1996); Breslauer, et al., *Proc. Natl. Acad. Sci. USA*, 83:3746-3750 (1986); Van Ness, et al., *Nucleic Acids Research*, 19: 5143-5151 (1991); McGraw, et al., *BioTechniques*, 8: 674-678 (1990); and Milner, et al., *Nature Biotechnology*, 15: 537-541 (1997), all expressly incorporated by reference.

In another embodiment, the probe/primer can comprise a sequence that hybridizes under moderately stringent conditions to at least about 7, preferably 12, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400, or more consecutive nucleotides of SEQ ID NOs: 1-93 of the present invention. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 x SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C to 60°C, 5 x SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2 x, 0.5 x, and 0.2 x SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed.

In particular, these probes are useful because they provide a method for detecting mutations in wild-type marker sequences of the present invention. Nucleic acid probes which are complementary to a wild-type marker sequence of the present invention and can form mismatches with mutant marker sequences are provided, allowing for detection by enzymatic or chemical cleavage or by shifts in electrophoretic mobility. Likewise, probes based on the subject sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins, for use, for example, in prognostic or diagnostic assays.

Nucleic acid probes may be generated using techniques which are well known to those of skill in the art (see, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989), or Current Protocols in Molecular Biology, F. Ausubel et al., ed. Greene Publishing and Wiley-Interscience, New York (1987).

In order to measure the hybridization of a nucleic acid probe to a target sequence in a biological sample, the probe is preferably labeled with a detectable label. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., DynabeadsTM), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, 35S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241.

Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

The labels may be incorporated into a nucleic acid probe by any of a number of means well known to those of skill in the art. However, in a preferred embodiment, the label is simultaneously incorporated into the probe during an amplification step in the preparation of the probe polynucleotides. Thus, for example, polymerase chain reaction (PCR), or other amplification reaction, with labeled primers or labeled nucleotides will provide a labeled amplification product, and thus a labeled probe.

Alternatively, a label may be added directly to the probe. Means of attaching labels to polynucleotides are well known to those of skill in the art and include, for example nick translation or end-labeling (e.g. with a labeled RNA) and subsequent attachment (ligation) of a polynucleotide linker joining the sample polynucleotide to a label (e.g., a fluorophore).

In a preferred embodiment, the fluorescent modifications are by cyanine dyes e.g. Cy-3/Cy-5 dUTP, Cy-3/Cy-5 dCTP (Amersham Pharmacia) or alexa dyes (Khan, J., Simon, R., Bittner, M., Chen, Y., Leighton, S. B., Pohida, T., Smith, P. D., Jiang, Y., Gooden, G. C., Trent, J. M. & Meltzer, P. S. (1998) *Cancer Res.* 58, 50095013.).

V Polynucleotide composition

Full-length cDNA molecules comprising the disclosed nucleic acids of the marker sequences, useful for the generation of probes, primers, or for transcription to produce the protein of the marker sequences, or antibodies thereto may be obtained as follows. The nucleic acid sequences of the marker sequences or a portion thereof comprising at least approximately 8, preferably about 12, preferably about 15, preferably about 25, more preferably about 40 nucleotides up to the full length of the sequence of SEQ ID NOs: 1-93, or a sequence complementary thereto, may be used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques as described in U.S. Patent No. 5,654,173, "Secreted Proteins and Polynucleotides Encoding Them," incorporated herein by reference. Libraries of cDNA may be made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical compound. Preferably, the tissue is the same as that used to generate the nucleic acids, as both the nucleic acid and the cDNA represent expressed genes. Alternatively, many cDNA libraries are available commercially. (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed. (Cold Spring Harbor Press, Cold Spring Harbor, NY 1989). The choice of cell type for library construction may be made after the identity of the protein encoded by the nucleic acid-related gene is known. This will indicate which tissue and cell types are likely to express the related gene, thereby containing the mRNA for generating the cDNA.

Members of the library that are larger than the nucleic acid, and preferably that contain the whole sequence of the native message, may be obtained. To confirm that the entire cDNA has been obtained, RNA protection experiments may be performed as follows. Hybridization of a full-length cDNA to an mRNA may protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that arc not hybridized may be subject to RNase degradation. This may be assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed. (Cold Spring Harbor Press, Cold Spring

Harbor, NY 1989). In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications* (Academic Press, Inc. 1990)) may be performed.

Genomic DNAs of the marker sequences may be isolated using nucleic acids in a manner similar to the isolation of full-length cDNAs. Briefly, the nucleic acids, or portions thereof, may be used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the nucleic acids. Most preferably, the genomic DNA is obtained from the biological material described herein in the Example. Such libraries may be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al.,pages 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking may be performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are isolated. These may be mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the nucleic acids of the invention, corresponding full length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, may be performed on a number of cell types to determine which cell lines express the gene of interest at the highest rate.

Classical methods of constructing cDNA libraries in Sambrook et al., *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant marker sequences or portions thereof as primers.

PCR methods may be used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert may contain sequence from the full length cDNA that corresponds to the sequence encoding Reg1α. Such PCR methods include gene trapping and RACE methods.

Gene trapping may entail inserting a member of a cDNA library into a vector. The vector then may be denatured to produce single stranded molecules. Next, a substrate-bound probe, such as biotinylated oligonucleotide, may be used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence may be based on the nucleic acid of SEQ ID NOs: 1-93, or a sequence complementary thereto. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber et al., PCT WO 95/04745 and Gruber et al., U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs may be ligated to an oligonucleotide linker and amplified by PCR using two primers. One primer may be based on sequence from the instant nucleic acids, for which full length sequence is desired, and a second primer may comprise a sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this method is reported in PCT Pub. No. WO 97/19110.

In preferred embodiments of RACE, a common primer may be designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* 15:890-893 (1993); Edwards et al., *Nuc. Acids Res.* 19:5227-5232 (1991)). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on the disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, such as serum, nucleic acid comprising nucleotides having the sequence of one or more nucleic acids of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from about 8 nucleotides (corresponding to at least 12 contiguous nucleotides

which hybridize under stringent conditions to or are at least 80% identical to the nucleic acid sequence of SEQ ID NOs:1-93, or a sequence complementary thereto) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid comprising the size of the full marker genes, or a sequence complementary thereto; (b) the nucleic acid of(a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral particle comprising (a) or (b).

The sequence of a nucleic acid of the present invention is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired.

In various embodiments described above, the polynucleotides of the present invention can be modified at the base moiety, sugar moiety, or phosphate backbone to improve the stability, hybridization, or solubility of the molecule. For example, detectable markers (avidin, biotin, radioactive elements, fluorescent tags and dyes, energy transfer labels, energy-emitting labels, binding partners, etc.) or moieties which improve hybridization, detection, and/or stability can be attached to the polynucleotides. The polynucleotides can also be attached to solid supports, e.g., nitrocellulose, magnetic or paramagnetic microspheres (e.g., as described in U.S. Pat. Nos. 5,411,863; 5,543,289; for instance, comprising ferromagnetic, super-magnetic, paramagnetic, superparamagnetic, iron oxide and polysaccharide), nylon, agarose, diazotized cellulose, latex solid microspheres, polyacrylamides, etc., according to a desired method. See, e.g., U.S. Pat. Nos. 5,470,967, 5,476,925, and 5,478,893.

Polynucleotide according to the present invention can be labeled according to any desired method. The polynucleotide can be labeled using radioactive tracers such as ^{32}P, ^{35}S, ^{3}H, or ^{14}C, to mention some commonly used tracers. The radioactive labeling can be carried out according to any method, such as, for example, terminal labeling at the 3' or 5' end using a radiolabeled nucleotide, polynucleotide kinase (with or without dephosphorylation with a phosphatase) or a ligase (depending on the end to be labeled). A non-radioactive labeling can also be used, combining a polynucleotide of the present invention with residues having immunological

properties (antigens, haptens), a specific affinity for certain recompounds (ligands), properties enabling detectable enzyme reactions to be completed (enzymes or coenzymes, enzyme substrates, or other substances involved in an enzymatic reaction), or characteristic physical properties, such as fluorescence or the emission or absorption of light at a desired wavelength, etc.

VI Vectors and host cells

The present invention further provides vectors and plasmids useful for directing the expression of marker sequences, and further provides host cells which express the vectors and plasmids provided herein. Nucleic acid sequences useful for the expression from a vector or plasmid as described below include, but are not limited to any nucleic acid or gene sequence identified as being differentially regulated by the methods described above, and further include therapeutic nucleic acid molecules, such as antisense molecules. The host cell may be any prokaryotic or eukaryotic cell. Ligating the polynucleotide sequence into a gene construct, such as an expression vector, and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard procedures well known in the art.

Vectors

There is a wide array of vectors known and available in the art that are useful for the expression of differentially expressed nucleic acid molecules according to the invention. The selection of a particular vector clearly depends upon the intended use the polypeptide encoded by the differentially expressed nucleic acid. For example, the selected vector must be capable of driving expression of the polypeptide in the desired cell type, whether that cell type be prokaryotic or eukaryotic. Many vectors comprise sequences allowing both prokaryotic vector replication and eukaryotic expression of operably linked gene sequences.

Vectors useful according to the invention may be autonomously replicating, that is, the vector, for example, a plasmid, exists extrachromosomally and its replication is not necessarily directly linked to the replication of the host cell's genome. Alternatively, the replication of the vector may be linked to the replication of the host's chromosomal DNA, for example, the vector may be integrated into the chromosome of the host cell as achieved by retroviral vectors.

Vectors useful according to the invention preferably comprise sequences operably linked to the sequence of interest (e.g., the marker sequences) that permit the transcription and translation of the sequence. Sequences that permit the transcription of the linked sequence of interest include a promoter and optionally also include an enhancer element or elements permitting the strong expression of the linked sequences. The term "transcriptional regulatory sequences" refers to the combination of a promoter and any additional sequences conferring desired expression characteristics (e.g., high level expression, inducible expression, tissue- or cell-type-specific expression) on an operably linked nucleic acid sequence.

The selected promoter may be any DNA sequence that exhibits transcriptional activity in the selected host cell, and may be derived from a gene normally expressed in the host cell or from a gene normally expressed in other cells or organisms. Examples of promoters include, but are not limited to the following: A) prokaryotic promoters - *E. coli* lac, tac, or trp promoters, lambda phage P_R or P_L promoters, bacteriophage T7, T3, Sp6 promoters, *B. subtilis* alkaline protease promoter, and the *B. stearothermophilus* maltogenic amylase promoter, etc.; B) eukaryotic promoters - yeast promoters, such as GAL1, GAL4 and other glycolytic gene promoters (see for example, Hitzeman et al., 1980, *J. Biol. Chem.* 255: 12073-12080; Alber & Kawasaki, 1982, *J. Mol. Appl. Gen.* 1: 419-434), LEU2 promoter (Martinez-Garcia et al., 1989, *Mol Gen Genet.* 217: 464-470), alcohol dehydrogenase gene promoters (Young et al., 1982, in *Genetic Engineering of Microorganisms for Chemicals*, Hollaender et al., eds., Plenum Press, NY), or the TPI1 promoter (U.S. Pat. No. 4,599,311); insect promoters, such as the polyhedrin promoter (U.S. Pat. No. 4,745,051; Vasuvedan et al., 1992, *FEBS Lett.* 311: 7-11), the P10 promoter (Vlak et al., 1988, *J. Gen. Virol.* 69: 765-776), the *Autographa californica* polyhedrosis virus basic protein promoter (EP 397485), the baculovirus immediate-early gene promoter gene 1 promoter (U.S. Pat. Nos. 5,155,037 and 5,162,222), the baculovirus 39K delayed-early gene promoter (also U.S. Pat. Nos. 5,155,037 and 5,162,222) and the OpMNPV immediate early promoter 2; mammalian promoters - the SV40 promoter (Subramani et al., 1981, *Mol. Cell. Biol.* 1: 854-864), metallothionein promoter (MT-1; Palmiter et al., 1983, *Science* 222: 809-814), adenovirus 2 major late promoter (Yu et al.,1984, *Nucl. Acids Res.* 12: 9309-21), cytomegalovirus (CMV) or other viral promoter (Tong et al., 1998, *Anticancer Res.* 18: 719-725), or even the endogenous promoter of a gene of interest in a particular cell type.

A selected promoter may also be linked to sequences rendering it inducible or tissue-specific. For example, the addition of a tissue-specific enhancer element upstream of a selected promoter may render the promoter more active in a given tissue or cell type. Alternatively, or in addition, inducible expression may be achieved by linking the promoter to any of a number of sequence elements permitting induction by, for example, thermal changes (temperature sensitive), chemical treatment (for example, metal ion- or IPTG-inducible), or the addition of an antibiotic inducing compound (for example, tetracycline).

Regulatable expression is achieved using, for example, expression systems that are drug inducible (e.g., tetracycline, rapamycin or hormone-inducible). Drug-regulatable promoters that are particularly well suited for use in mammalian cells include the tetracycline regulatable promoters, and glucocorticoid steroid-, sex hormone steroid-, ecdysone-, lipopolysaccharide (LPS)- and isopropylthiogalactoside (IPTG)-regulatable promoters. A regulatable expression system for use in mammalian cells should ideally, but not necessarily, involve a transcriptional regulator that binds (or fails to bind) nonmammalian DNA motifs in response to a regulatory agent, and a regulatory sequence that is responsive only to this transcriptional regulator.

Tissue-specific promoters may also be used to advantage in differentially expressed sequence-encoding constructs of the invention. A wide variety of tissue-specific promoters is known. As used herein, the term "tissue-specific" means that a given promoter is transcriptionally active (i.e., directs the expression of linked sequences sufficient to permit detection of the polypeptide product of the promoter) in less than all cells or tissues of an organism. A tissue specific promoter is preferably active in only one cell type, but may, for example, be active in a particular class or lineage of cell types (e.g., hematopoietic cells). A tissue specific promoter useful according to the invention comprises those sequences necessary and sufficient for the expression of an operably linked nucleic acid sequence in a manner or pattern that is essentially the same as the manner or pattern of expression of the gene linked to that promoter in nature. The following is a non-exclusive list of tissue specific promoters and literature references containing the necessary sequences to achieve expression characteristic of those promoters in their respective tissues; the entire content of each of these literature references is incorporated herein by reference. Examples of tissue specific promoters useful in the present invention are as follows:

Bowman et al., 1995 *Proc. Natl. Acad. Sci. USA* 92,12115-12119 describe a brain-specific transferrin promoter; the synapsin I promoter is neuron specific (Schoch et al., 1996 J. *Biol. Chem.* 271, 3317-3323); the nestin promoter is post-mitotic neuron specific (Uetsuki et al., 1996 J. Biol. Chem. 271, 918-924); the neurofilament light promoter is neuron specific (Charron et al., 1995 *J. Biol. Chem.* 270, 30604-30610); the acetylcholine receptor promoter is neuron specific (Wood et al., 1995 *J. Biol. Chem.* 270, 30933-30940); and the potassium channel promoter is high-frequency firing neuron specific (Gan et al., 1996 *J. Biol. Chem* 271, 5859-5865). Any tissue specific transcriptional regulatory sequence known in the art may be used to advantage with a vector encoding a differentially expressed nucleic acid sequence obtained from an animal subjected to pain.

In addition to promoter/enhancer elements, vectors useful according to the invention may further comprise a suitable terminator. Such terminators include, for example, the human growth hormone terminator (Palmiter et al., 1983, *supra*), or, for yeast or fungal hosts, the TPI1 (Alber & Kawasaki, 1982, *supra*) or ADH3 terminator (McKnight et al., 1985, *EMBO J.* 4: 2093-2099).

Vectors useful according to the invention may also comprise polyadenylation sequences (e.g., the SV40 or Ad5E1b poly(A) sequence), and translational enhancer sequences (e.g., those from Adenovirus VA RNAs). Further, a vector useful according to the invention may encode a signal sequence directing the recombinant polypeptide to a particular cellular compartment or, alternatively, may encode a signal directing secretion of the recombinant polypeptide.

a. Plasmid vectors.

Any plasmid vector that allows expression of a coding sequence of interest (e.g., the coding sequence of Reg1α)in a selected host cell type is acceptable for use according to the invention. A plasmid vector useful in the invention may have any or all of the above-noted characteristics of vectors useful according to the invention. Plasmid vectors useful according to the invention include, but are not limited to the following examples: Bacterial - pQE70, pQE60, pQE-9 (Qiagen) pBs, phagescript, psiX174, pBluescript SK, pBsKS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, and pRIT5 (Pharmacia); Eukaryotic - pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other plasmid or vector may be used as long as it is replicable and viable in the host.

b. Bacteriophage vectors.

There are a number of well known bacteriophage-derived vectors useful according to the invention. Foremost among these are the lambda-based vectors, such as Lambda Zap II or Lambda-Zap Express vectors (Stratagene) that allow inducible expression of the polypeptide encoded by the insert. Others include filamentous bacteriophage such as the M13-based family of vectors.

c. Viral vectors.

A number of different viral vectors are useful according to the invention, and any viral vector that permits the introduction and expression of one or more of the polynucleotides of the invention in cells is acceptable for use in the methods of the invention. Viral vectors that can be used to deliver foreign nucleic acid into cells include but are not limited to retroviral vectors, adenoviral vectors, adeno-associated viral vectors, herpesviral vectors, and Semliki forest viral (alphaviral) vectors. Defective retroviruses are well characterized for use in gene transfer (for a review see Miller, A.D. (1990) *Blood* 76:271). Protocols for producing recombinant retroviruses and for infecting cells *in vitro* or *in vivo* with such viruses can be found in *Current Protocols in Molecular Biology*, Ausubel, F.M. et al. (eds.) Greene Publishing Associates, (1989), Sections 9.10-9.14, and other standard laboratory manuals.

In addition to retroviral vectors, Adenovirus can be manipulated such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a normal lytic viral life cycle (see for example Berkner et al., 1988, *BioTechniques* 6:616; Rosenfeld et al., 1991, *Science* 252:431-434; and Rosenfeld et al., 1992, *Cell* 68:143-155). Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, Ad7 etc.) are well known to those skilled in the art.
Adeno-associated virus (AAV) is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle. (For a review see Muzyczka et al., 1992, *Curr. Topics in Micro. and Immunol.* 158:97-129). An AAV vector such as that described in Traschin et al. (1985, *Mol. Cell. Biol.* 5:3251-3260) can be used to introduce nucleic acid into cells. A variety of nucleic acids have been introduced into different cell types using AAV vectors (see, for example,

Hermonat et al., 1984, *Proc. Natl. Acad. Sci. USA* 81: 6466-6470; and Traschin et al., 1985, *Mol. Cell. Biol.* 4: 2072-2081).

Host cells

Any cell into which a recombinant vector carrying a gene of interest (e.g., a sequence encoding the marker sequences) may be introduced and wherein the vector is permitted to drive the expression of the peptide encoded by the differentially expressed sequence is useful according to the invention. Any cell in which a differentially expressed molecule of the invention may be expressed and preferably detected is a suitable host, wherein the host cell is preferably a mammalian cell and more preferably a human cell. Vectors suitable for the introduction of nucleic acid sequences to host cells from a variety of different organisms, both prokaryotic and eukaryotic, are described herein above or known to those skilled in the art.

Host cells may be prokaryotic, such as any of a number of bacterial strains, or may be eukaryotic, such as yeast or other fungal cells, insect or amphibian cells, or mammalian cells including, for example, rodent, simian or human cells. Cells may be primary cultured cells, for example, primary human fibroblasts or keratinocytes, or may be an established cell line, such as NIH3T3, 293T or CHO cells. Further, mammalian cells useful in the present invention may be phenotypically normal or oncogenically transformed. It is assumed that one skilled in the art can readily establish and maintain a chosen host cell type in culture.

Introduction of vectors to host cells.

Vectors useful in the present invention may be introduced to selected host cells by any of a number of suitable methods known to those skilled in the art. For example, vector constructs may be introduced to appropriate bacterial cells by infection, in the case of E. coli bacteriophage vector particles such as lambda or M13, or by any of a number of transformation methods for plasmid vectors or for bacteriophage DNA. For example, standard calcium-chloride-mediated bacterial transformation is still commonly used to introduce naked DNA to bacteria (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY), but electroporation may also be used (Ausubel et al., 1988, *Current Protocols in Molecular Biology*, (John Wiley & Sons, Inc., NY, NY)).

For the introduction of vector constructs to yeast or other fungal cells, chemical transformation methods are generally used (e.g. as described by Rose et al., 1990, *Methods in Yeast Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). For transformation of *S. cerevisiae*, for example, the cells are treated with lithium acetate to achieve transformation efficiencies of approximately 10^4 colony-forming units (transformed cells)/μg of DNA. Transformed cells are then isolated on selective media appropriate to the selectable marker used. Alternatively, or in addition, plates or filters lifted from plates may be scanned for GFP fluorescence to identify transformed clones.

For the introduction of vectors comprising a sequence of interest to mammalian cells, the method used will depend upon the form of the vector. Plasmid vectors may be introduced by any of a number of transfection methods, including, for example, lipid-mediated transfection ("lipofection"), DEAE-dextran-mediated transfection, electroporation or calcium phosphate precipitation. These methods are detailed, for example, in Current Protocols in Molecular Biology (Ausubel et al., 1988, John Wiley & Sons, Inc., NY, NY).

Lipofection reagents and methods suitable for transient transfection of a wide variety of transformed and non-transformed or primary cells are widely available, making lipofection an attractive method of introducing constructs to eukaryotic, and particularly mammalian cells in culture. For example, LipofectAMINE™ (Life Technologies) or LipoTaxi™(Stratagene) kits are available. Other companies offering reagents and methods for lipofection include Bio-Rad Laboratories, CLONTECH, Glen Research, InVitrogen, JBL Scientific, MBI Fermentas, PanVera, Promega, Quantum Biotechnologies, Sigma-Aldrich, and Wako Chemicals USA.

Following transfection with a vector of the invention, eukaryotic (e.g., human) cells successfully incorporating the construct (intra- or extrachromosomally) may be selected, as noted above, by either treatment of the transfected population with a selection agent, such as an antibiotic whose resistance gene is encoded by the vector, or by direct screening using, for example, FACS of the cell population or fluorescence scanning of adherent cultures. Frequently, both types of screening may be used, wherein a negative selection is used to enrich for cells taking up the construct and FACS or fluorescence scanning is used to further enrich for cells expressing differentially expressed polynucleotides or to identify specific clones of cells, respectively. For example, a negative selection with the neomycin analog G418 (Life Technologies, Inc.) may be used to identify cells that have received the vector, and fluorescence

scanning may be used to identify those cells or clones of cells that express the vector construct to the greatest extent.

VII Polypeptides

One aspect of the present invention pertains to isolated polypeptides which correspond to individual marker sequences of the present invention, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a polypeptide encoded by a nucleic acid marker sequence of the present invention. In one embodiment, the native polypeptide encoded by a marker sequence can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, polypeptides encoded by a nucleic acid marker sequence of the invention are produced by recombinant DNA techniques. Alternative to recombinant expression, a polypeptide encoded by a nucleic acid marker sequence of the invention can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a polypeptide encoded by a nucleic acid marker sequence of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the protein encoded by the nucleic acid marker sequence (e.g., the amino acid sequence listed in the GenBank and IMAGE Consortium database records described herein), which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

The polypeptides may contain amino acid substitutions, deletions or insertions made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues involved. Such substitutions may be conservative in nature when the substituted residue has structural or chemical properties similar to the original residue (e.g., replacement of leucine with isoleucine or valine) or they may be nonconservative when the replacement residue is radically different (e.g., a glycine replaced by a tryptophan). Computer programs included in LASERGENE software (DNASTAR, Madison, Wis.) and algorithms included in RasMol software (University of Massachusetts, Amherst, Mass.) may be used to help determine which and how many amino acid residues in a particular portion of the protein may be substituted, inserted, or deleted without abolishing biological or immunological activity.

The present invention also provides chimeric or fusion proteins corresponding to a marker sequence of the invention. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a polypeptide encoded by a nucleic acid marker sequence of the invention operably linked to a heterologous polypeptide (i.e., a polypeptide other than the polypeptide encoded by the nucleic acid marker sequence). Within the fusion protein, the term "operably linked" is intended to indicate that the polypeptide of the invention and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the polypeptide of the invention.

One useful fusion protein is a GST fusion protein in which a polypeptide encoded by a nucleic acid marker sequence of the invention is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a polypeptide encoded by a nucleic acid marker sequence of the invention can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel et al., ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, Calif.). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook et al., *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, N.J.). A signal sequence can be used to facilitate secretion and isolation of the secreted protein or other proteins of interest.

In addition to recombinant production, proteins or portions thereof may be produced manually, using solid-phase techniques (Stewart et al. (1969) Solid-Phase Peptide Synthesis, WH Freeman, San Francisco, Calif.; Merrifield (1963) *J Am Chem Soc* 5:2149-2154), or using machines such as the 431A peptide synthesizer (Applied Biosystems (ABI), Foster City, Calif.). Proteins produced by any of the above methods may be used as pharmaceutical compositions to treat disorders associated with null or inadequate expression of the genomic sequence.

VIII Antibodies

Another aspect of the present invention pertains to antibodies directed to polypeptides and fragments thereof of the marker sequences of the present invention. An isolated polypeptide encoded by a nucleic acid marker sequence of the present invention, or fragment thereof, can be used as an immunogen to generate antibodies using standard techniques. Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized, or chimeric antibodies, single chain antibodies, Fab fragments, Fv fragments F(ab') fragments, fragments produced by a Fab expression library, anti-iodiotypic antibodies, or other epitope binding polypeptide. Preferably, an antibody, useful in the present invention for the

detection of the individual marker sequences (and optionally at least one additional colon cancer-specific marker), is a human antibody or fragment thereof, including scFv, Fab, Fab', F(ab'), Fd, single chain antibody, of Fv. Antibodies, useful in the invention may include a complete heavy or light chain constant region, or a portion thereof, or an absence thereof. An antibody, useful in the invention, may be obtained from an art recognized host, such as rabbit, mouse, rat, donkey, sheep, goat, guinea pig, camel, horse, or chicken. In one embodiment, an antibody, useful in the invention can be a humanized antibody, in which amino acids have been replaced in the non-antigen binding regions in order to more closely resemble a human antibody, while still retaining the original binding ability. Methods for making humanized antibodies are described in Teng et al., 1983, *Proc. Natl. Acad. Sci. USA* 80: 7308-7312; Kozbor et al., 1983, *Immunology Today* 4: 7279; Olsson et al., 1982, *Meth. Enzymol.* 92: 3-16; WO 92/06193; EP 0239400.

Antibodies of the present invention may be monospecific, dispecfic, trispecific, or of greater multispecificity. As such, the individual marker sequences useful for the detection of cancer maybe detected with separate antibodies, or may be detected with the same antibody. Alternatively, a multispecific antibody may exhibit different specificities for different epitopes on the same protein (e.g., different epitopes on a marker sequence). While specificity of an antibody useful in the present invention to one or more additional cancer-specific markers is preferred, antibodies that bind polypeptides with at least 95%, 90%, 85%, 75%, 65%, 55%, and at least 50% identity to a polypeptide useful in the present invention for the detection of cancer, particularly colon cancer are also included in the present invention. Also encompassed in the present invention are antibodies which bind to polypeptide molecules which are encoded by one or more nucleic acid sequences which are complementary to, or hybridize to the sequences of SEQ ID NOs: 1-93.

Antibodies of the present invention which are useful for the detection of colon cancer may further act as agonists or antagonists of the activity of the polypeptide molecules to which they bind, and may thus be useful as therapeutic molecules for the treatment or prevention of colon cancer.

An important, but not limiting, role of an antibody of the present invention is to provide for the purification, or detection of individual marker sequences in a patient sample, including both *in vitro* and *in vivo* detection methods. Antibodies useful for the detection of colon cancer as described herein do not have to be used alone, and can be fused to other polypeptides,

including a heterologous polypeptide at the N- or C-terminus of the antibody polypeptide sequence. For example, an antibody useful in the present invention may be fused with a detectable label to facilitate detection of the antibody when bound to a target polypeptide. Methods for detectably labeling an antibody polypeptide are known to those of skill in the art.

For the production of antibodies useful in the present invention, various hosts including goats, rabbits, rats, mice, etc., may be immunized by injection with the protein products (or any portion, fragment, or oligonucleotide thereof which retains immunogenic properties) of the candidate genes of the invention. Depending on the host species, various adjuvants may be used to increase the immunological response. Such adjuvants include but are not limited to Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. BCG (bacilli Calmette-Guerin) and *Corynebacterium parvum* are potentially useful human adjuvants.

Polyclonal antisera or monoclonal antibodies can be made using methods known in the art. A mammal such as a mouse, hamster, or rabbit, can be immunized with an immunogenic form of a marker polypeptide, fragment, modified form thereof, or variant form thereof. Alternatively, an animal may be immunized with an immunogenic form of one or more additional colon cancer-specific marker polypeptides. Techniques for conferring immunogenicity on such molecules include conjugation to carriers or other techniques well known in the art. For example, the immunogenic molecule can be administered in the presence of adjuvant as described above. Immunization can be monitored by detection of antibody titers in plasma or serum. Standard immunoassay procedures can be used with the immunogen as antigen to assess the levels and the specificity of antibodies. Following immunization, antisera can be obtained and, if desired, polyclonal antibodies isolated from the sera.

To produce monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from an immunized animal and fused with myeloma cells by standard somatic cell fusion procedures thus immortalizing these cells and yielding hybridoma cells. Such techniques are well known in the art (see, e.g., Kohler and Milstein, 1975, *Nature* 256: 495-497; Kozbor et al., 1983, *Immunol. Today* 4: 72, Cole et al., 1985, In *Monoclonal Antibodies in Cancer Therapy*, Allen R. Bliss, Inc., pages 77-96). Additionally, techniques described for the production of

single-chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce antibodies according to the invention.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Pat. No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J.* 12:725-734.

Antibody fragments which can specifically bind to a marker polypeptide of the present invention, or fragments thereof, modified forms thereof, and variants thereof, also may be generated by known techniques. For example, such fragments include, but are not limited to, $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. VH regions and FV regions can be expressed in bacteria using phage expression libraries (e.g., Ward et al., 1989, *Nature* 341: 544-546; Huse et al., 1989, *Science* 246: 1275-1281; McCafferty et al., 1990, *Nature* 348: 552-554).

Chimeric antibodies, i.e., antibody molecules that combine a non-human animal variable region and a human constant region also are within the scope of the invention. Chimeric antibody molecules include, for example, the antigen binding domain from an antibody of a mouse, rat, or other species, with human constant regions. Standard methods may be used to make chimeric antibodies containing the immunoglobulin variable region which recognizes the gene product of individual marker antigens of the invention (see, e.g., Morrison et al., 1985,

Proc. Natl. Acad. Sci. USA 81: 6851; Takeda et al., 1985, *Nature* 314: 452; U.S. Patent No. 4,816,567; U.S. Patent No. 4,816,397).

Antibodies of the invention may be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having cervical cancer. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide encoded by a nucleic acid marker sequences of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Pat. No. 5,625,126; U.S. Pat. No. 5,633,425; U.S. Pat. No. 5,569,825; U.S. Pat. No. 5,661,016; and U.S. Pat. No. 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, Calif.), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

An antibody directed against a polypeptide encoded by a nucleic acid marker sequence of the invention (e.g., a monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker sequence (e.g., in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker sequence. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (e.g. in an ovary-associated body fluid) as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and

radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, .beta.-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

Further, an antibody (or fragment thereof) can be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), .sup.bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine). Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described in U.S. Pat. No. 4,676,980.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies* '84; Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in

Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982).

IX Detection of the marker sequences

In one aspect, the expression levels of the differentially expressed marker sequences are determined in normal and cancer cells and/or tissue, especially the colon cancer cells and/or tissue. In general, the present invention relates to methods of detecting a differentially-expressed nucleic acid sequence in a sample comprising nucleic acid. Such methods can comprise one or more of the following steps in any effective order, e.g., contacting said sample with polynucleotide probes under conditions effective for said probe to hybridize specifically to the nucleic acids of the marker sequences in said sample, and detecting the presence or absence of the nucleic acid marker sequences in said sample. In one preferred embodiment, said probes are polynucleotides designed to identify the marker sequences either in Table 1 or Table 2. The detection method can be applied to any sample, e.g., cultured primary, secondary, or established cell lines, tissue biopsy, blood, urine, stool, cerebral spinal fluid, and other bodily fluids, for any purpose.

In one embodiment, the probes of the individual and/or combinations of the marker sequences are applied to the samples obtained from both the normal and colon cancer cell lines, and the presence of the marker sequences are detected with the methods describes herein. In another embodiment, the probes of the individual and/or combinations of the marker sequences are applied to the samples obtained from both the normal and colon cancer tissue, and the amount of the marker sequences are detected with the methods describes herein. For example, one determination assay can employ the over-expressed marker sequences in combination with an the over-expressed or an under-expressed marker sequences. Moreover, the determination assay can employ a panel of at least two, or at least three, or at least four or more marker sequences, selected from both the over-expressed and the under-expressed marker sequences.

The methods of detecting the presence of the marker sequences can be carried out by any effective process, e.g., by Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, in situ hybridization, etc.. When PCR based techniques are used, two or more probes are generally used. One probe can be specific for a defined sequence

which is characteristic of a selective polynucleotide, but the other probe can be specific for the selective polynucleotide, or specific for a more general sequence, e.g., a sequence such as polyA which is characteristic of mRNA, a sequence which is specific for a promoter, ribosome binding site, or other transcriptional features, a consensus sequence (e.g., representing a functional domain). For the former aspects, 5' and 3' probes (e.g., polyA, Kozak, etc.) are preferred which are capable of specifically hybridizing to the ends of transcripts. When PCR is utilized, the probes can also be referred to as "primers" in that they can prime a DNA polymerase reaction.

In addition to testing for the presence or absence of the marker polynucleotides, the present invention also relates to determining the amounts at which the marker sequences of the present invention are expressed in samples and determining the differential expression of such marker sequences in samples. Such methods can involve substantially the same steps as described above for presence/absence detection, e.g., contacting with probe, hybridizing, and detecting hybridized probe, but using more quantitative methods and/or comparisons to standards. The amount of hybridization between the probe and target can be determined by any suitable methods, e.g., PCR, RT-PCR, RACE PCR, Northern blot, polynucleotide microarrays, Rapid-Scan, etc., and includes both quantitative and qualitative measurements.

In one embodiment, reverse transcription PCR (RT-PCR) is performed using primers designed to specifically hybridize to a predetermined portion of the marker mRNA sequences isolated from a clinical sample. Generation of a PCR product by such a reaction is thus indicative of the presence of the marker sequences in the sample. The technique of designing primers for PCR amplification is well known in the art. Oligonucleotide primers and probes are about 5 to 100 nucleotides in length, ideally from about 17 to 40 nucleotides, although primers and probes of different length are of use. Primers for amplification are preferably about 17-25 nucleotides. Primers useful according to the invention are also designed to have a particular melting temperature (Tm) by the method of melting temperature estimation. Commercial programs, including Oligo™ (MBI, Cascade, CO), Primer Design and programs available on the internet, including Primer3 and Oligo Calculator can be used to calculate a Tm of a nucleic acid sequence useful according to the invention. Preferably, the Tm of an amplification primer useful according to the invention, as calculated for example by Oligo Calculator, is preferably between about 45 and 65° C and more preferably between about 50 and 60° C. Preferably, the Tm of a probe useful according to the invention is 7° C higher than the Tm of the corresponding

amplification primers. It is preferred that, following generation of cDNA by RT-PCR, the cDNA fragment is cloned into an appropriate sequencing vector, such as a PCRII vector (TA cloning kit; Invitrogen). The identity of each cloned fragment is then confirmed by sequencing in both directions. It is expected that the sequence obtained from sequencing would be the same as the known sequences of the marker sequences as described herein.

Alternatively, the presence of mRNA sequences encoding the marker sequences may be detected by Northern analysis. Sequence confirmed cDNAs, that is, cDNAs encoding the marker sequences are used to produce ^{32}P-labeled cDNA probes using techniques well known in the art (see, for example, Ausubel, *supra*). Labeled probes for Northern analysis may also be produced using commercially available kits (Prime-It Kit, Stratagene, La Jolla, CA). Northern analysis of total RNA obtained from a clinical sample may be performed using classically described techniques. For example, total RNA samples are denatured with formaldehyde / formamide and run for two hours in a 1% agarose, MOPS-acetate-EDTA gel. RNA is then transferred to nitrocellulose membrane by upward capillary action and fixed by UV cross-linkage. Membranes are pre-hybridized for at least 90 minutes and hybridized overnight at 42° C. Post hybridization washes are performed as known in the art (Ausubel, *supra*). The membrane is then exposed to x-ray film overnight with an intensifying screen at -80° C. Labeled membranes are then visualized after exposure to film. The signal produced on the x-ray film by the radiolabeled cDNA probes can then be quantified using any technique known in the art, such as scanning the film and quantifying the relative pixel intensity using a computer program such as NIH Image (National Institutes of Health, Bethesda, MD), wherein the detection of hybridization of a marker-specific probe to the clinical sample is indicative of the presence of the marker sequences and thus may be used to detect cancer such as colon cancer.

In an alternative embodiment, the presence and optionally the quantity of the marker sequences in a clinical sample may be determined using the Taqman™ (Perkin-Elmer, Foster City, CA) technique, which is performed with a transcript-specific antisense probe (i.e., a probe capable of specifically hybridizing to a marker sequence). This probe is specific for a marker sequence PCR product and is prepared with a quencher and fluorescent reporter probe complexed to the 5' end of the oligonucleotide. Different fluorescent markers can be attached to different reporters, allowing for measurement of two products in one reaction (e.g., measurement of the marker sequence). When Taq DNA polymerase is activated, it cleaves off the fluorescent

reporters by its 5'-to-3' nucleolytic activity. The reporters, now free of the quenchers, fluoresce. The color change is proportional to the amount of each specific product and is measured by fluorometer; therefore, the amount of each color can be measured and the RT-PCR product can be quantified. The PCR reactions can be performed in 96 well plates so that samples derived from many individuals can be processed and measured simultaneously. The Taqman™ system has the additional advantage of not requiring gel electrophoresis and allows for quantification when used with a standard curve.

The marker sequence-specific antibodies described above may be used to detect the presence of one or more marker sequences in a biological sample by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay),"sandwich" immunoassays, immunoprecipitation assays, precipitation reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e. g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X-100,1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCI, 0.01 M sodium phosphate at pH 7.2,1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e. g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e. g., 1-4 hours) at 4 C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4 C, washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. In the case of immunonprecipitation of a serum sample, however the above protocol is carried out absent the cell lysis step. The ability of the antibody to immunoprecipitate Reg1α or TIMP1 (or other colon cancer marker) antigen can be assessed by, e. g., western blot analysis. The parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e. g., preclearing the cell lysate with sepharose beads) are well known to those of skill in the art (Ausubel et al, *supra*).

The individual and/or the combinations of the marker sequences may be detected in a biological sample obtained from a patient using Western blot analysis. Briefly, Western blot analysis comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e. g., 8%-20% SDS-PAGE), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e. g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e. g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e. g., an antihuman antibody) conjugated to an enzymatic substrate (e. g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e. g., 32P or 125I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. Methods for the optimization of such an analysis are well known in the art (Ausubel, et al., *supra*).

Alternatively, the presence of one or more cancer specific marker sequences in a clinical sample may be detected by ELISA. ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate (or other suitable container) with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e. g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest, that is, the antibody which will bind to a cancer-specific marker) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. This method may be modified or optimized according techniques which are known to those of skill in the art.

The binding affinity of an antibody to an antigen and the off-rate of an antibody/antigen interaction can be determined by competitive binding assays. One example of such an assay is a radioimmunoassay comprising the incubation of labeled antigen (e. g., marker labeled with 3H or 125I) with an anti-marker antibody in the presence of increasing amounts of unlabeled antigen,

and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e. g., 3H or 125I) in the presence of increasing amounts of an unlabeled second antibody.

Preferably, the above detection assays may be carried out using antibodies to detect the protein product encoded by a nucleic acid having the sequence of SEQ ID NOs:1-93, or a sequence complementary thereto. In addition, the above detection assays may be conducted using one or more antibodies which specifically recognize and bind to at least one cancer-specific marker. Accordingly, in one embodiment, the assay would include contacting the proteins of the test cell with an antibody specific for the gene product of a nucleic acid represented by SEQ ID NO:1-93, or a sequence complementary thereto, and determining the approximate amount of immunocomplex formation by the antibody and the proteins of the test cell, wherein a detection of such an immunocomplex is indicative of the presence of the antigen, and thus, permits the detection of colon cancer.

Immunoassays, useful in the present invention include those described above, and can also include both homogeneous and heterogeneous procedures such as fluorescence polarization immunoassay (FPIA), fluorescence immunoassay (FIA), enzyme immunoassay (EIA), and nephelometric inhibition immunoassay (NIA).

In another embodiment, the level of the encoded polypeptide product, i.e., the polypeptide product encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO:1-93, or a sequence complementary thereto, in a biological fluid (e.g., blood or urine) of a patient may be determined as a way of monitoring the level of expression of the marker nucleic acid sequence in cells of that patient. Such a method would include the steps of obtaining a sample of a biological sample from the patient, contacting the sample (or proteins from the sample) with an antibody specific for an encoded marker polypeptide, and determining the amount of immune complex formation by the antibody, with the amount of immune complex formation being indicative of the level of the marker encoded polypeptide product in the sample. This determination is particularly instructive when compared to the amount of immune complex

formation by the same antibody in a control sample taken from a normal individual or in one or more samples previously or subsequently obtained from the same person.

In another embodiment, the method can be used to determine the amount of marker polypeptide present in a cell, which in turn can be correlated with progression of a hyperproliferative disorder, e.g., colon cancer. The level of the marker polypeptide can be used predictably to evaluate whether a sample of cells contains cells which are, or are predisposed towards becoming, transformed cells. Moreover, the subject method can be used to assess the phenotype of cells which are known to be transformed, the phenotyping results being useful in planning a particular therapeutic regimen. For instance, very high levels of the marker polypeptide in sample cells is a powerful diagnostic and prognostic marker for a cancer, such as colon cancer. The observation of marker polypeptide level can be utilized in decisions regarding, e.g., the use of more aggressive therapies.

X Diagnostic assays

The determination of a detectable increase or decrease in the expression level of one or more marker sequences in a cancer patient compared to a normal patient provides a means of diagnosing or monitoring the patient's disease status, and/or patient response or benefit to cancer therapy. The present invention provides methods for detecting cancer, or alternatively, determining whether a subject is at risk for developing cancer by detecting the disclosed cancer-specific markers (i.e., the nucleic acid sequences of one or more nucleic acid sequences encoding the cancer specific marker and/or polypeptide sequences of one or more cancer specific markers) for the disease or condition encoded thereby. Examples of cancer include but not limited to, adenocarcinoma, lymphoma, blastoma, melanoma, sarcoma, and leukemia. More particularly, examples of cancer also include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, Hodgkin's and non-Hodgkin's lymphoma, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer such as hepatic carcinoma and hepatoma, bladder cancer, breast cancer, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer such as renal cell carcinoma and Wilms' tumors, basal cell carcinoma, melanoma, prostate cancer, vulval cancer, thyroid cancer, testicular cancer, esophageal cancer, and various types of head and neck cancer. Preferably, the cancers include breast, colon, and lung cancer. In a more preferred embodiment, the cancer is colon cancer, and

the marker sequences are the ones comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-93.

In clinical applications, human tissue samples can be screened for the presence and/or absence of the biomarkers identified herein. Such samples may comprise tissue samples, whole cells, cell lysates, or isolated nucleic acids, including, for example, needle biopsy cores, surgical resection samples, lymph node tissue, plasma, or serum. For example, these methods include obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. In certain embodiments, nucleic acids extracted from these samples may be amplified using techniques well known in the art. The levels of selected markers detected would be compared with statistically valid groups of metastatic, non-metastatic malignant, benign, or normal colon tissue samples.

In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA or cDNA and/or protein level of the marker sequences. The method comprises using a nucleic acid probe to determine the expression level of the individual and/or the combinations of the marker sequences in a biological sample obtained from a patient. Specifically, the method comprises:

1. Providing a nucleic acid probe comprising a nucleotide sequence at least about 8 nucleotides in length, at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of the coding sequence which is complementary to a portion of the coding sequence of a nucleic acid sequence represented by SEQ ID NOs:1-93, or a sequence complementary thereto;

2. Obtaining a clinical sample from a patient potentially comprising one or more nucleic acid marker sequences;

3. Providing a second clinical sample from an individual known to not have colon cancer;

4. Contacting the nucleic acid probe under stringent conditions with RNA of each of said first and second clinical samples (e.g., in a Northern blot or in situ hybridization assay); and

5. Comparing (a) the amount of hybridization of the probe with RNA of the first clinical sample, with (b) the amount of hybridization of the probe with RNA of the second clinical sample; wherein a statistically difference (e.g., by at least 0.5 fold, at least 2 fold, at least 5 fold, at least 20 fold, or at least 50 fold) in the amount of hybridization with the RNA of the first clinical sample as compared to the amount of hybridization with the RNA of the second clinical sample is indicative of the presence of one or more marker sequences in the first clinical sample.

In one embodiment, the method comprises *in situ* hybridization with a probe derived from a given marker nucleic acid sequence, which nucleic acid sequence is represented by SEQ ID NO:1-93, or a sequence complementary thereto. The method comprises contacting the labeled hybridization probe with a sample of a given type of tissue potentially containing cancerous or pre-cancerous cells as well as normal cells, and determining whether the probe labels some cells of the given tissue type to a degree significantly different (e.g., by at least 0.5 fold, at least 2 fold, at least 5 fold, at least 20 fold, or at least 50 fold) than the degree to which it labels other cells of the same tissue type.

Determining by hybridization whether the target is differentially expressed (e.g., up-regulated or down-regulated) in the sample can also be accomplished by any effective means. For instance, the target's expression pattern in the sample can be compared to its pattern in a known control, such as in a normal tissue, or it can be compared to another target in the same sample. When a second sample is utilized for the comparison, it can be a sample of normal tissue that is known not to contain diseased cells. The comparison can be performed on samples which contain the same amount of RNA (such as polyadenylated RNA or total RNA), or, on RNA extracted from the same amounts of starting tissue. Such a second sample can also be referred to as a control or standard. Hybridization can also be compared to a second target in the same tissue sample. Experiments can be performed that determine a ratio between the target nucleic acid and a second nucleic acid (a standard or control), e.g., in a normal tissue. When the ratio between the target and control are substantially the same in a normal sample, the sample is

determined or diagnosed not to contain cancer cells. However, if the ratio is at least 2 fold different between the normal and sample tissues, the sample is determined to contain cancer cells. The approaches can be combined, and one or more second samples, or second targets can be used. Any second target nucleic acid can be used as a comparison, including "housekeeping" genes, such as beta-actin, alcohol dehydrogenase, or any other gene whose expression does not vary depending upon the disease status of the cell.

Alternatively, the above diagnostic assays may be carried out using antibodies to detect the polypeptides encoded by the nucleic acid marker sequences, which nucleic acid sequences are represented by SEQ ID NOs:1-93, or a sequence complementary thereto. Preferably, the polypeptides have the sequence of one or more of SEQ ID NOs: 94-186. Accordingly, in one embodiment, the assay would include contacting the polypeptides of the test cell or tissue with one or more antibodies specific for the polypeptides represented by SEQ ID NOs: 94-186, and determining the approximate amount of immunocomplex formation by the antibodies and polypeptides of the test cell or tissue, wherein a statistically significant difference in the amount of the immunocomplex formed with the polypeptides of a test or tissue as compared to a normal cell or tissue is an indication that the test cell is cancerous or pre-cancerous. The term "significant difference" refers to a cell phenotype wherein the cell possesses a changed cellular amount of the marker polypeptide relative to a normal cell of similar tissue origin. For example, a cell may have either more or less than about 50%, 25%, 10%, or 5% of the marker polypeptide that a normal control cell. In particular, the assay evaluates the level of marker polypeptide in the test cells, and, preferably, compares the measured level with marker polypeptide detected in at least one control cell, e.g., a normal cell and/or a transformed cell of known phenotype.

In one embodiment, the assay is performed as a dot blot assay. The dot blot assay finds particular application where tissue samples are employed as it allows determination of the average amount of the marker polypeptide associated with a single cell by correlating the amount of marker polypeptide in a cell-free extract produced from a predetermined number of cells.

It is well established in the cancer literature that tumor cells of the same type (e.g., breast and/or colon tumor cells) may not show uniformly increased expression of individual oncogenes or uniformly decreased expression of individual tumor suppressor genes. There may also be varying levels of expression of a given marker sequence even between cells of a given type of cancer, further emphasizing the need for reliance on a battery of tests rather than a single test.

Accordingly, in one aspect, the invention provides for a battery of tests utilizing a number of probes of the invention, in order to improve the reliability and/or accuracy of the diagnostic test.

XI Arrays

In one aspect, the present invention also provides a method wherein nucleic acid probes are immobilized on a DNA chip in an organized array. Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. These nucleic acid probes comprise a nucleotide sequence at least about 8 nucleotides in length, preferably at least about 12 preferably at least about 15 nucleotides, more preferably at least about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of a marker nucleic acid sequence represented by SEQ ID NO:1-93 and is differentially expressed in cancer cells, such as colon cancer cells. In some embodiments, the microarrays comprise at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15, or more nucleic acids that are complimentary to at least a portion of the coding sequences of the marker sequences comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-93. The present invention provides significant advantages over the available tests for various cancers, such as colon cancer, because it increases the reliability of the test by providing an array of nucleic acid markers on a single chip.

The method includes obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumor cells to about 80% of the total cell population. The DNA or RNA is then extracted, amplified, and analyzed with a DNA chip to determine the presence of absence of the marker nucleic acid sequences.

In one embodiment, the nucleic acid probes are spotted onto a substrate in a two-dimensional matrix or array. Samples of nucleic acids can be labeled and then hybridized to the probes. Double-stranded nucleic acids, comprising the labeled sample nucleic acids bound to probe nucleic acids, can be detected once the unbound portion of the sample is washed away.

The probe nucleic acids can be spotted on substrates including glass, nitrocellulose, etc. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. The sample nucleic acids can be labeled using radioactive labels, fluorophores, chromophores, etc.

Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/292 12; PCT No. WO 97127317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.

In another aspect, the present invention also provides a protein microarrays. Protein microarray technology, which is also known by other names including: protein chip technology and solid-phase protein array technology, is well known to those of ordinary skill in the art and is based on, but not limited to, obtaining an array of identified peptides or proteins on a fixed substrate, binding target molecules or biological constituents to the peptides, and evaluating such binding. See, e.g., G. MacBeath and S. L. Schreiber, "Printing Proteins as Microarrays for High-Throughput Function Determination," *Science* 289(5485):1760-1763, 2000. In general, the protein microarrays include antigen-binding ligands such as antibodies or fragments thereof, fixed to a solid substrate, wherein the ligands specifically bind to the polypeptides encoded by the marker sequences of the present invention. In one embodiment, the protein microarrays further include at least one control polypeptide molecule. In some embodiments, the microarray comprises antibodies or antigen-binding fragments thereof, that bind specifically to least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 different polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-93. In certain embodiment, the antibodies are monoclonal or polyclonal antibodies. In another certain embodiment, the antibodies are chimeric, human, or humanized antibodies. In yet another certain embodiment, the antibodies are single chain antibodies, and the antigen-binding fragments are F(ab')2, Fab, Fd, or Fv fragments.

The solid microarray substrate may include, but not limited to, glass, silica, aluminosilicates, borosilicates, metal oxides such as alumina and nickel oxide, various clays, nitrocellulose, or nylon. The microarray substrates may be coated with a compound to enhance synthesis of a probe (peptide or nucleic acid) on the substrate. Coupling agents or groups on the substrate can be used to covalently link the first nucleotide or amino acid to the substrate. A variety of coupling agents or groups are known to those of skill in the art. Peptide or nucleic acid probes thus can be synthesized directly on the substrate in a predetermined grid.

Alternatively, peptide or nucleic acid probes can be spotted on the substrate, and in such cases the substrate may be coated with a compound to enhance binding of the probe to the substrate. In these embodiments, presynthesized probes are applied to the substrate in a precise, predetermined volume and grid pattern, preferably utilizing a computer- controlled robot to apply probe to the substrate in a contact-printing manner or in a non-contact manner such as ink jet or piezo-electric delivery. Probes may be covalently linked to the substrate.

XII Prognosis, staging, and monitoring of cancer

In one aspect, the present invention provides methods for determining cancer prognosis and stage based on examining the expression levels of the nucleic acid marker sequences and polypeptides using the methods described in the present invention. If cancer is detected in a subject using a technique other than by determining the expression levels of the marker sequences, then the differential expression level of the marker sequences can be used to determine the prognosis and stage for the subject. As used herein, prognosis refers to the prediction of the probable course and outcome of a disease.

In general, methods used for prognosis or stage of cancer involve comparison of the amount of the marker sequences in a sample of interest with that of a control to detect relative differences in the expression of the marker sequences, wherein the difference can be measured qualitatively and/or quantitatively. For example, the expression levels of one or more marker RNAs or polypeptides can be compared with the expression levels of the same marker RNAs or polypeptides in cancer free or normal samples. Alternatively, the expression levels of one or more marker RNAs or polypeptides can also be compared with the expression levels of the same marker RNAs or polypeptides observed in cancers that are known not to progress. In addition, the expression levels of one or more marker RNAs or polylpeptides can also be compared with the expression levels of the same marker RNAs or polypeptides observed in cancers that are known to progress and/or metastasize.

Also, as used herein, cancer stage refers to the sequence of the events, in which cancer develops and causes symptoms. In addition, staging is a process used to describe how advanced the cancerous state is in patient. Staging systems vary with the types of cancer, but generally involve the following "TNM" system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to

more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage. Methods of the present invention are useful in assaying the staging of cancer. The staging of cancer can be accomplished by determining the expression levels of one or more marker RNAs or polypeptides to a reference expression levels of the same marker RNAs or polypeptides. The reference expression levels of the marker RNAs or polypeptides can be that from cancer free or healthy or cancer samples, wherein the cancer can be at different stages in development.

The present invention further provides methods of monitoring cancer progression or recurrence by measuring the expression levels of the marker RNAs or polypeptides over the time. In one embodiment, the methods comprise:

(1). detecting in a biological sample of the subject at a first point in time, the expression of one or more nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93;

(2). repeating step (a) at a subsequent point in time; and

(3). comparing the expression level detected in steps (a) and (b), wherein a change in the expression level is indicative of progression of cancer or a pre-malignant condition thereof in the subject.

In another embodiment, the methods comprise:

(1). detecting in a biological sample of the subject at a first point in time, the expression of one or more polypeptides comprising one or more polypeptide sequences selected from the group consisting of SEQ ID NOs: 94-186;

(2). repeating step (a) at a subsequent point in time; and

(3). comparing the expression level detected in steps (a) and (b), wherein a change in the expression level is indicative of progression of cancer or a pre-malignant condition thereof in the subject.

For example, elevated expression levels of one or more over-expressed marker RNAs or polypeptides, or reduced expression levels of one or more under-expressed marker RNAs or polypeptides in a subsequent point in time relative to an earlier point in time, indicate that the cancer is progressing to a more severe stage. On the other hand, reduced expression levels of one or more over-expressed marker RNAs or polypeptides, or elevated expression levels of one or more under-expressed marker RNAs or polypeptides in a subsequent point in time relative to an earlier point in time, indicate that the cancer is not progressing or is progressing slowly.

The methods used in prognosis, staging, and monitoring cancer can be applied to various types of cancer. Examples of cancer include but not limited to, adenocarcinoma, lymphoma, blastoma, melanoma, sarcoma, and leukemia. More particularly, examples of cancer also include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, Hodgkin's and non-Hodgkin's lymphoma, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer such as hepatic carcinoma and hepatoma, bladder cancer, breast cancer, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer such as renal cell carcinoma and Wilms' tumors, basal cell carcinoma, melanoma, prostate cancer, vulval cancer, thyroid cancer, testicular cancer, esophageal cancer, and various types of head and neck cancer. Preferably, the cancers include breast, colon, and lung cancer. More preferably, the cancer is colon cancer, and the marker sequences are the ones comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-93.

XIII Efficacy of therapy and therapeutic compositions

In one aspect, the present invention also provides methods that permit the assessment and/or monitoring of patients who will be likely to benefit from both traditional and non-traditional treatments and therapies for cancers, particularly colon cancer. The present invention thus embraces testing, screening and monitoring of patients undergoing anti-cancer treatments and therapies, used alone, in combination with each other, and/or in combination with anti-cancer drugs, anti-neoplastic agents, chemotherapeutics and/or radiation and/or surgery, to treat cancer patients.

An advantage of the present invention is the ability to monitor, or screen over time, those patients who can benefit from one, or several, of the available cancer therapies, and preferably, to monitor patients receiving a particular type of therapy, or a combination therapy, over time to determine how the patient is faring from the treatment(s), if a change, alteration, or cessation of treatment is warranted; if the patient's disease has been reduced, ameliorated, or lessened; or if the patient's disease state or stage has progressed, or become metastatic or invasive. The cancer treatments embraced herein also include surgeries to remove or reduce in size a tumor, or tumor burden, in a patient. Accordingly, the methods of the invention are useful to monitor patient progress and disease status post-surgery.

The identification of the correct patients for a cancer therapy according to this invention can provide an increase in the efficacy of the treatment and can avoid subjecting a patient to unwanted and life-threatening side effects of the therapy. By the same token, the ability to monitor a patient undergoing a course of therapy using the methods of the present invention can determine whether a patient is adequately responding to therapy over time, to determine if dosage or amount or mode of delivery should be altered or adjusted, and to ascertain if a patient is improving during therapy, or is regressing or is entering a more severe or advanced stage of disease, including invasion or metastasis, as discussed further herein.

A method of monitoring according to this invention reflects the serial, or sequential, testing or analysis of a cancer patient by testing or analyzing the patient's body fluid sample over a period of time, such as during the course of treatment or therapy, or during the course of the patient's disease. For instance, in serial testing, the same patient provides a body fluid sample, e.g., serum or plasma, or has sample taken, for the purpose of observing, checking, or examining the expression levels of one or more of the markers (RNA or polypeptide) of the invention in the patient by measuring the levels of one or more of these markers during the course of treatment, and/or during the course of the disease, according to the methods of the invention.

Similarly, a patient can be screened over time to assess the levels of one or more of the markers in a biological sample for the purposes of determining the status of his or her disease and/or the efficacy, reaction, and response to cancer or neoplastic disease treatments or therapies that he or she is undergoing. It will be appreciated that one or more pretreatment sample(s) is/are optimally taken from a patient prior to a course of treatment or therapy, or at the start of the treatment or therapy, to assist in the analysis and evaluation of patient progress and/or response

at one or more later points in time during the period that the patient is receiving treatment and undergoing clinical and medical evaluation.

In monitoring a patient's levels of one or more of the markers of the invention over a period of time, which may be days, weeks, months, and in some cases, years, or various intervals thereof, the patient's body fluid sample, e.g., a serum or plasma sample, is collected at intervals, as determined by the practitioner, such as a physician or clinician, to determine the levels of one or more of the markers in the cancer patient compared to the respective levels of one or more of these analytes in normal individuals over the course or treatment or disease. For example, patient samples can be taken and monitored every month, every two months, or combinations of one, two, or three month intervals according to the invention. Quarterly, or more frequent monitoring of patient samples, is advisable.

The levels of the one or more markers found in the patient are compared with the respective levels of the one or more of these markers in normal individuals, and with the patient's own marker levels, for example, obtained from prior testing periods, to determine treatment or disease progress or outcome. Accordingly, use of the patient's own marker levels monitored over time can provide, for comparison purposes, the patient's own values as an internal personal control for long-term monitoring of marker levels, and thus cancer presence and/or progression. As described herein, following a course of treatment or disease, the determination of an increase or a decrease in one or more of the marker levels in the cancer patient over time compared to the respective levels of one or more of these markers in normal individuals reflects the ability to determine the severity or stage of a patient's cancer, or the progress, or lack thereof, in the course or outcome of a patient's cancer therapy or treatment.

Increases or decreases in the levels of the markers in cancer patients are determined by comparing the values obtained from analyzing cancer patient samples compared to the normal control range expression levels. A biomarker is said to be over-expressed if expression of the marker is at least 2 fold greater in the cancer patient relative to a normal control, and a biomarker is said to be under expressed if the expression of the marker is at least 2 fold greater in the normal control relative to in the cancer patient.

In monitoring a patient over time, a reduction in the levels of one or more of a patient's marker levels from increased levels (i.e., at least 2 fold over-expressed) compared to normal

range values to levels at or near to the levels of the analytes found in normal individuals is indicative of treatment progress or efficacy, and/or disease improvement, remission, tumor reduction or elimination, and the like. Likewise, in all of the methods described in the embodiments of this invention, a determination of a reduction of one or more of a patient's marker levels from an elevated level (i.e., at least 2 fold over-expressed) to, or approximately to, the respective levels of one or more of these analytes found in normal individuals provides a further aspect of the methods of the invention, in which a patient's improvement, recovery or remission, and/or treatment progress or efficacy, is able to be ascertained over time following performance of the method.

Another embodiment of the present invention encompasses a method of monitoring a cancer patient's course of disease, or the efficacy of a cancer patient's treatment or therapy. The patient's treatment or therapy can involve traditional therapies, such as hormone therapy, chemotherapeutic drug therapy, radiation, or novel therapies, or a combination of any of the foregoing. The method involves measuring levels of one or more markers in a body fluid sample of the cancer patient and determining if the levels of one or more of the markers in the patient's sample are changed by at least 2 fold compared to the respective levels of one or more of these analytes in normal controls during the course of disease or cancer treatment. In accordance with the method, a change in the levels of the marker in the cancer patient compared to the respective levels of the marker in normal controls is indicative of a change in stage, grade, severity or progression of the patient's cancer and/or a lack of efficacy or benefit of the cancer treatment or therapy provided to the patient during a course of treatment, e.g., poor treatment or clinical outcome.

As will be understood by the skilled practitioner in the art, the monitoring method according to this invention is preferably, performed in a serial or sequential fashion, using samples taken from a patient during the course of disease, or a disease treatment regimen, (e.g., after a number of days, weeks, months, or occasionally, years, or various multiples of these intervals) to allow a determination of disease progression or outcome, and/or treatment efficacy or outcome. If the sample is amenable to freezing or cold storage, the samples may be taken from a patient (or normal individual) and stored for a period of time prior to analysis.

In another of its embodiments, the present invention encompasses the determination of the amounts or levels of one or more additional cancer markers in conjunction with the

determination of the levels of one or more of the markers of the invention in a sample to be analyzed.

The present invention also includes a method of assessing the efficacy of a test composition for inhibiting cancers, such as colon cancer. As described above, differential expression levels of the marker sequences of the invention correlate with the cancerous state of cancer cells, particularly colon cancer cells. It is recognized that changes in the expression levels of the marker sequences of the present invention result from the cancerous state of cells. Thus, composition which inhibit cancer in a patient will cause the expression levels of the marker sequences to change to a level near the normal level of expression for the marker sequences. The method thus comprises comparing expression levels of one or more marker sequences in a first biological sample maintained in the presence of a test composition with those of the same marker sequences in a second biological sample maintained in the absence of the test composition. A significant difference in the expression levels of one or more marker sequences is an indication that the test composition inhibits the cancer. In a preferred embodiment, the cancer is colon cancer, and the marker sequences are the ones listed in Tables 1 and 2. In another embodiment, the cell samples may be aliquots of a single sample obtained from either a healthy subject or a patient with cancerous conditions.

XIV Modulators of the marker sequences

It is recognized that changes in the expression levels of the marker sequences likely induce, maintain, and promote the cancerous state of cells. Thus, another aspect of the present invention is directed to the modulators of the marker sequences capable of modulating the differentiation and proliferation of cells. In this regard, the present invention provides assays for determining compounds that modulate the expression of the marker sequences. The compounds can be used to modulate the biological activity of the polypeptides encoded by the marker sequences or the marker sequences themselves. Compounds can also be useful in a variety of different environments, including as medicinal agents to treat or prevent disorders associated with cancer.

Methods of identifying compounds generally comprise steps in which a compound is placed in contact with a marker sequence, its transcription product, its translation product, or other target, and determination of whether the compound modulates the marker sequence. For

modulating the expression of a marker sequence, a method can comprise, in any effective order, one or more of the following steps, e.g. , contacting the marker sequence (e.g., in a cell population) with a test compound under conditions effective for said test compound to modulate the expression of the marker sequence, and determining whether said test agent modulates said sequence. A compound can modulate expression of a sequence at any level, including transcription (e.g., by modulating the promoter), translation, and/or perdurance of the nucleic acid (e.g., degradation, stability, etc.) in the cell.

For modulating the biological activity of polypeptides, a method can comprise, in any effective order, one or more of the following steps, e.g. , contacting a polypeptide (e.g., in a cell, lysate, or isolated) with a test compound under conditions effective for said test agent to modulate the biological activity of said polypeptide, and determining whether said test compound modulates said biological activity.

Contacting the polynucleotide or polypeptide with the test compound can be accomplished by any suitable method and/or means that places the compound in a position to functionally control expression or biological activity of the gene or its product in the sample. Functional control indicates that the compound can exert its physiological effect through whatever mechanism it works. The choice of the method and/or means can depend upon the nature of the compound and the condition and type of environment in which the gene or its product is presented, e.g., lysate, isolated, or in a cell population (such as, in vivo, in vitro, organ explants, etc.). For example, if the cell population is an *in vitro* cell culture, the compound can be contacted with the cells by adding it directly into the culture medium. If the compound cannot dissolve readily in an aqueous medium, it can be incorporated into liposomes, or another lipophilic carrier, and then administered to the cell culture. Contact can also be facilitated by incorporation of compound with carriers and delivery molecules and complexes, by injection, by infusion, etc.

After the agent has been administered in such a way that it can gain access to the gene or gene product (including DNA, mRNA, and polypeptides), it can be determined whether the test compound modulates its expression or biological activity. Modulation can be of any type, quality, or quantity, e.g., increase, facilitate, enhance, up-regulate, stimulate, activate, amplify, augment, induce, decrease, down-regulate, diminish, lessen, reduce, etc. The modulatory quantity can also encompass any value, e.g., 1%, 5%, 10%, 50%, 75%, 1-fold, 2-fold, 5-fold, 10-

fold, 100-fold, etc. To modulate gene expression means, e.g., that the test compound has-an effect on its expression, e.g., to effect the amount of transcription, to effect RNA splicing, to effect translation of the RNA into polypeptide, to effect RNA or polypeptide stability, to effect polyadenylation or other processing of the RNA, to effect post-transcriptional or post-translational processing, etc. To modulate biological activity means, e.g. , that a functional activity of the polypeptide is changed in comparison to its normal activity in the absence of the compound. This effect includes, increase, decrease, block, inhibit, enhance, etc.

A test compound can be of any molecular composition, e.g., chemical compounds, biomolecules, such as polypeptides, lipids, nucleic acids (e.g. , antisense to a polynucleotide) carbohydrates, antibodies, ribozymes, double-stranded RNA, aptamers, etc. For example, if a polypeptide to be modulated is a cell-surface molecule, a test compound can be an antibody that specifically recognizes it and, e.g., causes the polypeptide to be internalized, leading to its down regulation on the surface of the cell. Such effect does not have to be permanent, but can require the presence of the antibody to continue the down-regulatory effect. Antibodies can also be used to modulate the biological activity of a polypeptide in a lysate or other cell-free form.

XV Drug screening

In one aspect, the present invention is also directed to methods for screening drugs that inhibit cancer, particularly colon cancer. Drug screening is performed by adding a test compound to a sample of cells, and monitoring the effect. A parallel sample which does not receive the test compound is also monitored as a control. The treated and untreated cells are then compared by any suitable phenotypic criteria, including but not limited to microscopic analysis, viability testing, ability to replicate, histological examination, the level of a particular RNA or polypeptide associated with the cells, the level of enzymatic activity expressed by the cells or cell lysates, and the ability of the cells to interact with other cells or compounds. Differences between treated and untreated cells indicates effects attributable to the test compound.

Desirable effects of a test compound include an effect on any phenotype that was conferred by the cancer-associated marker nucleic acid sequence. Examples include a test compound that limits the overabundance of mRNA, limits production of the encoded protein, or limits the functional effect of the protein. The effect of the test compound would be apparent when comparing results between treated and untreated cells. For example, candidate compounds

may be identified that down-regulate expression of one specific gene. In one embodiment, candidate compounds may be identified that up-regulate expression of one specific gene. Generally a plurality of assay mixtures are run in parallel with different compound concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cancerous cell (preferably a cancerous colon cell) with a candidate agent, and assessing the effect upon biological activity of a differentially expressed gene product. The effect upon a biological activity can be detected by, for example, detection of expression of a gene product of a differentially expressed gene (e.g., a decrease in mRNA or polypeptide levels, would in turn cause a decrease in biological activity of the gene product). Alternatively or in addition, the effect of the candidate agent can be assessed by examining the effect of the candidate agent in a functional assay. For example, where the differentially expressed gene product is an enzyme, then the effect upon biological activity can be assessed by detecting a level of enzymatic activity associated with the differentially expressed gene product. The functional assay will be selected according to the differentially expressed gene product.

The screening methods may include both *in vitro* and *in vivo* screening of a cell or tissue. One particular embodiment of *in vitro* method comprises a method of determining the efficacy of a test compound for inhibiting cancer in a subject, the method comprising comparing a) the expression level of one or more nucleic acid sequences in a first biological sample from the subject wherein the sample has been exposed to the test compound, with b) the expression level of said nucleic acid sequences in a second biological sample from the subject wherein the sample has not been exposed to the test compound, said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93, wherein a change of at least two fold in the expression level of said nucleic acid sequences is an indication that the test compound is efficacious for inhibiting cancer in the subject.

In another embodiment, the *in vivo* methods of screening for compounds that alter the expression of the marker sequences comprise exposing a subject, preferably a mammal having cancer cells in which the marker sequences (either at mRNA or polypeptide level) are detectable,

to a compound, and determining the level of the marker sequences. Where the differentially expressed gene is increased in expression in a cancerous cell, the compound of interest is those that decrease activity of the differentially expressed gene product, and where the differentially expressed gene is decreased in expression in a cancerous cell, the compound of interest is those that increase activity of the differentially expressed gene product.

Assays for determining the differentially expressed marker sequences (described *supra*) can be readily adapted in the screening assay embodiments of the present invention. Exemplary assays useful in screening candidate compounds include, but are not limited to, hybridization-based assays (e.g. use of nucleic acid probes or primers to assess expression levels), antibody-based assays (e.g. to assess levels of polypeptide gene products), binding assays (e.g. to detect interaction of a candidate agent with a differentially expressed polypeptide, which assays may be competitive assays where a natural or synthetic ligand for the polypeptide is available), and the like. Additional exemplary assays include, but are not necessarily limited to, cell proliferation assays, antisense knockout assays, assays to detect inhibition of cell cycle, assays of induction of cell death/apoptosis, and the like.

In one embodiment, the candidate compound is naturally occurring or modified proteins. In another embodiment, candidate compounds are peptides. The peptides may be digests of naturally occurring proteins, or the one made by chemical synthesis. Furthermore, the synthetic process can be designed to generate randomized proteins, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate proteinaceous drugs.

In another embodiment, the candidate compounds are nucleic acids, either naturally occurring or modified. In a preferred embodiment, the nucleic acid compounds are antisense nucleic acids. Drug candidates that are antisense molecules include antisense or sense oligonucleotides comprising a single-strand nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA or DNA sequences for lung cancer molecules identified by the methods of the invention.

In yet another preferred embodiment, drug candidates are antibodies. An antibody used in methods for screening for a candidate drug may either bind a full length protein or a fragment thereof. In a preferred embodiment, the antibody binds a unique epitope on a target protein and

shows little or no cross-reactivity. The term "antibody" is understood to include antibody fragments, as are known in the art, including Fab, Fab_2, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies known in the art. Antibodies as used herein as drug candidates include both polyclonal and monoclonal antibodies. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an antigenic agent and, if desired, an adjuvant. It may be useful to conjugate the antigenic agent to a protein known to be immunogenic in the mammal being immunized.

In yet another embodiment, the candidate compounds are chemical compounds. In a preferred embodiment, the candidate compounds are small organic compounds having a molecular weight of more than 100 and less than about 2500 daltons. Candidate compounds may also include functional groups necessary for structural interaction with proteins or nucleic acids.

XVI Kits

The present invention also provides for kits that contain the necessary reagents for detection of the expression levels (either at RNA or polypeptide level) of the individual and/or combinations of marker sequences in a biological sample. Reagents can include marker sequence-specific probes/primers and antibodies as described *supra*. Kits can also contain a control/reference value or a set of control/reference values indicating normal and various clinical progression stages of cancer. In a preferred embodiment, the control/reference value or a set of control/reference values are indicative of normal and various clinical progression stages of colon cancer. Moreover, kits can contain positive controls, and/or negative controls for comparison with the test sample. A negative control can contain a sample that does not have any marker RNA or polypeptide. A positive control can contain a sample that have various known levels of marker RNA or polypeptide. Kits can also contain any combinations of the marker sequence-specific probes/primers and/or antibodies. Kits can also contain instructions for conducting the assays and for interpreting the results. For antibody-based kit, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable label. For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a

polypeptide corresponding to a marker sequence of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

Such kits can be used to determine whether a subject is suffering from or at an increased risk of developing cancer, particularly colon cancer. Furthermore, such kits can be used to determine the prognosis, stage, or monitoring the progression of cancer, particularly colon cancer. Furthermore, such kits can be used for drug screening or for selection of treatment for cancer, particularly colon cancer.

Examples

The examples below are non-limiting and are merely representative of various aspects and features of the present invention.

Example 1. Identification of differentially expressed marker sequences

Twenty well characterized, microdissected samples of colorectal cancer tissue were obtained from consenting patients. A second set of twenty, microdissected samples of normal adjacent colon tissue were also obtained. Total RNA was extracted from these samples using RNeasy kits (QIAGEN, Valencia, CA) according to the manufacturer's instructions. Expression profiling was performed using the GeneChip expression arrays from Affymetrix (Santa Clara, CA). Reverse transcription, second-strand synthesis, and probe generation was accomplished by standard Affymetrix protocols. The Human Genome U133A GeneChip, which contains more than 15,000 substantiated human genes, was hybridized, washed, and scanned according to Affymetrix protocols. Changes in cellular mRNA levels in the cancerous tissues were compared with mRNA levels in the normal colon tissues. GeneSpring v4.2 (Silicon Genetics, Redwood City, CA) was used to normalize and scale results and compare gene expression levels in the cancer tissue relative to that in the normal tissue.

Applying a set of filters to the normalized data identified the up- and down-regulated genes. First, a non-parametric test defined the genes that were statistically associated with either the cancer or the normal samples. Next, a pair of filters was used to remove the genes with low signals and to set a high threshold for a minimum expression levels. The final filter required a three-fold average expression difference between the two conditions (cancer and normal).

This analysis resulted in 47 genes that were up-regulated in the colorectal cancer tissue relative to the normal adjacent colon tissue. These genes are identified in Table 1. Likewise, 46 down-regulated genes were identified in the colorectal cancer tissue relative to the normal adjacent colon tissue. These genes are listed in Table 2.

Other embodiments

Other embodiments will be evident to those of skill in the art. It should be understood that the foregoing detailed description is provided for clarity only and is merely exemplary. The spirit and scope of the present invention are not limited to the above examples, but are encompassed by the following claims.

Claims

1. A method of detecting differential expression of one or more nucleic acid sequences in a biological sample, comprising:

(a) obtaining the sample from a subject; and

(b) detecting a change in the expression level of one or more nucleic acid sequences relative to a control expression level of the nucleic acid sequences, said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93.

2. The method of claim 1, wherein said step of detecting comprises:

(a) contacting said sample with a polynucleotide probe comprising at least 12 consecutive nucleotides of a nucleic acid sequence, said probe is capable of hybridizing under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-93;

(b) detecting the hybridization of said polynucleotide probe to said nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-93, wherein the signal intensity of hybridization is indicative of the expression level of a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-93.

3. The method of claim 2, wherein said probe comprises a detectable label.

4. The method of claim 1, wherein said change in the expression level is either an increase or an decrease in expression level.

5. The method of claim 1, wherein said change in the expression level is at least two fold.

6. A method of detecting cancer or a pre-malignant condition thereof in a subject comprising comparing a) the expression level of one or more nucleic acid sequences in a biological sample from the subject with b) a control expression level of said nucleic acid sequences, said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93, wherein a change of at least two-fold in the

expression level of said nucleic acid sequences is indicative of cancer or pre-malignant condition.

7. The method of claim 6, wherein said change in the expression level is either an increase or decrease in the expression level.

8. A method of monitoring the onset, progression, or regression of cancer or a pre-malignant condition thereof in a subject, the method comprising:

(a) detecting in a biological sample of the subject at a first point in time, the expression of one or more nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93;

(b) repeating step (a) at a subsequent point in time; and

(c) comparing the expression level detected in steps (a) and (b), wherein a change in the expression level is indicative of progression of cancer or a pre-malignant condition thereof in the subject.

9. The method of claim 8, wherein the change in the expression level is either an increase or decrease.

10. A method of determining prognosis for cancer or a pre-malignant condition thereof in a subject, comprising:

(a) detecting in a biological sample of the subject, the expression level of one or more nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93;

(b) comparing the expression level detected in steps (a) with a reference expression level of said nucleic acid sequences; and

(c) evaluating the prognosis of the subject based on the comparison in step (b).

11. The method of claim 10, wherein the reference expression level is the expression level of said nucleic acid sequences in cancer free or normal sample.

12. The method of claim 10, wherein the reference expression level is the expression level of said nucleic acid sequences cancer samples that are known not to progress to aggressive form.

13. A method of determining the efficacy of a test compound for inhibiting cancer in a subject, the method comprising comparing a) the expression level of one or more nucleic acid sequences in a first biological sample from the subject wherein the sample has been exposed to the test compound, with b) the expression level of said nucleic acid sequences in a second biological sample from the subject wherein the sample has not been exposed to the test compound, said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93, wherein a change of at least two fold in the expression level of said nucleic acid sequences is an indication that the test compound is efficacious for inhibiting cancer in the subject.

14. The method of claim 13, wherein the change in the expression level is either an increase or decrease.

15. A method of determining the efficacy of a therapy for inhibiting cancer in a subject, the method comprising comparing a) the expression level of one or more nucleic acid sequences in a first biological sample from the subject prior to providing at least a portion of the therapy to the subject, with b) the expression level of said nucleic acid sequences in a second biological sample from the subject following the provision of the portion of the therapy, said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93, wherein a change of at least two fold in the expression level of said nucleic acid sequences is an indication that the therapy is efficacious for inhibiting cancer in the subject.

16. The method of claim 15, wherein the change in the expression level is either an increase or decrease.

17. A method of selecting a composition for inhibiting cancer in a subject, the method comprising:

(a) obtaining a first biological sample comprising cancer cells from the subject;

(b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;

(c) comparing the expression level of one or more nucleic acid sequences in each of the aliquots from (b) with the expression level in the sample produced by (a), said nucleic acid sequences comprising one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 1-93; and

(d) selecting one of the test compositions which induces a change of at least two fold in the expression level of said nucleic acid sequences in one aliquot containing the test composition.

18. The method of claim 17, wherein the change in the expression level is either an increase or decrease.

19. A method of inhibiting cancer in a subject, the method comprising:

(a) obtaining a first biological sample comprising cells from the subject;

(b) administering to the subject one or more test compositions;

(c) obtaining a second biological sample comprising cells from the subject of (b); and

(d) comparing the expression level of one or more nucleic acid sequences in the first sample with the expression level of said nucleic acid sequences in the second sample, wherein a change of at least two fold in the expression level is indicative of inhibition of cancer by said test compositions.

20. A polypeptide comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186.

21. An antibody that specifically binds to a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186.

22. The antibody of claim 21, wherein said antibody is polyclonal antibody.

23. The antibody of claim 21, wherein said antibody is monoclonal antibody.

24. A method of detecting in a biological sample the presence of a polypeptide comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, said method comprising:

(a) obtaining said biological sample from a subject;

(b) contacting said sample with a polypeptide ligand which is capable of binding to one or more of SEQ ID NOs: 94-186; and

(c) detecting the binding of said polypeptide ligand to said polypeptide, wherein detecting of binding is indicative of the presence of said polypeptide sequence comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186 in said biological sample.

25. The method of claim 24, wherein the polypeptide ligand is an antibody.

26. The method of claim 24, wherein the polypeptide ligand comprises a detectable label.

27. The method of claim 25, wherein the antibody is a monoclonal antibody.

28. A method of detecting cancer or a pre-malignant condition thereof in a subject comprising:

(a) obtaining a biological sample from a subject;

(b) contacting the sample with one or more polypeptide ligands that bind specifically to one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186;

(c) determining specific binding; and

(d) comparing the specific binding between the polypeptide ligands and the polypeptides in the sample with the specific binding between the polypeptide ligands and the polypeptides in a cancer-free sample, wherein a significant change in the specific binding is diagnostic for cancer in the subject.

29. A method of monitoring the onset, progression, or regression of cancer in a subject, comprising:

(a) contacting at a first point in time a first biological sample with one or more polypeptide ligands that specifically bind to one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, determining specific binding between the polypeptide ligands and the polypeptides;

(b) contacting at a subsequent point in time a second biological sample with said polypeptide ligands that specifically bind to one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, determining specific binding between the polypeptide ligands and the polypeptides; and

(c) comparing the specific binding in the first biological sample to the specific binding in the second biological sample, wherein a significant change in the specific binding is an indication of the onset, progression, or regression of cancer.

30. A method of determining prognosis for cancer or a pre-malignant condition thereof in a subject, comprising:

(a) contacting a biological sample obtained from a subject having cancer with one or more polypeptide ligands that bind specifically to one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186;

(b) determining specific binding;

(c) comparing the specific binding between the polypeptide ligands and the polypeptides in the sample with the specific binding between the polypeptide ligands and the polypeptides either in a cancer-free sample or in a cancer sample that is known not to progress to aggressive form; and

(d) evaluating the prognosis of the subject based on the comparison in step (c).

31. A method of determining the efficacy of a test compound for inhibiting cancer in a subject, the method comprising comparing a) in a first biological sample from the subject binding between one or more polypeptide ligands that specifically bind to one or more

polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186 and one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, wherein the sample has not been exposed to the test compound, with b) in a second biological sample from the subject, the specific binding of said polypeptide ligands and said polypeptides, wherein the sample has been exposed to the test compound, and wherein a significant change in the specific binding is an indication that the test compound is efficacious for inhibiting cancer in the subject.

32. A method of determining the efficacy of a therapy for inhibiting cancer in a subject, comprising comparing a) in a first biological sample from the subject prior to a treatment, binding between one or more polypeptide ligands that specifically bind to one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186 and one or more polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, with b) in a second biological sample from the subject following the treatment, the specific binding of said polypeptide ligands and said polypeptides, and wherein a significant change in the specific binding is an indication that the test compound is efficacious for inhibiting cancer in the subject.

33. A method of selecting a composition for inhibiting cancer in a subject, comprising

(a) obtaining a first biological sample comprising cancer cells from the subject;

(b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;

(c) comparing the specific binding between one or more polypeptide ligands and one or more polypeptides in each of the aliquots from (b) with the specific binding between said polypeptide ligands and said polypeptides in each of the aliquots from (a), wherein said ligands comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, and wherein said polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186; and

(d) selecting one of the test compositions which induces a significant change in specific binding .

34. A method of inhibiting cancer in a subject with cancer, comprising:

(a) obtaining a first biological sample comprising cells from the subject;

(b) administering to the subject one or more test compositions;

(c) obtaining a second biological sample comprising cells from the subject of (b); and

(d) comparing the specific binding between one or more polypeptide ligands and one or more polypeptides in the first sample with the specific binding between said polypeptide ligands and said polypeptides in the second sample, wherein said ligands comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, and wherein said polypeptides comprising a polypeptide sequence selected from the group consisting of SEQ ID NOs: 94-186, and wherein a significant change in the specific binding is an indication of inhibition cancer by said test compositions.

SEQUENCE LISTING

<110> Mayo Foundation for Medical Education and Research
Bayer Healthcare LLC
Burgess, Christopher
Myerow, Susan
Thiagalingam, Arunthathi
Maimonis, Peter
Molino, Gary
Burgart, Lawrence
Boardman, Lisa A.
Thibodeau, Steven
Lewis, Marcia

<120> Use of Differentially Expressed Nucleic Acid Sequences as Biomarkers for Cancer

<130> 1657/2022

<140> US 10/700,439
<141> 2003-11-04

<160> 186

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2163
<212> DNA
<213> Homo sapiens

<400> 1
ggcagatgaa atataagatt catcaaccac atttgacagc ccatggcagg tttcctgttt 60
tccatcgtcc ctctgcaggt cacagacaca cagagcccag ccgtggcagg ctcagccggg 120
gtccggggct gctaacaacg gctacattcc tcccccaggg ccaagggaaa tcctgagcgc 180
aggccagggt tgtttggttt tgaggtgtgc tgggatgaaa ggcaccctgg aagtggaagg 240
taaatgaaca atggaaaaac ttcacggcaa gattagaaag atacctgagc ccaatacccg 300
cctgatgtcg tgggccacac ctccgggtta ccaggggaag ggaggaagca aactgtcata 360
ttgatgtggc tctaaacaac aacagtgtgc gaaggcccag gggcactttg ggattgacca 420
agaggaaaca caagttgcac aatgatacaa tcttgttggt acaattgtca gagaagggaa 480
ctcccacagc aaaggccata aaaccatcca gggcagtctg gggcggctca gttctgcggt 540
gccagggagt ggagcagagc tcagccccgt cccaaacaca gatgggacca tgaactccgg 600
acacagcttc agccagaccc cctcggcctc cttccatggc gccggaggtg gctggggccg 660
gcccaggagc ttccccaggg ctcccaccgt ccatggcggt gcgggggggag cccgcatctc 720
cctgtccttc accacgcgga gctgcccacc ccctggaggg tcttggggtt ctggaagaag 780
cagcccccta ctaggcggaa atgggaaggc caccatgcag aatctcaacg accgcctggc 840
ctcctacctg gagaaggttc gcgccctgga ggaggccaac atgaagctgg aaagccgcat 900
cctgaaatgg caccagcaga gagatcctgg cagtaagaaa gattattccc agtatgagga 960
aaacatcaca cacctgcagg agcagatagt ggatggtaag atgaccaatg ctcagattat 1020
tcttctcatt gacaatgcca ggatggcagt ggatgacttc aacctcaagt atgaaaatga 1080
acactccttt aagaaagact tggaaattga agtcgagggc ctccgaagga ccttagacaa 1140
cctgaccatt gtcacaacag acctagaaca ggaggtggaa ggaatgagga aagagctcat 1200
tctcatgaag aagcaccatg agcaggaaat ggagaagcat catgtgccaa gtgacttcaa 1260
tgtcaatgtg aaggtggata caggtcccag ggaagatctg attaaggtcc tggaggatat 1320
gagacaagaa tatgagctta taataaagaa gaagcatcga gacttggaca cttggtataa 1380
agaacagtct gcagccatgt cccaggaggc agccagtcca gccactgtgc agagcagaca 1440
aggtgacatc cacgaactga agcgcacatt ccaggccctg gagattgacc tgcagacaca 1500
gtacagcacg aaatctgctt tggaaaacat gttatccgag acccagtctc ggtactcctg 1560
caagctccag gacatgcaag agatcatctc ccactatgag gaggaactga cgcagctacg 1620
ccatgaactg gagcggcaga acaatgaata ccaagtgctg ctgggcatca aaacccacct 1680
ggagaaggaa atcaccacgt accgacggct cctggaggga gagagtgaag ggacacggga 1740
agaatcaaag tcgagcatga aagtgtctgc aactccaaag atcaaggcca taacccagga 1800
gaccatcaac ggaagattag ttctttgtca agtgaatgaa atccaaaagc acgcatgaga 1860
ccaatgaaag tttccgcctg ttgtaaaatc tattttcccc caaggaaagt ccttgcacag 1920
acaccagtga gtgagttcta aaagataccc ttggaattat cagactcaga aacttttatt 1980
ttttttttct gtaacagtct caccagactt ctcataatgc tcttaatata ttgcactttt 2040

ctaatcaaag tgcgagttta tgagggtaaa gctctacttt cctactgcag ccttcagatt 2100
ctcatcattt tgcatctatt ttgtagccaa taaaactccg cactagcaaa aaaaaaaaaa 2160
aaa 2163

<210> 2
<211> 808
<212> DNA
<213> Homo sapiens

<400> 2
gatataaagc tcctacagct acctggcctg agaagccaac tcagactcag ccaacagaga 60
ttgttgattt gcctcttaag caagagattc attgcagctc agcatggctc agaccagctc 120
atacttcatg ctgatctcct gcctgatgtt tctgtctcag agccaaggcc aagaggccca 180
gacagagttg ccccaggccc ggatcagctg cccagaaggc accaatgcct atcgctccta 240
ctgctactac tttaatgaag accgtgagac ctgggttgat gcagatctct attgccagaa 300
catgaattcg ggcaacctgg tgtctgtgct cacccaggcc gagggtgcct ttgtggcctc 360
actgattaag gagagtggca ctgatgactt caatgtctgg attggcctcc atgaccccaa 420
aaagaaccgc cgctggcact ggagcagtgg gtccctggtc tcctacaagt cctggggcat 480
tggagcccca agcagtgtta atcctggcta ctgtgtgagc ctgacctcaa gcacaggatt 540
ccagaaatgg aaggatgtgc cttgtgaaga caagttctcc tttgtctgca agttcaaaaa 600
ctagaggcaa ctggaaaata catgtctaga actgatccag caattacaac ggagtcaaaa 660
attaaaccgg accatctctc caactcaact caacctggac actctcttct ctgctgagtt 720
tgccttgtta atcttcaata gttttaccta ccccagtctt tggaacccta aataataaaa 780
ataaacatgt ttccactatt gtgctgtc 808

<210> 3
<211> 773
<212> DNA
<213> Homo sapiens

<400> 3
aagccacctc aagtggacaa ggcacttacc aacagagatt gctgatttgc tccttaagca 60
agagattcac tgccgctaag catggctcag accaactcgt tcttcatgct gatctcctcc 120
ctgatgttcc tgtctctgag ccaaggccag gagtcccaga cagagctgcc taatccccga 180
atcagctgcc cagaaggcac caatgcctat cgctcctact gctactactt taatgaagac 240
cctgagacct gggttgatgc agatctctat tgccagaaca tgaattcagg caacctggtg 300
tctgtgctca cccaggcgga gggtgccttc gtggcctcac tgattaagga gagtagcact 360
gatgacagca atgtctggat tggcctccat gacccaaaaa agaaccgccg ctggcactgg 420
agtagtgggt ccctggtctc ctacaagtcc tgggacactg gatccccgag cagtgctaat 480
gctggctact gtgcaagcct gacttcatgc tcaggattca agaaatggaa ggatgaatct 540
tgtgagaaga agttctcctt tgtttgcaag ttcaaaaact agaggaagct gaaaaatgga 600
tgtctagaac tggtcctgca attactatga agtcaaaaat taaactagac tatgtctcca 660
actcagttca gaccatctcc tccctaatga gtttgcatcg ctgatcttca gtaccttcac 720
ctgtctcagt ctctagagcc ctgaaaaata aaaacaaact tatttttatc cag 773

<210> 4
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 4
cgggggggta ctgtgcgagc cctcaaggag gtggctgttc tgtagctgga gagctccgtg 60
ggtggcagga ctgaacttga acaccagaaa caacccccaa gccttgtgac ctgggaggca 120
ggaggcgggt ctgtctccct gggacttggg tggctgagcc gaggtactcg ggaccctgtc 180
ccgcgcatgg cagagtggct cctcacagcc tgaagctcat ccttctgcac gggccagcca 240
ggccagcaca gaggcaccag ggcagcagtg cacacaggtc cccggggacc ccaccatgtg 300
gagcggatgg tggctgtggc cccttgtggc cgtctgcact gcagacttct ttcgggacga 360
ggcagagagg atcatgaggg actcccctgt cattgatggg cacaatgacc tcccctggca 420
gctgctggat atgttcaaca accggctgca ggacgagagg gccaacctga ccaccttggc 480
cggcacacac accaacatcc ccaagctgag ggccggcttt gtgggaggcc agttctggtc 540
cgtgtacacg ccctgcgaca cccagaacaa agacgccgtg cggaggacgc tggagcagat 600
ggacgtggtc caccgcatgt gccggatgta cccggagacc ttcctgtatg tcaccagcag 660
tgcaggcatt cggcaggcct tccgggaagg gaaggtggcc agcctgatcg gcgtggaggg 720
cggccactcc attgacagca gtttgggcgt cctgcgggca ctctatcagc tgggcatgcg 780
gtacctgacc ctcacccaca gctgcaacac gccctgggct gacaactggc tggtggacac 840
gggagacagc gagccccaga gccaaggctt gtcacccttt gggcagcgtg tggtgaagga 900
gctgaaccgt ctgggggtcc tcatcgactt ggctcacgtg tctgtggcca ccatgaaggc 960

caccctgcag ctgtccagag ccccggtcat cttcagccac tcctcggcct acagcgtgtg 1020
cgcaagccgg cgcaacgtgc ctgacgacgt cctgaggctg gtgaaacaga cagacagcct 1080
ggtgatggtg aacttctaca acaattacat ttcctgcacc aacaaggcca acctgtccca 1140
agtggccgac catctggatc acatcaagga ggtggcagga gccagagccg tgggttttgg 1200
tggggacttt gatggtgttc caagggtccc tgaggggctg gaggacgtct ccaagtatcc 1260
agacctgatc gctgagctgc tcaggaggaa ctggacggag gcggaggtca agggcgcact 1320
ggctgacaac ctgctgaggg tcttcgaggc tgtggaacag gccagcaacc tcacacaggc 1380
tcccgaggag gagcccatcc cgctggacca gctgggtggc tcctgcagga cccattacgg 1440
ctactcctct ggggcttcca gcctccatcg ccactggggg ctcctgctgg cctccctcgc 1500
tcccctggtc ctctgtctgt ctctcctgtg aaacctggga gaccagagtc ccctttaggg 1560
ttcccggagc tccgggaaga cccgcccatc ccaggactcc agatgccagg agccctgctg 1620
cccacatgca aggaccagca tctcctgaga ggacgcctgg gcttacctgg ggggcaggat 1680
gcctggggac agttcaggac acacacacag taggcccgca ataaaagcaa caccccctt 1738

<210> 5
<211> 1666
<212> DNA
<213> Homo sapiens

<400> 5
ctccataagg cacaaacttt cagagacagc agagcacaca agcttctagg acaagagcca 60
ggaagaaacc accggaagga accatctcac tgtgtgtaaa catgacttcc aagctggccg 120
tggctctctt ggcagccttc ctgatttctg cagctctgtg tgaaggtgca gttttgccaa 180
ggagtgctaa agaacttaga tgtcagtgca taaagacata ctccaaacct ttccacccca 240
aatttatcaa agaactgaga gtgattgaga gtggaccaca ctgcgccaac acagaaatta 300
ttgtaaagct ttctgatgga agagagctct gtctggaccc caaggaaaac tgggtgcaga 360
gggttgtgga gaagtttttg aagagggctg agaattcata aaaaaattca ttctctgtgg 420
tatccaagaa tcagtgaaga tgccagtgaa acttcaagca aatctacttc aacacttcat 480
gtattgtgtg ggtctgttgt agggttgcca gatgcaatac aagattcctg gttaaatttg 540
aatttcagta aacaatgaat agtttttcat tgtaccatga aatatccaga acatacttat 600
atgtaaagta ttatttattt gaatctacaa aaaacaacaa ataatttta aatataagga 660
ttttcctaga tattgcacgg gagaatatac aaatagcaaa attgaggcca agggccaaga 720
gaatatccga actttaattt caggaattga atgggtttgc tagaatgtga tatttgaagc 780
atcacataaa aatgatggga caataaattt tgccataaag tcaaatttag ctggaaatcc 840
tggatttttt tctgttaaat ctggcaaccc tagtctgcta gccaggatcc acaagtcctt 900
gttccactgt gccttggttt ctcctttatt tctaagtgga aaaagtatta gccaccatct 960
tacctcacag tgatgttgtg aggacatgtg gaagcacttt aagtttttc atcataacat 1020
aaattatttt caagtgtaac ttattaacct atttattatt tatgtattta tttaagcatc 1080
aaatatttgt gcaagaattt ggaaaaatag aagatgaatc attgattgaa tagttataaa 1140
gatgttatag taaatttatt ttattttaga tattaaatga tgttttatta gataaatttc 1200
aatcagggtt tttagattaa acaaacaaac aattgggtac ccagttaaat tttcatttca 1260
gataaacaac aaataatttt ttagtataag tacattattg tttatctgaa attttaattg 1320
aactaacaat cctagtttga tactcccagt cttgtcattg ccagctgtgt tggtagtgct 1380
gtgttgaatt acggaataat gagttagaac tattaaaaca gccaaaactc cacagtcaat 1440
attagtaatt tcttgctggt tgaaacttgt ttattatgta caaatagatt cttataatat 1500
tatttaaatg actgcatttt taaatacaag gctttatatt tttaacttta agatgttttt 1560
atgtgctctc caaatttttt ttactgtttc tgattgtatg gaaatataaa agtaaatatg 1620
aaacatttaa aatataattt gttgtcaaag taaaaaaaaa aaaaaa 1666

<210> 6
<211> 1973
<212> DNA
<213> Homo sapiens

<400> 6
gggatattgg agtagcaaga ggctgggaag ccatcactta ccttgcactg agaaagaaga 60
caaaggccag tatgcacagc tttcctccac tgctgctgct gctgttctgg ggtgtggtgt 120
ctcacagctt cccagcgact ctagaaacac aagagcaaga tgtggactta gtccagaaat 180
acctggaaaa atactacaac ctgaagaatg atgggaggca agttgaaaag cggagaaata 240
gtggcccagt ggttgaaaaa ttgaagcaaa tgcaggaatt ctttgggctg aaagtgactg 300
ggaaaccaga tgctgaaacc ctgaaggtga tgaagcagcc cagatgtgga gtgcctgatg 360
tggctcagtt tgtcctcact gaggggaacc ctcgctggga gcaaacacat ctgacctaca 420
ggattgaaaa ttacacgcca gatttgccaa gagcagatgt ggaccatgcc attgagaaag 480
ccttccaact ctggagtaat gtcacacctc tgacattcac caaggtctct gagggtcaag 540
cagacatcat gatatctttt gtcaggggag atcatcggga caactctcct tttgatggac 600
ctggaggaaa tcttgctcat gcttttcaac caggcccagg tattggaggg gatgctcatt 660
ttgatgaaga tgaaaggtgg accaacaatt tcagagagta caacttacat cgtgttgcgg 720

ctcatgaact cggccattct cttggactct cccattctac tgatatcggg gctttgatgt 780
accctagcta caccttcagt ggtgatgttc agctagctca ggatgacatt gatggcatcc 840
aagccatata tggacgttcc caaaatcctg tccagcccat cggcccacaa accccaaaag 900
cgtgtgacag taagctaacc tttgatgcta taactacgat tcggggagaa gtgatgttct 960
ttaaagacag attctacatg cgcacaaatc ccttctaccc ggaagttgag ctcaatttca 1020
tttctgtttt ctggccacaa ctgccaaatg ggcttgaagc tgcttacgaa tttgccgaca 1080
gagatgaagt ccggtttttc aaagggaata agtactgggc tgttcaggga cagaatgtgc 1140
tacacggata ccccaaggac atctacagct cctttggctt ccctagaact gtgaagcata 1200
tcgatgctgc tctttctgag gaaaacactg gaaaaaccta cttctttgtt gctaacaaat 1260
actggaggta tgatgaatat aaacgatcta tggatccagg ttatcccaaa atgatagcac 1320
atgactttcc tggaattggc cacaaagttg atgcagtttt catgaaagat ggatttttct 1380
atttctttca tggaacaaga caatacaaat ttgatcctaa aacgaagaga attttgactc 1440
tccagaaagc taatagctgg ttcaactgca ggaaaaattg aacattacta atttgaatgg 1500
aaaacacatg gtgtgagtcc aaagaaggtg ttttcctgaa gaactgtcta ttttctcagt 1560
catttttaac ctctagagtc actgatacac agaatataat cttatttata cctcagtttg 1620
catatttttt tactatttag aatgtagccc tttttgtact gatataattt agttccacaa 1680
atggtgggta caaaaagtca agtttgtggc ttatggattc atataggcca gagttgcaaa 1740
gatcttttcc agagtatgca actctgacgt tgatcccaga gagcagcttc agtgacaaac 1800
atatcctttc aagacagaaa gagacaggag acatgagtct ttgccggagg aaaagcagct 1860
caagaacaca tgtgcagtca ctggtgtcac cctggatagg caagggataa ctcttctaac 1920
acaaaataag tgttttatgt ttggaataaa gtcaaccttg tttctactgt ttt 1973

<210> 7
<211> 1127
<212> DNA
<213> Homo sapiens

<400> 7
accaaatcaa ccataggtcc aagaacaatt gtctctggac ggcagctatg cgactcaccg 60
tgctgtgtgc tgtgtgcctg ctgcctggca gcctggccct gccgctgcct caggaggcgg 120
gaggcatgag tgagctacag tgggaacagg ctcaggacta tctcaagaga ttttatctct 180
atgactcaga aacaaaaaat gccaacagtt tagaagccaa actcaaggag atgcaaaaat 240
tctttggcct acctataact ggaatgttaa actcccgcgt catagaaata atgcagaagc 300
ccagatgtgg agtgccagat gttgcagaat actcactatt tccaaatagc ccaaaatgga 360
cttccaaagt ggtcacctac aggatcgtat catatactcg agacttaccg catattacag 420
tggatcgatt agtgtcaaag gctttaaaca tgtggggcaa agagatcccc ctgcatttca 480
ggaaagttgt atggggaact gctgacatca tgattggctt tgcgcgagga gctcatgggg 540
actcctaccc atttgatggg ccaggaaaca cgctggctca tgcctttgcg cctgggacag 600
gtctcggagg agatgctcac ttcgatgagg atgaacgctg gacggatggt agcagtctag 660
ggattaactt cctgtatgct gcaactcatg aacttggcca ttctttgggt atgggacatt 720
cctctgatcc taatgcagtg atgtatccaa cctatggaaa tggagatccc caaaatttta 780
aactttccca ggatgatatt aaaggcattc agaaactata tggaaagaga agtaattcaa 840
gaaagaaata gaaacttcag gcagaacatc cattcattca ttcattggat tgtatatcat 900
tgttgcacaa tcagaattga taagcactgt tcctccactc catttagcaa ttatgtcacc 960
ctttttatt gcagttggtt tttgaatgtc tttcactcct tttattggtt aaactccttt 1020
atggtgtgac tgtgtcttat tccatctatg agctttgtca gtgcgcgtag atgtcaataa 1080
atgttacata cacaaataaa taaaatgttt attccatggt aaattta 1127

<210> 8
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 8
gcagagcaca gcatcgtcgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca 60
aacgccgacc aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta 120
ggcatcacct gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag 180
ctttacaaca aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag 240
cagaatctcc tagccccaca gacccttcca agtaagtcca acgaaagcca tgaccacatg 300
gatgatatgg atgatgaaga tgatgatgac catgtggaca gccaggactc cattgactcg 360
aacgactctg atgatgtaga tgacactgat gattctcacc agtctgatga gtctcaccat 420
tctgatgaat ctgatgaact ggtcactgat tttcccacgg acctgccagc aaccgaagtt 480
ttcactccag ttgtccccac agtagacaca tatgatggcc gaggtgatag tgtggtttat 540
ggactgaggt caaaatctaa gaagtttcgc agacctgaca tccagtaccc tgatgctaca 600
gacgaggaca tcacctcaca catggaaagc gaggagttga atggtgcata caaggccatc 660
cccgttgccc aggacctgaa cgcgccttct gattgggaca gccgtgggaa ggacagttat 720
gaaacgagtc agctggatga ccagagtgct gaaacccaca gccacaagca gtccagatta 780

tataagcgga aagccaatga tgagagcaat gagcattccg atgtgattga tagtcaggaa 840
ctttccaaag tcagccgtga attccacagc catgaatttc acagccatga agatatgctg 900
gttgtagacc ccaaaagtaa ggaagaagat aaacacctga aatttcgtat ttctcatgaa 960
ttagatagtg catcttctga ggtcaattaa aaggagaaaa aatacaattt ctcactttgc 1020
atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcttt 1080
ctcagtttat tggttgaatg tgtatctatt tgagtctgga aataactaat gtgtttgata 1140
attagtttag tttgtggctt catggaaact ccctgtaaac taaaagcttc agggttatgt 1200
ctatgttcat tctatagaag aaatgcaaac tatcactgta ttttaatatt tgttattctc 1260
tcatgaatag aaatttatgt agaagcaaac aaaatacttt tacccactta aaaagagaat 1320
ataacatttt atgtcactat aatcttttgt tttttaagtt agtgtatatt ttgttgtgat 1380
tatctttttg tggtgtgaat aaatctttta tcttgaatgt aataagaatt tggtggtgtc 1440
aattgcttat ttgttttccc acggttgtcc agcaattaat aaaacataac ctttttttact 1500
gcctaaaaaa aaaaaaaaaa aaaa 1524

<210> 9
<211> 1172
<212> DNA
<213> Homo sapiens

<400> 9
gagacattcc tcaattgctt agacatattc tgagcctaca gcagaggaac ctccagtctc 60
agcaccatga atcaaactgc gattctgatt tgctgcctta tctttctgac tctaagtggc 120
attcaaggag tacctctctc tagaaccgta cgctgtacct gcatcagcat tagtaatcaa 180
cctgttaatc caaggtcttt agaaaaactt gaaattattc ctgcaagcca attttgtcca 240
cgtgttgaga tcattgctac aatgaaaaag aagggtgaga agagatgtct gaatccagaa 300
tcgaaggcca tcaagaattt actgaaagca gttagcaagg aaatgtctaa aagatctcct 360
taaaaccaga ggggagcaaa atcgatgcag tgcttccaag gatggaccac acagaggctg 420
cctctcccat cacttcccta catggagtat atgtcaagcc ataattgttc ttagtttgca 480
gttacactaa aaggtgacca atgatggtca ccaaatcagc tgctactact cctgtaggaa 540
ggttaatgtt catcatccta agctattcag taataactct accctggcac tataatgtaa 600
gctctactga ggtgctatgt tcttagtgga tgttctgacc ctgcttcaaa tatttccctc 660
acctttccca tcttccaagg gtactaagga atctttctgc tttggggttt atcagaattc 720
tcagaatctc aaataactaa aaggtatgca atcaaatctg ctttttaaag aatgctcttt 780
acttcatgga cttccactgc catcctccca aggggcccaa attctttcag tggctaccta 840
catacaattc caaacacata caggaaggta gaaatatctg aaaatgtatg tgtaagtatt 900
cttatttaat gaaagactgt acaaagtata agtcttagat gtatatattt cctatattgt 960
tttcagtgta catggaataa catgtaatta agtactatgt atcaatgagt aacaggaaaa 1020
ttttaaaaat acagatagat atatgctctg catgttacat aagataaatg tgctgaatgg 1080
ttttcaaata aaaatgaggt actctcctgg aaatattaag aaagactatc taaatgttga 1140
aagatcaaaa ggttaataaa gtaattataa ct 1172

<210> 10
<211> 5699
<212> DNA
<213> Homo sapiens

<400> 10
ggagttctca gacctccagt ttcagccctg ccctcagcct ccaatccgta agagacaccc 60
agccccagca attggattgg gcagcccgtc ttgacacacc actgtgctga gtgcttgagg 120
acgtgtttca acagatggtt ggggttagtg tgtgtcatca cattcgagtg gggattaaga 180
gaaggaaggc tgccttgctg gagctgtgtg gtcttctcca agtgagagtc gcaggcaata 240
gaactacttt gcttttggag gaaaaggagg aattcatttt cagcagacac aagaaaagca 300
gtttttttt cagggattct tcacttctct tgaacaagga actcactcag agactaacac 360
aaaggaagta atttcttacc tggtcattat ttagtctaca ataagttcat ccttcttcag 420
tgtgaccagt aaattcttcc catactcttg aagagagcat aattggaatg gagaggtggt 480
gctgacggcc acccaccatc atctaaagaa gataaacttg gcaaatgaca tgcaggttct 540
tcaaggcaga ataattgcag aaaatcttca aaggacccta tctgcagatg ttctgaatac 600
ctctgagaat agagattgat tattcaacca ggatacctaa ttcaagaact ccagaaatca 660
ggagacggag acattttgtc agttttgcaa cattggacca aatacaatga agtattcttg 720
ctgtgctctg gttttggctg tcctgggcac agaattgctg ggaagcctct gttcgactgt 780
cagatccccg aggttcagag gacggataca gcaggaacga aaaaacatcc gacccaacat 840
tattcttgtg cctaccgatg atcaagatgt ggagctgggg tccctgcaag tcatgaacaa 900
aacgagaaag attatggaac atgggggggc caccttcatc aatgcctttg tgactacacc 960
catgtgctgc ccgtcacggt cctccatgct caccgggaag tatgtgcaca atcacaatgt 1020
ctacaccaac aacgagaact gctcttcccc ctcgtggcag gccatgcatg agcctcggac 1080
ttttgctgta tatcttaaca acactggcta cagaacagcc ttttttggaa aatacctcaa 1140
tgaatataat ggcagctaca tccccctgg gtggcgagaa tggcttggat taatcaagaa 1200

ttctcgcttc tataattaca ctgtttgtcg caatggcatc aaagaaaagc atggatttga 1260
ttatgcaaag gactacttca cagacttaat cactaacgag agcattaatt acttcaaaat 1320
gtctaagaga atgtatcccc ataggcccgt tatgatggtg atcagccacg ctgcgcccca 1380
cggccccgag gactcagccc cacagttttc taaactgtac cccaatgctt cccaacacat 1440
aactcctagt tataactatg caccaaatat ggataaacac tggattatgc agtacacagg 1500
accaatgctg cccatccaca tggaatttac aaacattcta cagcgcaaaa ggctccagac 1560
tttgatgtca gtggatgatt ctgtggagag gctgtataac atgctcgtgg agacggggga 1620
gctggagaat acttacatca tttacaccgc cgaccatggt taccatattg ggcagtttgg 1680
actggtcaag gggaaatcca tgccatatga ctttgatatt cgtgtgcctt tttttattcg 1740
tggtccaagt gtagaaccag gatcaatagt cccacagatc gttctcaaca ttgacttggc 1800
ccccacgatc ctggatattg ctgggctcga cacacctcct gatgtggacg gcaagtctgt 1860
cctcaaactt ctggacccag aaaagccagg taacaggttt cgaacaaaca agaaggccaa 1920
aatttggcgt gatacattcc tagtggaaag aggcaaattt ctacgtaaga aggaagaatc 1980
cagcaagaat atccaacagt caaatcactt gcccaaatat gaacgggtca aagaactatg 2040
ccagcaggcc aggtaccaga cagcctgtga acaaccgggg cagaagtggc aatgcattga 2100
ggatacatct ggcaagcttc gaattcacaa gtgtaaagga cccagtgacc tgctcacagt 2160
ccggcagagc acgcggaacc tctacgctcg cggcttccat gacaaagaca aagagtgcag 2220
ttgtagggag tctggttacc gtgccagcag aagccaaaga aagagtcaac ggcaattctt 2280
gagaaaccag gggactccaa agtacaagcc cagatttgtc catactcggc agacacgttc 2340
cttgtccgtc gaatttgaag gtgaaatata tgacataaat ctggaagaag aagaagaatt 2400
gcaagtgttg caaccaagaa acattgctaa gcgtcatgat gaaggccaca aggggccaag 2460
agatctccag gcttccagtg gtggcaacag gggcaggatg ctggcagata gcagcaacgc 2520
cgtgggccca cctaccactg tccgagtgac acacaagtgt tttattcttc ccaatgactc 2580
tatccattgt gagagagaac tgtaccaatc ggccagagcg tggaaggacc ataaggcata 2640
cattgacaaa gagattgaag ctctgcaaga taaaattaag aatttaagag aagtgagagg 2700
acatctgaag agaaggaagc ctgaggaatg tagctgcagt aaacaaagct attacaataa 2760
agagaaaggt gtaaaaaagc aagagaaatt aaagagccat cttcacccat tcaaggaggc 2820
tgctcaggaa gtagatagca aactgcaact tttcaaggag aacaaccgta ggaggaagaa 2880
ggagaggaag gagaagagac ggcagaggaa gggggaagag tgcagcctgc ctggcctcac 2940
ttgcttcacg catgacaaca accactggca gacagccccg ttctggaacc tgggatcttt 3000
ctgtgcttgc acgagttcta acaataacac ctactggtgt ttgcgtacag ttaatgagac 3060
gcataatttt cttttctgtg agtttgctac tggcttttg gagtattttg atatgaatac 3120
agatccttat cagctcacaa atacagtgca cacggtagaa cgaggcattt tgaatcagct 3180
acacgtacaa ctaatggagc tcagaagctg tcaaggatat aagcagtgca acccaagacc 3240
taagaatctt gatgttggaa ataaagatgg aggaagctat gacctacaca gaggacagtt 3300
atgggatgga tgggaaggtt aatcagcccc gtctcactgc agacatcaac tggcaaggcc 3360
tagaggagct acacagtgtg aatgaaaaca tctatgagta cagacaaaac tacagactta 3420
gtctggtgga ctggactaat tacttgaagg atttagatag agtatttgca ctgctgaaga 3480
gtcactatga gcaaaataaa acaaataaga ctcaaactgc tcaaagtgac gggttcttgg 3540
ttgtctctgc tgagcacgct gtgtcaatgg agatggcctc tgctgactca gatgaagacc 3600
caaggcataa ggttgggaaa acacctcatt tgaccttgcc agctgacctt caaaccctgc 3660
atttgaaccg accaacatta agtccagaga gtaaacttga atggaataac gacattccag 3720
aagttaatca tttgaattct gaacactgga gaaaaaccga aaaatggacg gggcatgaag 3780
agactaatca tctggaaacc gatttcagtg gcgatggcat gacagagcta gagctcgggc 3840
ccagccccag gctgcagccc attcgcaggc acccgaaaga acttccccag tatggtggtc 3900
ctggaaagga catttttgaa gatcaactat atcttcctgt gcattccgat ggaatttcag 3960
ttcatcagat gttcaccatg gccaccgcag aacaccgaag taattccagc atagcgggga 4020
agatgttgac caaggtggag aagaatcacg aaaaggagaa gtcacagcac ctagaaggca 4080
gcgcctcctc ttcactctcc tctgattaga tgaaactgtt accttaccct aaacacagta 4140
tttctttta actttttat ttgtaaacta ataaaggtaa tcacagccac caacattcca 4200
agctaccctg ggtacctttg tgcagtagaa gctagtgagc atgtgagcaa gcggtgtgca 4260
cacggagact catcgttata atttactatc tgccaagagt agaaagaaag gctggggata 4320
tttgggttgg cttggttttg atttttgct tgtttgtttg ttttgtacta aaacagtatt 4380
atcttttgaa tatcgtaggg acataagtat atacatgtta tccaatcaag atggctagaa 4440
tggtgccttt ctgagtgtct aaaacttgac acccctggta aatctttcaa cacacttcca 4500
ctgcctgcgt aatgaagttt tgattcattt ttaaccactg gaatttttca atgccgtcat 4560
tttcagttag atgattttgc actttgagat taaaatgcca tgtctatttg attagtctta 4620
ttttttatt tttacaggct tatcagtctc actgttggct gtcattgtga caaagtcaaa 4680
taaaccccca aggacgacac acagtatgga tcacatattg tttgacatta agcttttgcc 4740
agaaaatgtt gcatgtgttt tacctcgact tgctaaaatc gattagcaga aaggcatggc 4800
taataatgtt ggtggtgaaa ataaataaat aagtaaacaa aatgaagatt gcctgctctc 4860
tctgtgccta gcctcaaagc gttcatcata catcatacct ttaagattgc tatattttgg 4920
gttattttct tgacaggaga aaaagatcta aagatctttt attttcatct tttttggttt 4980
tcttggcatg actaagaagc ttaaatgttg ataaaatatg actagttttg aatttacacc 5040
aagaacttct caataaaaga aaatcatgaa tgctccacaa tttcaacata ccacaagaga 5100
agttaatttc ttaacattgt gttctatgat tatttgtaag accttcacca agttctgata 5160
tcttttaaag acatagttca aaattgcttt tgaaaatctg tattcttgaa aatatccttg 5220

SEQUENCE LISTING 1657-2022.txt

ttgtgtatta ggtttttaaa taccagctaa aggattacct cactgagtca tcagtaccct 5280
cctattcagc tccccaagat gatgtgtttt tgcttaccct aagagaggtt ttcttcttat 5340
ttttagataa ttcaagtgct tagataaatt atgttttctt taagtgttta tggtaaactc 5400
ttttaaagaa aatttaatat gttatagctg aatctttttg gtaactttaa atctttatca 5460
tagactctgt acatatgttc aaattagctg cttgcctgat gtgtgtatca tcggtgggat 5520
gacagaacaa acatatttat gatcatgaat aatgtgcttt gtaaaaagat ttcaagttat 5580
taggaagcat actctgtttt ttaatcatgt ataatattcc atgatacttt tatagaacaa 5640
ttctggcttc aggaaagtct agaagcaata tttcttcaaa taaaaggtgt ttaaacttt 5699

<210> 11
<211> 6217
<212> DNA
<213> Homo sapiens

<400> 11
cgcagactgt gctggagctg gtgctgaaaa agggggtttg cagaggctgc cctggggctg 60
gtgctgaaag aagagcccac agctgacttc atggtgctac aataacctca gaatctactt 120
ttcactctca ggagaaccca cagtctaata tttagacatg atggcaaact gggcggaagc 180
aagacctctc ctcattctta ttgttttatt agggcaattt gtctcaataa aagcccagga 240
agaagacgag gatgaaggat atggtgaaga aatagcctgc actcagaatg gccagatgta 300
cttaaacagg gacatttgga aacctgcccc ttgtcagatc tgtgtctgtg acaatggagc 360
cattctctgt gacaagatag aatgccagga tgtgctggac tgtgccgacc ctgtaacgcc 420
ccctggggaa tgctgtcctg tctgttcaca aacacctgga ggtggcaata caaattttgg 480
tagaggaaga aagggacaaa agggagaacc aggattagtg cctgttgtaa caggcatacg 540
tggtcgtcca ggaccggcag gacctccagg atcacaggga ccaagaggag agcgagggcc 600
aaaaggaaga cctggccctc gtggacctca gggaattgat ggagaaccag gtgttcctgg 660
tcaacctggt gctccaggac ctcctggaca tccgtcccac ccaggacccg atggcttgag 720
caggccgttt tcagctcaaa tggctgggtt ggatgaaaaa tctggacttg ggagtcaagt 780
aggactaatg cctggctctg tgggtcctgt tggcccaagg ggaccacagg gtttacaagg 840
acagcaaggt ggtgcaggac ctacaggacc tcctggtgaa cctggtgatc ctggaccaat 900
gggtccgatt ggttcacgtg gaccagaggg ccctcctggt aaacctgggg aagatggtga 960
acctggcaga aatggaaatc ctggtgaagt gggatttgca ggatctccgg gagctcgtgg 1020
atttcctggg gctcctggtc ttccaggtct gaagggtcac cgaggacaca aaggtcttga 1080
aggccctaaa ggtgaagttg gagcacctgg ttccaagggt gaagctggcc ccactggtcc 1140
aatgggtgcc atgggtcctc tgggtccgag gggaatgcca ggagagagag ggagacttgg 1200
gccacagggt gctcctggac aacgaggtgc acatggtatg cctggaaaac ctggaccaat 1260
gggtcctctt gggataccag gctcttctgg ttttccagga aatcctggaa tgaagggaga 1320
agcaggtcct acaggggcgc gaggccctga aggtcctcag gggcagagag gtgaaactgg 1380
gcccccaggt ccagttggct ctccaggtct tcctggtgca ataggaactg atggtactcc 1440
tggtcccaaa ggcccaacgg gctctccggg tacctctggt cctcctggct cagcagggcc 1500
tcctggatct ccaggacctc agggtagcac tggtcctcag gggaattcgg gccttccggg 1560
tgatccaggt ttcaaaggag aagctggccc aaaaggggaa ccagggccac atggtattca 1620
gggtccgata ggcccacccg gtgaagaagg caaaagaggt cccagaggtg acccaggaac 1680
acttggtcct ccagggccag tgggagaaag gggtgctcct ggcaatcgtg gttttccagg 1740
ctctgatggt ttacctgggc caaagggtgc tcaaggagaa cggggtcctg taggttcttc 1800
aggacccaaa ggaagccagg gggatccagg acgtccaggg gaacctgggc ttccaggtgc 1860
tcggggtttg acaggaaatc ctggtgttca aggtcctgaa ggaaaacttg gacctttggg 1920
tgcgccaggg gaagatggcc gtccaggtcc tccaggctcc ataggaatca aagggcagcc 1980
cgggaccatg ggccttccag gccccaaagg tagcaatggt gaccctggga aacctggaga 2040
agcaggaaat cctggagttc ctgggcaaag gggagctcct ggaaaagatg gtaaagttgg 2100
tccttatggt cctcctgggc cgccgggtct acgtggtgaa agaggagaac aaggacctcc 2160
agggcccaca ggttttcagg ggcatcctgg tcctccaggt cctcctggag aaggtggaaa 2220
accaggtgat caaggtgttc ctggaggtcc cggagcagtt ggcccgttag gacctagagg 2280
agaacgagga aatcctgggg aaagaggaga acctgggata actggactcc ctggtgagaa 2340
gggaatggct ggaggacatg gtcctgatgg cccaaaaggc agtccaggtc catctgggac 2400
ccctggagat acaggcccac caggtcttca aggtatgccg ggagaaagag gaattgcagg 2460
aactcctggc cccaagggtg acagaggtgg cataggagaa aaaggtgctg aaggcacagc 2520
tggaaatgat ggtgcaggag gtcttccagg tcctttgggc cctccaggtc cggcaggcct 2580
actgggagaa aagggtgaac ctggtcctcg aggtttagtt ggtcctcctg gctcccgggg 2640
caatcctggt tctcgaggtg aaaatgggcc aactggagct gttggttttg ccggacccca 2700
ggggtctgac ggacagcctg gagtaaaagg tgaacctgga gagccaggac agaagggaga 2760
tgctggttct cctggaccac aaggtttagc aggatcccct ggccctcatg gtcctaatgg 2820
tgttcctgga ctaaaaggtg gtcgaggaac ccaaggtccg cctggtgcta caggatttcc 2880
tggttctgcg ggcagagttg gacctccagg ccctgctgga gctccaggac ctgcgggacc 2940
cctaggggaa cccgggaagg agggacctcc aggtcctcgt ggggaccctg gctctcatgg 3000
gcgtgtggga gtccgaggac cagctggccc ccctggtggc ccaggagaca aaggggaccc 3060
aggagaagat gggcaacctg gtccagatgg ccccccctggt ccagctggaa cgaccgggca 3120

gagaggaatt gttggcatgc ctgggcaacg tggagagaga ggcatgcccg gcctaccagg 3180
cccagcggga acaccaggaa aagtaggacc aactggtgca acaggagata aaggtccacc 3240
tggacctgtg gggcccccag gctccaatgg tcctgtaggg gaacctggac cagaaggtcc 3300
agctggcaat gatggtaccc caggacggga tggtgctgtt ggagaacgtg gtgatcgtgg 3360
agaccctggg cctgcaggtc tgccaggctc tcagggtgcc cctggaactc ctggccctgt 3420
gggtgctcca ggagatgcag gacaaagagg agatccgggt tctcggggtc ctataggaca 3480
cctgggtcga gctggaaaac gtggattacc tggaccccaa ggacctcgtg gtgacaaagg 3540
tgatcatgga gaccgaggcg acagaggtca gaagggccac agaggcttta ctggtcttca 3600
gggtcttcct ggccctcctg gtccaaatgg tgaacaagga agtgctggaa tccctggacc 3660
atttggccca agaggtcctc caggcccagt tggtccttca ggtaaagaag gaaaccctgg 3720
gccacttggg ccattgggac ctccaggtgt acgaggcagt gtaggagaag caggacctga 3780
gggccctcct ggtgagcctg gcccacctgg ccctccgggt ccccctggcc accttacagc 3840
tgctcttggg gatatcatgg ggcactatga tgaaagcatg ccagatccac ttcctgagtt 3900
tactgaagat caggcggctc ctgatgacaa aaacaaaacg gacccagggg ttcatgctac 3960
cctgaagtca ctcagtagtc agattgaaac catgcgcagc cccgatggct cgaaaaagca 4020
cccagcccgc acgtgtgatg acctaaagct ttgccattcc gcaaagcaga gtggtgaata 4080
ctggattgat cctaaccaag gatctgttga agatgccatc aaagtttact gcaacatgga 4140
aacaggagaa acatgtattt cagcaaaccc atccagtgta ccacgtaaaa cctggtgggc 4200
cagtaaatct cctgacaata aacctgtttg gtatggtctt gatatgaaca gagggtctca 4260
gttcgcttat ggagaccacc aatcacctaa tacagccatt actcagatga ctttttgcg 4320
ccttttatca aaagaagcct cccagaacat cacttacatc tgtaaaaaca gtgtaggata 4380
catggacgat caagctaaga acctcaaaaa agctgtggtt ctcaaagggg caaatgactt 4440
agatatcaaa gcagagggaa atattagatt ccggtatatc gttcttcaag acacttgctc 4500
taagcggaat ggaaatgtgg gcaagactgt ctttgaatat agaacacaga atgtggcacg 4560
cttgcccatc atagatcttg ctcctgtgga tgttggcggc acagaccagg aattcggcgt 4620
tgaaattggg ccagtttgtt ttgtgtaaag taagccaaga cacatcgaca atgagcacca 4680
ccatcaatga ccaccgccat tcacaagaac tttgactgtt tgaagttgat cctgagactc 4740
ttgaagtaat ggctgatcct gcatcagcat tgtatatatg gtcttaagtg cctggcctcc 4800
ttatccttca gaatatttat tttacttaca atcctcaagt tttaattgat tttaaatatt 4860
tttcaataca acagtttagg tttaagatga ccaatgacaa tgaccacctt tgcagaaagt 4920
aaactgattg aataaataaa tctccgtttt cttcaattta tttcagtgta atgaaaaagt 4980
tgcttagtat ttatgaggaa attcttcttc ctggcaggta gcttaaagag tggggtatat 5040
agagccacaa cacatgttta ttttgcttgg ctgcagttga aaaatagaaa ttagtgccct 5100
tttgtgacct ctcattccaa gattgtcaat taaaaatgag tttaaaatgt ttaacttgtg 5160
atcgagacct acatgcatgt cttgatattg tgtaactata atagagactc tttaaggaga 5220
atcttaaaaa aaaaaaacgt ttctcactgt cttaaataga atttttaaat agtatatatt 5280
cagtggcatt ttggagaaca aagtgaattt acttcgactt cttaaatttt tgtaaaagac 5340
tataagttta gacatctttc tcattcaaat ttaaagatat ctttctcctc ttgatcaatc 5400
tatcaatatt gatagaagtc acactagtat ataccattta atacatttac actttcttat 5460
ttaagaagat attgaatgca aaataattga catatagaac tttacaaaca tatgtccaag 5520
gactctaaat tgagactctt ccacatgtac aatctcatca tcctgaagcc tataatgaag 5580
aaaaagatct agaaactgag ttgtggagct gactctaatc aaatgtgatg attggaatta 5640
gaccatttgg cctttgaact ttcataggaa aaatgaccca acatttctta gcatgagcta 5700
cctcatctct agaagctggg atggacttac tattcttgtt tatattttag atactgaaag 5760
gtgctatgct tctgttatta ttccaagact ggagataggc agggctaaaa aggtattatt 5820
atttttcctt taatgatggt gctaaaattc ttcctataaa attccttaaa aataaagatg 5880
gtttaatcac taccattgtg aaaacataac tgttagactt cccgtttctg aaagaaagag 5940
catcgttcca atgcttgttc actgttcctc tgtcatactg tatctggaat gctttgtaat 6000
acttgcatgc ttcttagacc agaacatgta ggtccccttg tgtctcaata ctttttttt 6060
cttaattgca tttgttggct ctattttaat ttttttcttt taaaataaac agctgggacc 6120
atcccaaaag acaagccatg catacaactt tggtcatgta tctctgcaaa gcatcaaatt 6180
aaatgcacgc ttttgtcatg tcaaaaaaaa aaaaaaa 6217

<210> 12
<211> 1103
<212> DNA
<213> Homo sapiens

<400> 12
cacagagccc gggccgcagg cacctcctcg ccagctcttc cgctcctctc acagccgcca 60
gacccgcctg ctgagcccca tggcccgcgc tgctctctcc gccgcccccа gcaatccccg 120
gctcctgcga gtggcactgc tgctcctgct cctggtagcc gctggccggc gcgcagcagg 180
agcgtccgtg gccactgaac tgcgctgcca gtgcttgcag accctgcagg gaattcaccc 240
caagaacatc caaagtgtga acgtgaagtc ccccggaccc cactgcgccc aaaccgaagt 300
catagccaca ctcaagaatg ggcggaaagc ttgcctcaat cctgcatccc ccatagttaa 360
gaaaatcatc gaaaagatgc tgaacagtga caaatccaac tgaccagaag ggaggaggaa 420
gctcactggt ggctgttcct gaaggaggcc ctgcccttat aggaacagaa gaggaaagag 480

agacacagct gcagaggcca cctggattgt gcctaatgtg tttgagcatc gcttaggaga 540
agtcttctat ttatttattt attcattagt tttgaagatt ctatgttaat attttaggtg 600
taaaataatt aagggtatga ttaactctac ctgcacactg tcctattata ttcattcttt 660
ttgaaatgtc aaccccaagt tagttcaatc tggattcata tttaatttga aggtagaatg 720
ttttcaaatg ttctccagtc attatgttaa tatttctgag gagcctgcaa catgccagcc 780
actgtgatag aggctggcgg atccaagcaa atggccaatg agatcattgt gaaggcaggg 840
gaatgtatgt gcacatctgt tttgtaactg tttagatgaa tgtcagttgt tatttattga 900
aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa actttaagaa ctaaaatgtt 960
ctaaatatcc cttggacatt ttatgtcttt cttgtaaggc atactgcctt gtttaatggt 1020
agttttacag tgtttctggc ttagaacaaa ggggcttaat tattgatgtt ttcatagaga 1080
atataaaaat aaagcactta tag 1103

<210> 13
<211> 793
<212> DNA
<213> Homo sapiens

<400> 13
aggagttgtg agtttccaag ccccagctca ctctgaccac ttctctgcct gcccagcatc 60
atgaagggcc ttgcagctgc cctccttgtc ctcgtctgca ccatggccct ctgctcctgt 120
gcacaagttg gtaccaacaa agagctctgc tgcctcgtct atacctcctg gcagattcca 180
caaaagttca tagttgacta ttctgaaacc agcccccagt gccccaagcc aggtgtcatc 240
ctcctaacca agagaggccg gcagatctgt gctgacccca ataagaagtg ggtccagaaa 300
tacatcagcg acctgaagct gaatgcctga ggggcctgga agctgcgagg gcccagtgaa 360
cttggtgggc ccaggaggga acaggagcct gagccagggc aatggccctg ccaccctgga 420
ggccacctct tctaagagtc ccatctgcta tgcccagcca cattaactaa ctttaatctt 480
agtttatgca tcatatttca ttttgaaatt gatttctatt gttgagctgc attatgaaat 540
tagtattttc tctgacatct catgacattg tctttatcat cctttccccc ttcccttcaa 600
ctcttcgtac attcaatgca tggatcaatc agtgtgatta gctttctcag cagacattgt 660
gccatatgta tcaaatgaca aatctttatt gaatggtttt gctcagcacc acctttttaat 720
atattggcag tacttattat ataaaaggta aaccagcatt ctcactgtga aaaaaaaaaa 780
aaaaaaaaaa aaa 793

<210> 14
<211> 3654
<212> DNA
<213> Homo sapiens

<400> 14
agatgccgcg ggggccgctc gcagccgccg ctgacttgtg aatgggaccg ggactggggc 60
cgggactgac accgcagcgc ttgccctgcg ccagggactg gcggctcgga ggttgcgtcc 120
accctcaagg gccccagaaa tcactgtgtt ttcagctcag cggccctgtg acattccttc 180
gtgttgtcat ttgttgagtg accaatcaga tgggtggagt gtgttacaga aattggcagc 240
aagtatccaa tgggtgaaga agaagctaac tggggacgtg ggcagccctg acgtgatgag 300
ctcaaccagc agagacattc catcccaaga gaggtctgcg tgacgcgtcc gggaggccac 360
cctcagcaag accaccgtac agttggtgga aggggtgaca gctgcattct cctgtgccta 420
ccacgtaacc aaaaatgaag gagaactact gtttacaagc cgccctggtg tgcctgggca 480
tgctgtgcca cagccatgcc tttgccccag agcggcgggg gcacctgcgg ccctccttcc 540
atgggcacca tgagaagggc aaggaggggc aggtgctaca gcgctccaag cgtggctggg 600
tctggaacca gttcttcgtg atagaggagt acaccgggcc tgaccccgtg cttgtgggca 660
ggcttcattc agatattgac tctggtgatg ggaacattaa atacattctc tcaggggaag 720
gagctggaac cattttgtg attgatgaca aatcagggaa cattcatgcc accaagacgt 780
tggatcgaga agagagagcc cagtacacgt tgatggctca ggcggtggac agggacacca 840
atcggccact ggagccaccg tcggaattca ttgtcaaggt ccaggacatt aatgacaacc 900
ctccggagtt cctgcacgag acctatcatg ccaacgtgcc tgagaggtcc aatgtgggaa 960
cgtcagtaat ccaggtgaca gcttcagatg cagatgaccc cacttatgga aatagcgcca 1020
agttagtgta cagtatcctc gaaggacaac cctatttttc ggtggaagca cagacaggta 1080
tcatcagaac agccctaccc aacatggaca gggaggccaa ggaggagtac cacgtggtga 1140
tccaggccaa ggacatgggt ggacatatgg gcggactctc agggacaacc aaagtgacga 1200
tcacactgac cgatgtcaat gacaacccac caaagtttcc gcagagcgta taccagatgt 1260
ctgtgtcaga agcagccgtc cctggggagg aagtaggaag agtgaaagct aaagatccag 1320
acattggaga aaatggctta gtcacataca atattgttga tggagatggt atggaatcgt 1380
ttgaaatcac aacggactat gaaacacagg agggggtgat aaagctgaaa aagcctgtag 1440
attttgaaac caaaagagcc tatagcttga aggtagaggc agccaacgtg cacatcgacc 1500
cgaagtttat cagcaatggc cctttcaagg acactgtgac cgtcaagatc tcagtagaag 1560
atgctgatga gcccccctatg ttcttggccc caagttacat ccacgaagtc caagaaaatg 1620
cagctgctgg caccgtggtt gggagagtgc atgccaaaga ccctgatgct gccaacagcc 1680

cgataaggta ttccatcgat cgtcacactg acctcgacag atttttcact attaatccag 1740
aggatggttt tattaaaact acaaaacctc tggatagaga ggaaacagcc tggctcaaca 1800
tcactgtctt tgcagcagaa atccacaatc ggcatcagga agccaaagtc ccagtggcca 1860
ttagggtcct tgatgtcaac gataatgctc ccaagtttgc tgccccttat gaaggtttca 1920
tctgtgagag tgatcagacc aagccacttt ccaaccagcc aattgttaca attagtgcag 1980
atgacaagga tgacacggcc aatggaccaa gatttatctt cagcctaccc cctgaaatca 2040
ttcacaatcc aaatttcaca gtcagagaca accgagataa cacagcaggc gtgtacgccc 2100
ggcgtggagg gttcagtcgg cagaagcagg acttgtacct tctgcccata gtgatcagcg 2160
atggcggcat cccgcccatg agtagcacca acaccctcac catcaaagtc tgcgggtgcg 2220
acgtgaacgg ggcactgctc tcctgcaacg cagaggccta cattctgaac gccggcctga 2280
gcacaggcgc cctgatcgcc atcctcgcct gcatcgtcat tctcctggtc attgtagtat 2340
tgtttgtgac cctgagaagg caaaagaaag aaccactcat tgtctttgag gaagaagatg 2400
tccgtgagaa catcattact tatgatgatg aaggggtgg ggaagaagac acagaagcct 2460
ttgatattgc caccctccag aatcctgatg gtatcaatgg atttatcccc cgcaaagaca 2520
tcaaacctga gtatcagtac atgcctagac ctgggctccg gccagcgccc aacagcgtgg 2580
atgtcgatga cttcatcaac acgagaatac aggaggcaga caatgacccc acggctcctc 2640
cttatgactc cattcaaatc tacggttatg aaggcagggg ctcagtggcc gggtccctga 2700
gctccctaga gtcggccacc acagattcag acttggacta tgattatcta cagaactggg 2760
gacctcgttt taagaaacta gcagatttgt atggttccaa agacactttt gatgacgatt 2820
cttaacaata acgatacaaa tttggcctta agaactgtgt ctggcgttct caagaatcta 2880
gaagatgtgt aaacaggtat ttttttaaat caaggaaagg ctcatttaaa acaggcaaag 2940
ttttacagag aggatacatt taataaaact gcgaggacat caaagtggta aatactgtga 3000
aataccttt ctcacaaaaa ggcaaatatt gaagttgttt atcaacttcg ctagaaaaaa 3060
aaaacacttg gcatacaaaa tatttaagtg aaggagaagt ctaacgctga actgacaatg 3120
aagggaaatt gtttatgtgt tatgaacatc caagtctttc ttctttttta agttgtcaaa 3180
gaagcttcca caaaattaga aaggacaaca gttctgagct gtaatttcgc cttaaactct 3240
ggacactcta tatgtagtgc atttttaaac ttgaaatata taatattcag ccagcttaaa 3300
cccatacaat gtatgtacaa tacaatgtac aattatgtct cttgagcatc aatcttgtta 3360
ctgctgattc ttgtaaatct ttttgcttct actttcatct taaactaata cgtgccagat 3420
ataactgtct tgtttcagtg agagacgccc tatttctatg tcatttttaa tgtatctatt 3480
tgtacaattt taaagttctt attttagtat acgtataaat atcagtattc tgacatgtaa 3540
gaaaatgtta cggcatcaca cttatatttt atgaacattg tactgttgct ttaatatgag 3600
cttcaatata agaagcaatc tttgaaataa aaaaagattt ttttttaaaa aaaa 3654

<210> 15
<211> 983
<212> DNA
<213> Homo sapiens

<400> 15
gtggaattca tggcatctac ttcgtatgac tattgcagag tgcccatgga agacggggat 60
aagcgctgta agcttctgct ggggatagga attctggtgc tcctgatcat cgtgattctg 120
ggggtgccct tgattatctt caccatcaag gccaacagcg aggcctgccg ggacggcctt 180
cgggcagtga tggagtgtcg caatgtcacc catctcctgc aacaagagct gaccgaggcc 240
cagaagggct ttcaggatgt ggaggcccag gccgccacct gcaaccacac tgtgatggcc 300
ctaatggctt ccctggatgc agagaaggcc caaggacaaa agaaagtgga ggagcttgag 360
ggagagatca ctacattaaa ccataagctt caggacgcgt ctgcagaggt ggagcgactg 420
agaagagaaa accaggtctt aagcgtgaga atcgcggaca agaagtacta ccccagctcc 480
caggactcca gctccgctgc ggcgccccag ctgctgattg tgctgctggg cctcagcgct 540
ctgctgcagt gagatcccag gaagctggca catcttggaa ggtccgtcct gctcggcttt 600
tcgcttgaac attcccttga tctcatcagt tctgagcggg tcatggggca acacggttag 660
cggggagagc acggggtagc cggagaaggg cctctggagc aggtctggag gggccatggg 720
gcagtcctgg gtgtggggac acagtcgggt tgacccaggg ctgtctccct ccagagcctc 780
cctccggaca atgagtcccc cctcttgtct cccaccctga gattgggcat ggggtgcggt 840
gtgggggggca tgtgctgcct gttgttatgg gttttttttg cgggggggt tgctttttc 900
tggggtcttt gagctccaaa aaataaacac ttcctttgag ggagagcaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaa 983

<210> 16
<211> 2257
<212> DNA
<213> Homo sapiens

<400> 16
gtgcgatccc gggcccgagg gcatcagacg gcggctgatt agctccggtt tgcatcaccc 60
ggaccggggg attagctccg gtttgcatca cccggaccgg gggccgggcg cgcacgagac 120
tcgcagcgga agtggaggcg gctccgcgcg cgtccgctgc taggacccgg gcagggctgg 180

agctgggctg ggatcccgag ctcggcagca gcgcagcggg ccggcccacc tgctggtgcc 240
ctggaggctc tgagccccgg cggcgcccgg gcccacgcgg aacgacgggg cgagatgcga 300
gccacccctc tagctgctcc tgcgggttcc ctgtccagga agaagcggtt ggagttggat 360
gacaacttag ataccgagcg tcccgtccag aaacgagctc gaagtgggcc ccagcccaga 420
ctgcccccct gcctgttgcc cctgagccca cctactgctc cagatcgtgc aactgctgtg 480
gccactgcct cccgtcttgg gccctatgtc ctcctggagc ccgaggaggg cgggcgggcc 540
taccaggccc tgcactgccc tacaggcact gagtatacct gcaaggtgta ccccgtccag 600
gaagccccgg ccgtgctgga gccctatgcg cggctgcccc cgcacaagca tgtggctcgg 660
cccactgagg tcctggctgg tacccagctc ctctacgcct ttttcactcg gacccatggg 720
gacatgcaca gcctggtgcg aagccgccac cgtatccctg agcctgaggc tgccgtgctc 780
ttccgccaga tggccaccgc cctggcgcac tgtcaccagc acggtctggt cctgcgtgat 840
ctcaagctgt gtcgctttgt cttcgctgac cgtgagagga agaagctggt gctggagaac 900
ctggaggact cctgcgtgct gactgggcca gatgattccc tgtgggacaa gcacgcgtgc 960
ccagcctacg tgggacctga gatactcagc tcacgggcct catactcggg caaggcagcc 1020
gatgtctgga gcctgggcgt ggcgctcttc accatgctgg ccggccacta ccccttccag 1080
gactcggagc ctgtcctgct cttcggcaag atccgccgcg gggcctacgc cttgcctgca 1140
ggcctctcgg cccctgcccg ctgtctggtt cgctgcctcc ttcgtcggga gccagctgaa 1200
cggctcacag ccacaggcat cctcctgcac ccctggctgc gacaggaccc gatgccctta 1260
gccccaaccc gatcccatct ctgggaggct gcccaggtgg tccctgatgg tctggggctg 1320
gacgaagcca gggaagagga gggagacaga gaagtggttc tgtatggcta ggaccaccct 1380
actacacgct cagctgccaa cagtggattg agtttggggg tagctccaag ccttctcctg 1440
cctctgaact gagccaaacc ttcagtgcct tccagaaggg agaaaggcag aagcctgtgt 1500
ggagtgtgct gtgtacacat ctgctttgtt ccacacacat gcagttcctg cttgggtgct 1560
tatcaggtgc caagccctgt tctcggtgct gggagtacag cagtgagcaa aggagacaat 1620
attccctgct cacagagatg acaaactggc atccttgagc tgacaacact tttccatgac 1680
cataggtcac tgtctacact gggtacactt tgtaccagtg tcggcctcca ctgatgctgg 1740
tgctcaggca cctctgtcca aggacaatcc ctttcacaaa caaaccagct gcctttgtat 1800
cttgtacctt ttcagagaaa gggaggtatc cctgtgccaa aggctccagg cctctccccc 1860
gcaactcagg acccaagccc agctcactct gggaactgtg ttcccagcat ctctgtcctc 1920
ttgattaaga gattctcctt ccaggcctaa gcctgggatt tgggccagag ataagaatcc 1980
aaactatgag gctagttctt gtctaactca agactgttct ggaatgaggg tccaggcctg 2040
tcaaccatgg ggcttctgac ctgagcacca aggttgaggg acaggattag gcagggtctg 2100
tcctgtggcc acctggaaag tcccaggtgg gactcttctg gggacacttg gggtccacaa 2160
tcccaggtcc atactctagg ttttggatac catgagtatg tatgtttacc tgtgcctaat 2220
aaaggagaat tatgaaataa aaaaaaaaaa aaaaaaa 2257

<210> 17
<211> 5784
<212> DNA
<213> Homo sapiens

<400> 17
acggcatcca gtacagaggg gctggacttg gacccctgca gcagccctgc acaggagaag 60
cggcatataa agccgcgctg cccgggagcc gctcggccac gtccaccgga gcatcctgca 120
ctgcagggcc ggtctctcgc tccagcagag cctgcgcctt tctgactcgg tccggaacac 180
tgaaaccagt catcactgca tctttttggc aaaccaggag ctcagctgca ggaggcagga 240
tggtctggag gctggtcctg ctggctctgt gggtgtggcc cagcacgcaa gctggtcacc 300
aggacaaaga cacgaccttc gacctttta gtatcagcaa catcaaccgc aagaccattg 360
gcgccaagca gttccgcggg cccgaccccg gcgtgccggc ttaccgcttc gtgcgctttg 420
actacatccc accggtgaac gcagatgacc tcagcaagat caccaagatc atgcggcaga 480
aggagggctt cttcctcacg gcccagctca agcaggacgg caagtccagg ggcacgctgt 540
tggctctgga gggccccggt ctctcccaga ggcagttcga gatcgtctcc aacggccccg 600
cggacacgct ggatctcacc tactggattg acggcacccg gcatgtggtc tccctggagg 660
acgtcggcct ggctgactcg cagtggaaga acgtcaccgt gcaggtggct ggcgagacct 720
acagcttgca cgtgggctgc gacctcatag gaccagttgc tctggacgag cccttctacg 780
agcacctgca ggcggaaaag agccggatgt acgtggccaa aggctctgcc agagagagtc 840
acttcagggg tttgcttcag aacgtccacc tagtgtttga aaactctgtg gaagatattc 900
taagcaagaa gggttgccag caaggccagg gagctgagat caacgccatc agtgagaaca 960
cagagacgct gcgcctgggt ccgcatgtca ccaccgagta cgtgggcccc agctcggaga 1020
ggaggcccga ggtgtgcgaa cgctcgtgcg aggagctggg aaacatggtc caggagctct 1080
cggggctcca cgtcctcgtg aaccagctca gcgagaacct caagagagtg tcgaatgata 1140
accagtttct ctgggagctc attggtggcc ctcctaagac aaggaacatg tcagcttgct 1200
ggcaggatgg ccggttcttt gcggaaaatg aaacgtgggt ggtggacagc tgcaccacgt 1260
gtacctgcaa gaaatttaaa accatttgcc accaaatcac ctgcccgcct gcaacctgcg 1320
ccagtccatc ctttgtggaa ggcgaatgct gcccttcctg cctccactcg gtggacggtg 1380
aggagggctg gtctccgtgg gcagagtgga cccagtgctc cgtgacgtgt ggctctggga 1440
cccagcagag aggccggtcc tgtgacgtca ccagcaacac ctgcttgggg ccctcgatcc 1500

agacacgggc ttgcagtctg agcaagtgtg acacccgcat ccggcaggac ggcggctgga 1560
gccactggtc accttggtct tcatgctctg tgacctgtgg agttggcaat atcacacgca 1620
tccgtctctg caactcccca gtgccccaga tgggggcaa gaattgcaaa gggagtggcc 1680
gggagaccaa agcctgccag ggcgccccat gcccaatcga tggccgctgg agcccctggt 1740
ccccgtggtc ggcctgcact gtcacctgtg ccggtgggat ccgggagcgc acccgggtct 1800
gcaacagccc tgagcctcag tacggaggga aggcctgcgt gggggatgtg caggagcgtc 1860
agatgtgcaa caagaggagc tgccccgtgg atggctgttt atccaacccc tgcttcccgg 1920
gagcccagtg cagcagcttc cccgatgggt cctggtcatg cggcttctgc cctgtgggct 1980
tcttgggcaa tggcacccac tgtgaggacc tggacgagtg tgccctggtc cccgacatct 2040
gcttctccac cagcaaggtg cctcgctgtg tcaacactca gcctggcttc cactgcctgc 2100
cctgcccgcc ccgatacaga gggaaccagc ccgtcggggt cggcctggaa gcagccaaga 2160
cggaaaagca agtgtgtgag cccgaaaacc catgcaagga caagacacac aactgccaca 2220
agcacgcgga gtgcatctac ctgggtcact tcagcgaccc catgtacaag tgcgagtgcc 2280
agacaggcta cgcgggcgac gggctcatct gcggggagga ctcggacctg gacggctggc 2340
ccaacctcaa tctggtctgc gccaccaacg ccacctacca ctgcatcaag gataactgcc 2400
cccatctgcc aaattctggg caggaagact ttgacaagga cgggattggc gatgcctgtg 2460
atgatgacga tgacaatgac ggtgtgaccg atgagaagga caactgccag ctcctcttca 2520
atccccgcca ggctgactat gacaaggatg aggttgggga ccgctgtgac aactgcccct 2580
acgtgcacaa ccctgcccag atcgacacag acaacaatgg agagggtgac gcctgctccg 2640
tggacattga tggggacgat gtcttcaatg aacgagacaa ttgtccctac gtctacaaca 2700
ctgaccagag ggacacggat ggtgacggtg tgggggatca ctgtgacaac tgccccctgg 2760
tgcacaaccc tgaccagacc gacgtggaca atgaccttgt tggggaccag tgtgacaaca 2820
acgaggacat agatgacgac ggccaccaga acaaccagga caactgcccc tacatctcca 2880
acgccaacca ggctgaccat gacagagacg gccagggcga cgcctgtgac cctgatgatg 2940
acaacgatgg cgtccccgat gacagggaca actgccggct tgtgttcaac ccagaccagg 3000
aggacttgga cggtgatgga cggggtgata tttgtaaaga tgattttgac aatgacaaca 3060
tcccagatat tgatgatgtg tgtcctgaaa acaatgccat cagtgagaca gacttcagga 3120
acttccagat ggtccccttg gatcccaaag ggaccaccca aattgatccc aactgggtca 3180
ttcgccatca aggcaaggag ctggttcaga cagccaactc ggaccccggc atcgctgtag 3240
gttttgacga gtttgggtct gtggacttca gtggcacatt ctacgtaaac actgaccggg 3300
acgacgacta tgctggcttc gtctttggtt accagtcaag cagccgcttc tatgtggtga 3360
tgtggaagca ggtgacgcag acctactggg aggaccagcc cacgcgggcc tatggctact 3420
ccggcgtgtc cctcaaggtg gtgaactcca ccacggggac gggcgagcac ctgaggaacg 3480
cgctgtggca cacggggaac acgccggggc aggtgcgaac cttatggcac gaccccagga 3540
acattggctg gaaggactac acggcctata ggtggcacct gactcacagg cccaagaccg 3600
gctacatcag agtcttagtg catgaaggaa aacaggtcat ggcagactca ggacctatct 3660
atgaccaaac ctacgctggc gggcggctgg gtctatttgt cttctctcaa gaaatggtct 3720
atttctcaga cctcaagtac gaatgcagag atatttaaac aagatttgct gcatttccgg 3780
caatgccctg tgcatgccat ggtccctaga cacctcagtt cattgtggtc cttgcggctt 3840
ctctctctag cagcacctcc tgtcccttga ccttaactct gatggttctt cacctcctgc 3900
cagcaacccc aaacccaagt gccttcagag gataaatatc aatggaactc agagatgaac 3960
atctaaccca ctagaggaaa ccagtttggt gatatatgag actttatgtg gagtgaaaat 4020
tgggcatgcc attacattgc tttttcttgt ttgtttaaaa agaatgacgt ttacatataa 4080
aatgtaatta cttattgtat ttatgtgtat atggagttga agggaatact gtgcataagc 4140
cattatgata aattaagcat gaaaaatatt gctgaactac ttttggtgct taaagttgtc 4200
actattcttg aattagagtt gctctacaat gacacacaaa tcccgctaaa taaattataa 4260
acaagggtca attcaaattt gaagtaatgt tttagtaagg agagattaga agacaacagg 4320
catagcaaat gacataagct accgattaac taatcggaac atgtaaaaca gttacaaaaa 4380
taaacgaact ctcctcttgt cctacaatga aagccctcat gtgcagtaga gatgcagttt 4440
catcaaagaa caaacatcct tgcaaatggg tgtgacgcgg ttccagatgt ggatttggca 4500
aaacctcatt taagtaaaag gttagcagag caaagtgcgg tgctttagct gctgcttgtg 4560
ccgttgtggc gtcggggagg ctcctgcctg agcttccttc cccagctttg ctgcctgaga 4620
ggaaccagag cagacgcaca ggccggaaaa ggcgcatcta acgcgtatct aggctttggt 4680
aactgcggac aagttgcttt tacctgattt gatgatacat ttcattaagg ttccagttat 4740
aaatattttg ttaatattta ttaagtgact atagaatgca actccattta ccagtaactt 4800
attttaaata tgcctagtaa cacatatgta gtataatttc tagaaacaaa catctaataa 4860
gtatataatc ctgtgaaaat atgaggcttg ataatattag gttgtcacga tgaagcatgc 4920
tagaagctgt aacagaatac atagagaata atgaggagtt tatgatggaa ccttaatata 4980
taatgttgcc agcgatttta gttcaatatt tgttactgtt atctatctgc tgtatatgga 5040
attcttttaa ttcaaacgct gaaaacgaat cagcatttag tcttgccagg cacacccaat 5100
aatcagtcat gtgtaatatg cacaagtttg tttttgtttt tgtttttttt gttggttggt 5160
ttttttgctt taagttgcat gatctttctg caggaaatag tcactcatcc cactccacat 5220
aaggggttta gtaagagaag tctgtctgtc tgatgatgga taggggcaa atctttttcc 5280
cctttctgtt aatagtcatc acatttctat gccaaacagg aacgatccat aactttagtc 5340
ttaatgtaca cattgcattt tgataaaatt aattttgttg tttcctttga ggttgatcgt 5400
tgtgttgttt tgctgcactt tttacttttt tgcgtgtgga gctgtattcc cgagacaacg 5460
aagcgttggg atacttcatt aaatgtagcg actgtcaaca gcgtgcaggt tttctgtttc 5520

tgtgttgtgg ggtcaaccgt acaatggtgt gggaatgacg atgatgtgaa tatttagaat 5580
gtaccatatt ttttgtaaat tatttatgtt tttctaaaca aatttatcgt ataggttgat 5640
gaaacgtcat gtgttttgcc aaagactgta aatatttatt tatgtgttca catggtcaaa 5700
atttcaccac tgaaaccctg cacttagcta gaacctcatt tttaaagatt aacaacagga 5760
aataaattgt aaaaaaggtt ttct 5784

<210> 18
<211> 841
<212> DNA
<213> Homo sapiens

<400> 18
gaaccgttta ctcgctgctg tgcccatcta tcagcaggct ccgggctgaa gattgcttct 60
cttctctcct ccaaggtcta gtgacggagc ccgcgcgcgg cgccaccatg cggcagaagg 120
cggtatcgct tttcttgtgc tacctgctgc tcttcacttg cagtggggtg gaggcaggtg 180
agaatgcggg taaggatgca ggtaagaaaa agtgctcgga gagctcggac agcggctccg 240
ggttctggaa ggccctgacc ttcatggccg tcggaggagg actcgcagtc gccgggctgc 300
ccgcgctggg cttcaccggc gccggcatcg cggccaactc ggtggctgcc tcgctgatga 360
gctggtctgc gatcctgaat gggggcggcg tgcccgccgg ggggctagtg gccacgctgc 420
agagcctcgg ggctggtggc agcagcgtcg tcataggtaa tattggtgcc ctgatgggct 480
acgccaccca caagtatctc gatagtgagg aggatgagga gtagccagca gctcccagaa 540
cctcttcttc cttcttggcc taactcttcc agttaggatc tagaactttg cctttttttt 600
ttttttttt ttttttgag atgggttctc actatattgt ccaggctaga gtgcagtggc 660
tattcacaga tgcgaacata gtacactgca gcctccaact cctagcctca agtgatcctc 720
ctgtctcaac ctcccaagta ggattacaag catgcgccga cgatgcccag aatccagaac 780
tttgtctatc actctcccca acaacctaga tgtgaaaaca gaataaactt cacccagaaa 840
a 841

<210> 19
<211> 555
<212> DNA
<213> Homo sapiens

<400> 19
atgagccgca cagcctacac ggtgggagcc ctgcttctcc tcttggggac cctgctgccg 60
gctgctgaag ggaaaaagaa agggtcccaa ggtgccatcc ccccgccaga caaggcccag 120
cacaatgact cagagcagac tcagtcgccc cagcagcctg gctccaggaa ccgggggcgg 180
ggccaagggc ggggcactgc catgcccggg gaggaggtgc tggagtccag ccaagaggcc 240
ctgcatgtga cggagcgcaa atacctgaag cgagactggt gcaaaaccca gccgcttaag 300
cagaccatcc acgaggaagg ctgcaacagt cgcaccatca tcaaccgctt ctgttacggc 360
cagtgcaact ctttctacat ccccaggcac atccggaagg aggaaggttc ctttcagtcc 420
tgctccttct gcaagcccaa gaaattcact accatgatgg tcacactcaa ctgccctgaa 480
ctacagccac ctaccaagaa gaagagagtc acacgtgtga agcagtgtcg ttgcatatcc 540
atcgatttgg attaa 555

<210> 20
<211> 2334
<212> DNA
<213> Homo sapiens

<400> 20
agacacctct gccctcacca tgagcctctg gcagcccctg gtcctggtgc tcctggtgct 60
gggctgctgc tttgctgccc ccagacagcg ccagtccacc cttgtgctct tccctggaga 120
cctgagaacc aatctcaccg acaggcagct ggcagaggaa tacctgtacc gctatggtta 180
cactcgggtg gcagagatgc gtggagagtc gaaatctctg gggcctgcgc tgctgcttct 240
ccagaagcaa ctgtccctgc ccgagaccgg tgagctggat agcgccacgc tgaaggccat 300
gcgaacccca cggtgcgggg tcccagacct gggcagattc caaacctttg agggcgacct 360
caagtggcac caccacaaca tcacctattg gatccaaaac tactcggaag acttgccgcg 420
ggcggtgatt gacgacgcct ttgcccgcgc cttcgcactg tggagcgcgg tgacgccgct 480
caccttcact cgcgtgtaca gccgggacgc agacatcgtc atccagtttg gtgtcgcgga 540
gcacggagac gggtatccct tcgacgggaa ggacgggctc ctggcacacg cctttcctcc 600
tggccccggc attcagggag acgcccattt cgacgatgac gagttgtggt ccctgggcaa 660
gggcgtcgtg gttccaactc ggtttggaaa cgcagatggc gcggcctgcc acttcccctt 720
catcttcgag ggccgctcct actctgcctg caccaccgac ggtcgctccg acggcttgcc 780
ctggtgcagt accacggcca actacgacac cgacgaccgg tttggcttct gccccagcga 840
gagactctac acccgggacg gcaatgctga tgggaaaccc tgccagtttc cattcatctt 900
ccaaggccaa tcctactccg cctgcaccac ggacggtcgc tccgacggct accgctggtg 960

cgccaccacc gccaactacg accgggacaa gctcttcggc ttctgcccga cccgagctga 1020
ctcgacggtg atgggggca actcggcggg ggagctgtgc gtcttccct tcactttcct 1080
gggtaaggag tactcgacct gtaccagcga gggccgcgga gatgggcgcc tctggtgcgc 1140
taccacctcg aactttgaca gcgacaagaa gtggggcttc tgcccggacc aaggatacag 1200
tttgttcctc gtggcggcgc atgagttcgg ccacgcgctg ggcttagatc attcctcagt 1260
gccggaggcg ctcatgtacc ctatgtaccg cttcactgag gggccccct tgcataagga 1320
cgacgtgaat ggcatccggc acctctatgg tcctcgccct gaacctgagc cacggcctcc 1380
aaccaccacc acaccgcagc ccacggctcc cccgacggtc tgccccaccg gacccccac 1440
tgtccacccc tcagagcgcc ccacagctgg ccccacaggt ccccctcag ctggccccac 1500
aggtcccccc actgctggcc cttctacggc cactactgtg cctttgagtc cggtggacga 1560
tgcctgcaac gtgaacatct tcgacgccat cgcggagatt gggaaccagc tgtatttgtt 1620
caaggatggg aagtactggc gattctctga gggcaggggg agccggccgc agggcccctt 1680
ccttatcgcc gacaagtggc ccgcgctgcc ccgcaagctg gactcggtct ttgaggagcc 1740
gctctccaag aagcttttct tcttctctgg gcgccaggtg tgggtgtaca caggcgcgtc 1800
ggtgctgggc ccgaggcgtc tggacaagct gggcctggga gccgacgtgg cccaggtgac 1860
cggggccctc cggagtggca gggggaagat gctgctgttc agcgggcggc gcctctggag 1920
gttcgacgtg aaggcgcaga tggtggatcc ccggagcgcc agcgaggtgg accggatgtt 1980
ccccggggtg cctttggaca cgcacgacgt cttccagtac cgagagaaag cctatttctg 2040
ccaggaccgc ttctactggc gcgtgagttc ccggagtgag ttgaaccagg tggaccaagt 2100
gggctacgtg acctatgaca tcctgcagtg ccctgaggac tagggctccc gtcctgcttt 2160
gcagtgccat gtaaatcccc actgggacca accctgggga aggagccagt ttgccggata 2220
caaactggta ttctgttctg gaggaaaggg aggagtggag gtgggctggg ccctctcttc 2280
tcacctttgt tttttgttgg agtgtttcta ataaacttgg attctctaac cttt 2334

<210> 21
<211> 921
<212> DNA
<213> Homo sapiens

<400> 21
ccctcggacg gccccggagg atgctgctga gccccggcac tgcctggctg cgagcacatg 60
atggcgatac gggagctcaa agtgtgcctt ctcggggaca ctggggttgg gaaatcaagc 120
atcgtgtgtc gatttgtcca ggatcacttt gaccacaaca tcagccctac tattggggca 180
tcttttatga ccaaaactgt gccttgtgga aatgaacttc acaagttcct catctgggac 240
actgctggtc aggaacggtt tcattcattg gctcccatgt actatcgagg ctcagctgca 300
gctgttatcg tgtatgatat taccaagcag gattcatttt ataccttgaa gaaatgggtc 360
aaggagctga aagaacatgg tccagaaaac attgtaatgg ccatcgctgg aaacaagtgc 420
gacctctcag atattaggga ggttcccctg aaggatgcta aggaatacgc tgaatccata 480
ggtgccatcg tggttgagac aagtgcaaaa aatgctatta atatcgaaga gctctttcaa 540
ggaatcagcc gccagatccc acccttggac ccccatgaaa atggaaacaa tggaacaatc 600
aaagttgaga agccaaccat gcaagccagc cgccggtgct gttgacccaa gggcgtggtc 660
cacggtactt gaagaagcca gagcccacat cctgtgcact gctgaaggac cctacgctcg 720
gtggcctggc acctcacttt gagaagagtg agcacactgg ctttgcatcc tggaaggcct 780
gcaggggcg gggcaggaaa tgtacctgaa aaggatttta gaaaaccctg ggaaacccac 840
cacaccacca caaaatggcc tttagtgtat gaaatgcaca tggaggggat gtagttgcat 900
ttttgctaaa aaaaaaaaaa a 921

<210> 22
<211> 345
<212> DNA
<213> Homo sapiens

<400> 22
atgtcggccc tcagcctcct cattctgggc ctgctcacgg cagtgccacc tgccagctgt 60
cagcaaggcc tggggaacct tcagccctgg atgcagggcc ttatcgcggt ggccgtgttc 120
ctggtcctcg ttgcaatcgc ctttgcagtc aaccacttct ggtgccagga ggagccggag 180
cctgcacaca tgatcctgac cgtcggaaac aaggcagatg gagtcctggt gggaacagat 240
ggaaggtact cttcgatggc ggccagtttc aggtccagtg agcatgagaa tgcctatgag 300
aatgtgcccg aggaggaagg caaggtccgc agcaccccga tgtaa 345

<210> 23
<211> 1499
<212> DNA
<213> Homo sapiens

<400> 23
tatttacttc ctgcgggtgc acaggctgtg gtcgtctatc tccctgttgt tcttcccatc 60

ggcgaagatg gccctggaga cggtgccgaa ggacctgcgg catctgcggg cctgtttgct 120
gtgttcgctg gtcaagacta tagaccagtt tgaatatgat ggttgtgaca attgtgatgc 180
atatctacaa atgaagggta accgagagat ggtatatgac tgcactagct cttcctttga 240
tggaatcatt gcgatgatga gtccagagga cagctgggtc tccaagtggc agcgagtcag 300
taactttaag ccaggtgtat atgcggtgtc agtcactggt cgcctgcccc aaggaatcgt 360
gcgggagctg aaaagtcgag gagtggccta caaatccaga gacacagcta taaagaccta 420
gcaagatgca aggctgccag catctttgct ctccacctcc tgcctctgct tatttcttgt 480
tctggaacta aatgaacaga acttcaaata cttcctaccc tccaattcag actcagctga 540
ctgttgagag agcagcacat cattttatca ttttatcttc tttggactac aggtggggtg 600
ggagggattt gggttggtgg attaacagat ggaattgagg agagagtagg atgctgattt 660
tcctacccgt ggcccaggtc tgtgccttcc ccatgccaag gactctaggt caaatgtcaa 720
taaatatgaa cctcgagaaa gttctgaagg ccatgacacc tgccttgcct ccctcttcca 780
ttctcttagg cacagtaata gcttatttgc cctataagaa ccttcccaga gcagcagagg 840
cccttctact ccctcttgac tgtctcagcc tctgggattg cagcctttgt agtgtgcttc 900
cttgcttcct atcagagggt gctgatccag aggctcagta accccatcaa cttggtggcc 960
ctggtgtctc acacttgtat ccttctgccc tcgagacctg gcacagcagt atcccttgaa 1020
gaaatcctga ggctttgtag agtgctcctt gaccatgttt aataattctt ccctcccctg 1080
cttgtctatt ttcttctctt cacggctctt cctatacctt aggccagtct caagcactca 1140
ctggagaccc ttgggccttg ggcgaccatt gagtcctagt ctcccttgtt tgtgcccctg 1200
taggaggtag gtccttttct cctccggcct agtaggggac cttgggtaac atcccatttt 1260
tcggccaagg tgagttgttt taggataaaa aaatttacca caaattctca tttaaatttc 1320
cacagaaatc ctgttcgtat ccccattttg atttccctaa gttccttgtt ctccctctaa 1380
aaagagaatg attgcaccct gcctgtttac ctcaggattg ttgtgattgt agaaacgaag 1440
ctatgtgaaa attatataag tattataaag gtgaaatact tttgctctca aaaaaaaaa 1499

<210> 24
<211> 946
<212> DNA
<213> Homo sapiens

<400> 24
ggaaacccaa gaggaaatga ctgagcccgt ctgggtcccc gcccgctcgc gctcccctgg 60
ccacaccctc cgcctggacg cagcagccac cgccgcgtcc ctctctccac gaggctgccg 120
gcttaggacc cccagctccg acatgtcgcc ctctggtcgc ctgtgtcttc tcaccatcgt 180
tggcctgatt ctccccacca gaggacagac gttgaaagat accacgtcca gttcttcagc 240
agactcaact atcatggaca ttcaggtccc gacacgagcc ccagatgcag tctacacaga 300
actccagccc acctctccaa ccccaacctg gcctgctgat gaaacaccac aaccccagac 360
ccagacccag caactggaag gaacggatgg gcctctagtg acagatccag agacacacaa 420
gagcaccaaa gcagctcatc ccactgatga caccacgacg ctctctgaga gaccatcccc 480
aagcacagac gtccagacag acccccagac cctcaagcca tctggttttc atgaggatga 540
ccccttcttc tatgatgaac acaccctccg gaaacggggg ctgttggtcg cagctgtgct 600
gttcatcaca ggcatcatca tcctcaccag tggcaagtgc aggcagctgt cccggttatg 660
ccggaatcgt tgcaggtgag tccatcagaa acaggagctg acaacctgct gggcacccga 720
agaccaagcc ccctgccagc tcaccgtgcc cagcctcctg catcccctcg aagagcctgg 780
ccagagaggg aagacacaga tgatgaagct ggagccaggg ctgccggtcc gagtctccta 840
cctcccccaa ccctgcccgc ccctgaaggc tacctggcgc cttgggggct gtccctcaag 900
ttatctcctc tgctaagaca aaaagtaaag cactgtggtc tttgcc 946

<210> 25
<211> 11185
<212> DNA
<213> Homo sapiens

<400> 25
gctgccccga gcctttctgg ggaagaactc caggcgtgcg gacgcaacag ccgagaacat 60
taggtgttgt ggacaggagc tgggaccaag atcttcggcc agccccgcat cctcccgcat 120
cttccagcac cgtcccgcac cctccgcatc cttccccggg ccaccacgct tcctatgtga 180
cccgcctggg caacgccgaa cccagtcgcg cagcgctgca gtgaattttc cccccaaact 240
gcaataagcc gccttccaag gccaagatgt tcataaatat aaagagcatc ttatggatgt 300
gttcaacctt aatagtaacc catgcgctac ataaagtcaa agtgggaaaa agcccaccgg 360
tgaggggctc cctctctgga aaagtcagcc taccttgtca tttttcaacg atgcctactt 420
tgccacccag ttacaacacc agtgaatttc tccgcatcaa atggtctaag attgaagtgg 480
acaaaaatgg aaaagatttg aaagagacta ctgtccttgt ggcccaaaat ggaaatatca 540
agattggtca ggactacaaa gggagagtgt ctgtgcccac acatcccgag gctgtgggcg 600
atgcctccct cactgtggtc aagctgctgg caagtgatgc gggtctttac cgctgtgacg 660
tcatgtacgg gattgaagac acacaagaca cggtgtcact gactgtggat ggggttgtgt 720
ttcactacag ggcggcaacc agcaggtaca cactgaattt tgaggctgct cagaaggctt 780

gtttggacgt tggggcagtc atagcaactc cagagcagct ctttgctgcc tatgaagatg 840
gatttgagca gtgtgacgca ggctggctgg ctgatcagac tgtcagatat cccatccggg 900
ctcccagagt aggctgttat ggagataaga tgggaaaggc aggagtcagg acttatggat 960
tccgttctcc ccaggaaact tacgatgtgt attgttatgt ggatcatctg gatggtgatg 1020
tgttccacct cactgtcccc agtaaattca ccttcgagga ggctgcaaaa gagtgtgaaa 1080
accaggatgc caggctggca acagtggggg aactccaggc ggcatggagg aacggctttg 1140
accagtgcga ttacgggtgg ctgtcggatg ccagcgtgcg ccaccctgtg actgtggcca 1200
gggcccagtg tggaggtggt ctacttgggg tgagaaccct gtatcgtttt gagaaccaga 1260
caggcttccc tccccctgat agcagatttg atgcctactg ctttaaacct aaagaggcta 1320
caaccatcga tttgagtatc ctcgcagaaa ctgcatcacc cagtttatcc aaagaaccac 1380
aaatggtttc tgatagaact acaccaatca tccctttagt tgatgaatta cctgtcattc 1440
caacagagtt ccctcccgtg ggaaatattg tcagttttga acagaaagcc acagtccaac 1500
ctcaggctat cacagatagt ttagccacca aattacccac acctactggc agtaccaaga 1560
agccctggga tatggatgac tactcacctt ctgcttcagg acctcttgga aagctagaca 1620
tatcagaaat taaggaagaa gtgctccaga gtacaactgg cgtctctcat tatgctacgg 1680
attcatggga tggtgtcgtg gaagataaac aaacacaaga atcggttaca cagattgaac 1740
aaatagaagt gggtcctttg gtaacatcta tggaaatctt aaagcacatt ccttccaagg 1800
aattccctgt aactgaaaca ccattggtaa ctgcaagaat gatcctggaa tccaaaactg 1860
aaaagaaaat ggtaagcact gtttctgaat tggtaaccac aggtcactat ggattcacct 1920
tgggagaaga ggatgatgaa gacagaacac ttacagttgg atctgatgag agcaccttga 1980
tctttgacca aattcctgaa gtcattacgg tgtcaaagac ttcagaagac accatccaca 2040
ctcatttaga agacttggag tcagtctcag catccacaac tgtttcccct ttaattatgc 2100
ctgataataa tggatcatcc atggatgact gggaagagag acaaactagt ggtaggataa 2160
cggaagagtt tcttggcaaa tatctgtcta ctacaccttt tccatcacag catcgtacag 2220
aaatagaatt gtttccttat tctggtgata aaatattagt agagggaatt tccacagtta 2280
tttatccttc tctacaaaca gaaatgacac atagaagaga aagaacagaa acactaatac 2340
cagagatgag aacagatact tatacagatg aaatacaaga agagatcact aaaagtccat 2400
ttatgggaaa aacagaagaa gaagtcttct ctgggatgaa actctctaca tctctctcag 2460
agccaattca tgttacagag tcttctgtgg aaatgaccaa gtcttttgat ttcccaacat 2520
tgataacaaa gttaagtgca gagccaacag aagtaagaga tatggaggaa gactttacag 2580
caactccagg tactacaaaa tatgatgaaa atattacaac agtgcttttg gcccatggta 2640
ctttaagtgt tgaagcagcc actgtatcaa aatggtcatg ggatgaagat aatacaacat 2700
ccaagccttt agagtctaca gaaccttcag cctcttcaaa attgcccccc gccttactca 2760
caactgtggg gatgaatgga aaggataaag acatcccaag tttcactgaa gatggagcag 2820
atgaatttac tcttattcca gatagtactc aaaagcagtt agaggaggtt actgatgaag 2880
acatagcagc ccatggaaaa ttcacaatta gatttcagcc aactacatca actggtattg 2940
cagaaaagtc aactttgaga gattctacaa ctgaagaaaa agttccacct atcacaagca 3000
ctgaaggcca agtttatgca accatggaag gaagtgcttt gggtgaagta gaagatgtgg 3060
acctctctaa gccagtatct actgttcccc aatttgcaca cacttcagag gtggaaggat 3120
tagcatttgt tagttatagt agcacccaag agcctactac ttatgtagac tcttcccata 3180
ccattcctct ttctgtaatt cccaagacag actggggagt gttagtacct tctgttccat 3240
cagaagatga agttctaggt gaaccctctc aagacatact tgtcattgat cagactcgcc 3300
ttgaagcgac tatttctcca gaaactatga gaacaacaaa aatcacagag ggaacaactc 3360
aggaagaatt cccttggaaa gaacagactg cagagaaacc agttcctgct ctcagttcta 3420
cagcttggac tcccaaggag gcagtaacac cactggatga acaagagggc gatggatcag 3480
catatacagt ctctgaagat gaattgttga caggttctga gagggtccca gttttagaaa 3540
caactccagt tggaaaaatt gatcacagtg tgtcttatcc accaggtgct gtaactgagc 3600
acaaagtgaa aacagatgaa gtggtaacac taacaccacg cattgggcca aaagtatctt 3660
taagtccagg gcctgaacaa aaatatgaaa cagaaggtag tagtacaaca ggatttacat 3720
catctttgag tccttttagt acccacatta cccagcttat ggaagaaacc actactgaga 3780
aaacatccct agaggatatt gatttaggct caggattatt tgaaaagccc aaagccacag 3840
aactcataga attttcaaca atcaaagtca cagttccaag tgatattacc actgccttca 3900
gttcagtaga cagacttcac acaacttcag cattcaagcc atcttccgcg atcactaaga 3960
aaccacctct catcgacagg gaacctggtg aagaaacaac cagtgacatg gtaatcattg 4020
gagaatcaac atctcatgtt cctcccacta cccttgaaga tattgtagcc aaggaaacag 4080
aaaccgatat tgatagagag tatttcacga cttcaagtcc tcctgctaca cagccaacaa 4140
gaccacccac tgtggaagac aaagaggcct ttggacctca ggcgctttct acgccacagc 4200
ccccagcaag cacaaaattt caccctgaca ttaatgttta tattattgag gtcagagaaa 4260
ataagacagg tcgaatgagt gatttgagtg taattggtca tccaatagat tcagaatcta 4320
aagaagatga accttgtagt gaagaaacag atccagtgca tgatctaatg gctgaaattt 4380
tacctgaatt ccctgacata attgaaatag acctatacca cagtgaagaa aatgaagaag 4440
aagaagaaga gtgtgcaaat gctactgatg tgacaaccac cccatctgtg cagtacataa 4500
atgggaagca tctcgttacc actgtgccca aggacccaga agctgcagaa gctaggcgtg 4560
gccagtttga aagtgttgca ccttctcaga atttctcgga cagctctgaa agtgatactc 4620
atccatttgt aatagccaaa acggaattgt ctactgctgt gcaacctaat gaatctacag 4680
aaacaactga gtcttcttgaa gttacatgga agcctgagac ttaccctgaa acatcagaac 4740
atttttcagg tggtgagcct gatgttttcc ccacagtccc attccatgag gaatttgaaa 4800

gtggaacagc caaaaaaggg gcagaatcag tcacagagag agatactgaa gttggtcatc 4860
aggcacatga acatactgaa cctgtatctc tgtttcctga agagtcttca ggagagattg 4920
ccattgacca agaatctcag aaaatagcct ttgcaagggc tacagaagta acatttggtg 4980
aagaggtaga aaaaagtact tctgtcacat acactcccac tatagttcca agttctgcat 5040
cagcatatgt ttcagaggaa gaagcagtta ccctaatagg aaatccttgg ccagatgacc 5100
tgttgtctac caaagaaagc tgggtagaag caactcctag acaagttgta gagctctcag 5160
ggagttcttc gattccaatt acagaaggct ctggagaagc agaagaagat gaagatacaa 5220
tgttcaccat ggtaactgat ttatcacaga gaaatactac tgatacactc attactttag 5280
acactagcag gataatcaca gaaagctttt ttgaggttcc tgcaaccacc atttatccag 5340
tttctgaaca accttctgca aaagtggtgc ctaccaagtt tgtaagtgaa acagacactt 5400
ctgagtggat ttccagtacc actgttgagg aaaagaaaag gaaggaggag gagggaacta 5460
caggtacggc ttctacattt gaggtatatt catctacaca gagatcggat caattaattt 5520
tacccttga attagaaagt ccaaatgtag ctacatctag tgattcaggt accaggaaaa 5580
gttttatgtc cttgacaaca ccaacacagt ctgaaaggga aatgacagat tctactcctg 5640
tctttacaga aacaaataca ttagaaaatt tgggggcaca gaccactgag cacagcagta 5700
tccatcaacc tggggttcag gaagggctga ccactctccc acgtagtcct gcctctgtct 5760
ttatggagca gggctctgga gaagctgctg ccgacccaga aaccaccact gtttcttcat 5820
tttcattaaa cgtagagtat gcaattcaag ccgaaaagga agtagctggc actttgtctc 5880
cgcatgtgga aactacattc tccactgagc caacaggact ggttttgagt acagtaatgg 5940
acagagtagt tgctgaaaat ataacccaaa catccaggga aatagtgatt tcagagcgat 6000
taggagaacc aaattatggg gcagaaataa ggggcttttc cacaggtttt cctttggagg 6060
aagatttcag tggtgacttt agagaatact caacagtgtc tcatcccata gcaaaagaag 6120
aaacggtaat gatggaaggc tctggagatg cagcatttag ggacacccag acttcaccat 6180
ctacagtacc tacttcagtt cacatcagtc acatatctga ctcagaagga cccagtagca 6240
ccatggtcag cacttcagcc ttcccctggg aagagtttac atcctcagct gagggctcag 6300
gtgagcaact ggtcacagtc agcagctctg ttgttccagt gcttcccagt gctgtgcaaa 6360
agttttctgg tacagcttcc tccattatcg acgaaggatt gggagaagtg ggtactgtca 6420
atgaaattga tagaagatcc accattttac caacagcaga agtggaaggt acgaaagctc 6480
cagtagagaa ggaggaagta aaggtcagtg gcacagtttc aacaaacttt ccccaaacta 6540
tagagccagc caaattatgg tctaggcaag aagtcaaccc tgtaagacaa gaaattgaaa 6600
gtgaaacaac atcagaggaa caaattcaag aagaaaagtc atttgaatcc cctcaaaact 6660
ctcctgcaac agaacaaaca atctttgatt cacagacatt tactgaaact gaactcaaaa 6720
ccacagatta ttctgtacta acaacaaaga aaacttacag tgatgataaa gaaatgaagg 6780
aggaagacac ttctttagtt aacatgtcta ctccagatcc agatgcaaat ggcttggaat 6840
cttacacaac tctccctgaa gctactgaaa agtcacattt tttcttagct actgcattag 6900
taactgaatc tataccagct gaacatgtag tcacagattc accaatcaaa aaggaagaaa 6960
gtacaaaaca ttttccgaaa ggcatgagac caacaattca agagtcagat actgagctct 7020
tattctctgg actgggatca ggagaagaag ttttacctac tctaccaaca gagtcagtga 7080
attttactga agtggaacaa atcaataaca cattatatcc ccacacttct caagtggaaa 7140
gtacctcaag tgacaaaatt gaagacttta acagaatgga aaatgtggca aaagaagttg 7200
gaccactcgt atctcaaaca gacatctttg aaggtagtgg gtcagtaacc agcacaacat 7260
taatagaaat tttaagtgac actggagcag aaggacccac ggtggcacct ctccctttct 7320
ccacggacat cggacatcct caaaatcaga ctgtcaggtg ggcagaagaa atccagacta 7380
gtagaccaca aaccataact gaacaagact ctaacaagaa ttcttcaaca gcagaaatta 7440
acgaaacaac aacctcatct actgattttc tggctagagc ttatggtttt gaaatggcca 7500
aagaatttgt tacatcagca ccaaaaccat ctgacttgta ttatgaacct tctggagaag 7560
gatctggaga agtggatatt gttgattcat ttcacacttc tgcaactact caggcaacca 7620
gacaagaaag cagcaccaca tttgtttctg atgggtccct ggaaaaacat cctgaggtgc 7680
caagcgctaa agctgttact gctgatggat tcccaacagt ttcagtgatg ctgcctcttc 7740
attcagagca gaacaaaagc tcccctgatc caactagcac actgtcaaat acagtgtcat 7800
atgagaggtc cacagacggt agtttccaag accgtttcag ggaattcgag gattccacct 7860
taaaacctaa cagaaaaaaa cccactgaaa atattatcat agacctggac aaagaggaca 7920
aggatttaat attgacaatt acagagagta ccatccttga aattctacct gagctgacat 7980
cggataaaaa tactatcata gatattgatc atactaaacc tgtgtatgaa gacattcttg 8040
gaatgcaaac agatatagat acagaggtac catcagaacc acatgacagt aatgatgaaa 8100
gtaatgatga cagcactcaa gttcaagaga tctatgaggc agctgtcaac ctttctttaa 8160
ctgaggaaac atttgagggc tctgctgatg ttctggctag ctacactcag gcaacacatg 8220
atgaatcaat gacttatgaa gatagaagcc aactagatca catgggcttt cacttcacaa 8280
ctgggatccc tgctcctagc acagaaacag aattagacgt tttacttccc acggcaacat 8340
ccctgccaat tcctcgtaag tctgccacag ttattccaga gattgaagga ataaaagctg 8400
aagcaaaagc cctggatgac atgtttgaat caagcacttt gtctgatggt caagctattg 8460
cagaccaaag tgaaataata ccaacattgg gccaatttga aaggactcag gaggagtatg 8520
aagacaaaaa acatgctggt ccttcttttc agccagaatt ctcttcagga gctgaggagg 8580
cattagtaga ccatactccc tatctaagta ttgctactac ccaccttatg gatcagagtg 8640
taacagaggt gcctgatgtg atggaaggat ccaatccccc atattacact gatacaacat 8700
tagcagtttc aacatttgcg aagttgtctt ctcagacacc atcatctccc ctcactatct 8760
actcaggcag tgaagcctct ggacacacag agatccccca gcccagtgct ctgccaggaa 8820

tagacgtcgg ctcatctgta atgtccccac aggattcttt taaggaaatt catgtaaata 8880
ttgaagcaac tttcaaacca tcaagtgagg aataccttca cataactgag cctccctctt 8940
tatctcctga cacaaaatta gaaccttcag aagatgatgg taaacctgag ttattagaag 9000
aaatggaagc ttctcccaca gaacttattg ctgtggaagg aactgagatt ctccaagatt 9060
tccaaaacaa aaccgatggt caagtttctg gagaagcaat caagatgttt cccaccatta 9120
aaacacctga ggctggaact gttattacaa ctgccgatga aattgaatta gaaggtgcta 9180
cacagtggcc acactctact tctgcttctg ccacctatgg ggtcgaggca ggtgtggtgc 9240
cttggctaag tccacagact tctgagaggc ccacgctttc ttcttctcca gaaataaacc 9300
ctgaaactca agcagcttta atcagagggc aggattccac gatagcagca tcagaacagc 9360
aagtggcagc gagaattctt gattccaatg atcaggcaac agtaaaccct gtggaattta 9420
atactgaggt tgcaacacca ccattttccc ttctggagac ttctaatgaa acagatttcc 9480
tgattggcat taatgaagag tcagtggaag gcacggcaat ctatttacca ggacctgatc 9540
gctgcaaaat gaacccgtgc cttaacggag gcacctgtta tcctactgaa acttcctacg 9600
tatgcacctg tgtgccagga tacagcggag accagtgtga acttgatttt gatgaatgtc 9660
actctaatcc ctgtcgtaat ggagccactt gtgttgatgg ttttaacaca ttcaggtgcc 9720
tctgccttcc aagttatgtt ggtgcacttt gtgagcaaga taccgagaca tgtgactatg 9780
gctggcacaa attccaaggg cagtgctaca aatactttgc ccatcgacgc acatgggatg 9840
cagctgaacg ggaatgccgt ctgcagggtg cccatctcac aagcatcctg tctcacgaag 9900
aacaaatgtt tgttaatcgt gtgggccatg attatcagtg gataggcctc aatgacaaga 9960
tgtttgagca tgacttccgt tggactgatg gcagcacact gcaatacgag aattggagac 10020
ccaaccagcc agacagcttc ttttctgctg gagaagactg tgttgtaatc atttggcatg 10080
agaatggcca gtggaatgat gttccctgca attaccatct cacctatacg tgcaagaaag 10140
gaacagttgc ttgcggccag ccccctgttg tagaaaatgc caagaccttt ggaaagatga 10200
aacctcgtta tgaaatcaac tccctgatta gataccactg caaagatggt ttcattcaac 10260
gtcaccttcc aactatccgg tgcttaggaa atggaagatg ggctatacct aaaattacct 10320
gcatgaaccc atctgcatac caaaggactt attctatgaa atactttaaa aattcctcat 10380
cagcaaagga caattcaata aatacatcca aacatgatca tcgttggagc cggaggtggc 10440
aggagtcgag gcgctgatcc ctaaaatggc gaacatgtgt tttcatcatt tcagccaaag 10500
tcctaacttc ctgtgccttt cctatcacct cgagaagtaa ttatcagttg gtttggattt 10560
ttggaccacc gttcagtcat tttgggttgc cgtgctccca aaacatttta aatgaaagta 10620
ttggcattca aaaagacagc agacaaaatg aaagaaaatg agagcagaaa gtaagcattt 10680
ccagcctatc taatttcttt agttttctat ttgcctccag tgcagtccat ttcctaatgt 10740
ataccagcct actgtactat ttaaaatgct caatttcagc accgatggcc atgtaaataa 10800
gatgatttaa tgttgatttt aatcctgtat ataaaataaa aagtcacaat gagtttgggc 10860
atatttaatg atgattatgg agccttagag gtctttaatc attggttcgg ctgcttttat 10920
gtagtttagg ctggaaatgg tttcacttgc tctttgactg tcagcaagac tgaagatggc 10980
ttttcctgga cagctagaaa acacaaaatc ttgtaggtca ttgcacctat ctcagccata 11040
ggtgcagttt gcttctacat gatgctaaag gctgcgaatg ggatcctgat ggaactaagg 11100
actccaatgt cgaactcttc tttgctgcat tccttttttct tcacttacaa gaaaggcctg 11160
aatggaggac ttttctgtaa ccagg 11185

<210> 26
<211> 2245
<212> DNA
<213> Homo sapiens

<400> 26
gaatctcgac ccttgaatgg agttacacga acggccagat gaaagaagga aggcccggac 60
ctccactcag ggccgactag gggactggcg gagggtgcac gctgatggat ttactcaccg 120
ggtgcttgga gctccagcag ctggctggag cccgcgatga cgtcacggac tcgggtcaca 180
tggccgagtc cgccccgccc cctccccgtc cccgccgctg cagccgtcgc cttcggagcg 240
aagggtaccg acccggcaga agctcggagc tctcggggta tcgaggaggc aggcccgcgg 300
gcgcacgggc gagcgggccg ggagccggag cggcggagga gccggcagca gcggcgcggc 360
gggctccagg cgaggcggtc gacgctcctg aaaacttgcg cgcgcgctcg cgccactgcg 420
cccggagcga tgaagatggt cgcgccctgg acgcggttct actccaacag ctgctgcttg 480
tgctgccatg tccgcaccgg caccatcctg ctcggcgtct ggtatctgat catcaatgct 540
gtggtactgt tgattttatt gagtgccctg gctgatccgg atcagtataa cttttcaagt 600
tctgaactgg gaggtgactt tgagttcatg gatgatgcca acatgtgcat tgccattgcg 660
atttctcttc tcatgatcct gatatgtgct atggctactt acggagcgta caagcaacgc 720
gcagcctgga tcatcccatt cttctgttac cagatctttg actttgccct gaacatgttg 780
gttgcaatca ctgtgcttat ttatccaaac tccattcagg aatacatacg gcaactgcct 840
cctaattttc cctacagaga tgatgtcatg tcagtgaatc ctacctgttt ggtccttatt 900
attcttctgt ttattagcat tatcttgact tttaagggtt acttgattag ctgtgtttgg 960
aactgctacc gatacatcaa tggtaggaac tcctctgatg tcctggttta tgttaccagc 1020
aatgacacta cggtgctgct acccccgtat gatgatgcca ctgtgaatgg tgctgccaag 1080
gagccaccgc caccttacgt gtctgcctaa gccttcaagt gggcggagct gagggcagca 1140
gcttgacttt gcagacatct gagcaatagt tctgttattt cacttttgcc atgagcctct 1200

ctgagcttgt ttgttgctga aatgctactt tttaaaattt agatgttaga ttgaaaactg 1260
tagttttcaa catatgcttt gctggaacac tgtgatagat taactgtaga attcttcctg 1320
tacgattggg gatataatgg gcttcactaa ccttccctag gcattgaaac ttcccccaaa 1380
tctgatggac ctagaagtct gcttttgtac ctgctgggcc ccaaagttgg gcatttttct 1440
ctctgttccc tctcttttga aaatgtaaaa taaaaccaaa aatagacaac tttttcttca 1500
gccattccag catagagaac aaaaccttat ggaaacagga atgtcaattg tgtaatcatt 1560
gttctaatta ggtaaataga agtccttatg tatgtgttac aagaatttcc cccacaacat 1620
cctttatgac tgaagttcaa tgacagtttg tgtttggtgg taaaggattt tctccatggc 1680
ctgaattaag accattagaa agcaccaggc cgtgggagca gtgaccatct gctgactgtt 1740
cttgtggatc ttgtgtccag ggacatgggg tgacatgcct cgtatgtgtt agagggtgga 1800
atggatgtgt ttggcgctgc atgggatctg gtgcccctct tctcctggat tcacatcccc 1860
acccagggcc cgcttttact aagtgttctg ccctagattg gttcaaggag gtcatccaac 1920
tgactttatc gagtggaatt gggatatatt tgatatactt ctgcctaaca acatggaaaa 1980
gggttttctt ttccctgcaa gctacatcct actgctttga acttccaagt atgtctagtc 2040
acctttttaaa atgtaaacat tttcagaaaa atgaggattg ccttccttgt atgcgctttt 2100
taccttgact acctgaattg caagggattt ttatatattc atatgttaca aagtcagcaa 2160
ctctcctgtt ggttcattat tgaatgtgct gtaaattaag ttgtttgcaa ttaaaacaag 2220
gtttgcccac aaaaaaaaaa aaaaa 2245

<210> 27
<211> 4912
<212> DNA
<213> Homo sapiens

<400> 27
attggggtct gctctaagct gcagcaagag aaactgtgtg tgaggggaag aggcctgttt 60
cgctgtcggg tctctagttc ttgcacgctc tttaagagtc tgcactggag gaactcctgc 120
cattaccagc tcccttcttg cagaagggag ggggaaacat acatttattc atgccagtct 180
gttgcatgca ggctttttgg cttcctacct tgcaacaaaa taattgcacc aactccttag 240
tgccgattcc gcccacagag agtcctggag ccacagtctt ttttgctttg cattgtagga 300
gagggactaa gtgctagaga ctatgtcgct ttcctgagct accgagagcg ctcgtgaact 360
ggaatcaact gcttcaggga aaaagaaaaa aaaaaaaaaa agacttgcct gggaggccgc 420
gagaaacttg cattggaagc ttcagcaacc agcattcgag aaactcctct ctactttagc 480
acggtctcca gactcagccg agagacagca aactgcagcg cggtgagaga gcgagagaga 540
gggagagaga gactctccag cctgggaact ataactcctc tgcgagaggc ggagaactcc 600
ttccccaaat cttttgggga cttttctctc tttacccacc tccgcccctg cgaggagttg 660
aggggccagt tcggccgccg cgcgcgtctt cccgttcggc gtgtgcttgg cccggggaac 720
cgggagggcc cggcgatcgc gcggcggccg ccgcgagggt gtgagcgcgc gtgggcgccc 780
gccgagccga ggccatggtg cagcaaacca acaatgccga gaacacggaa gcgctgctgg 840
ccggcgagag ctcggactcg ggcgccggcc tcgagctggg aatcgcctcc tcccccacgc 900
ccggctccac cgcctccacg ggcggcaagg ccgacgaccc gagctggtgc aagaccccga 960
gtgggcacat caagcgaccc atgaacgcct tcatggtgtg gtcgcagatc gagcggcgca 1020
agatcatgga gcagtcgccc gacatgcaca acgccgagat ctccaagcgg ctgggcaaac 1080
gctggaagct gctcaaagac agcgacaaga tccctttcat tcgagaggcg gagcggctgc 1140
gcctcaagca catggctgac taccccgact acaagtaccg gcccaggaag aaggtgaagt 1200
ccggcaacgc caactccagc tcctcggccg ccgcctcctc caagccgggg gagaagggag 1260
acaaggtcgg tggcagtggc gggggcggcc atgggggcgg cggcggcggc gggagcagca 1320
acgcgggggg aggaggcggc ggtgcgagtg gcggcggcgc caactccaaa ccggcgcaga 1380
aaaagagctg cggctccaaa gtggcgggcg gcgcgggcgg tggggttagc aaaccgcacg 1440
ccaagctcat cctggcaggc ggcggcggcg gcgggaaagc agcggctgcc gccgccgcct 1500
ccttcgccgc cgaacaggcg ggggccgccg ccctgctgcc cctgggcgcc gccgccgacc 1560
accactcgct gtacaaggcg cggactccca gcgcctcggc ctccgcctcc tcggcagcct 1620
cggcctccgc agcgctcgcg gccccgggca agcacctggc ggagaagaag gtgaagcgcg 1680
tctacctgtt cggcggcctg ggcacgtcgt cgtcgcccgt gggcggcgtg ggcgcgggag 1740
ccgaccccag cgacccccctg ggcctgtacg aggaggaggg cgcgggctgc tcgcccgacg 1800
cgcccagcct gagcggccgc agcagcgccg cctcgtcccc cgccgccggc cgctcgcccg 1860
ccgaccaccg cggctacgcc agcctgcgcg ccgcctcgcc cgccccgtcc agcgcgccct 1920
cgcacgcgtc ctcctcggcc tcgtcccact cctcctcttc ctcctcctcg ggctcctcgt 1980
cctccgacga cgagttcgaa gacgacctgc tcgacctgaa ccccagctca aactttgaga 2040
gcatgtccct gggcagcttc agttcgtcgt cggcgctcga ccgggacctg gattttaact 2100
tcgagcccgg ctccggctcg cacttcgagt tcccggacta ctgcacgccc gaggtgagcg 2160
agatgatctc gggagactgg ctcgagtcca gcatctccaa cctggttttc acctactgaa 2220
gggcgcgcag gcagggagaa gggccggggg gggtaggaga ggagaaaaaa aaagtgaaaa 2280
aaagaaacga aaaggacaga cgaagagttt aaagagaaaa gggaaaaaag aaagaaaaag 2340
taagcagggc tggcttcgcc cgcgttctcg tcgtcggatc aaggagcgcg gcggcgtttt 2400
ggacccgcgc tcccatcccc caccttcccg ggccggggac ccactctgcc cagccggagg 2460
gacgcggagg aggaagaggg tagacagggg cgacctgtga ttgttgttat tgatgttgtt 2520

gttgatggca aaaaaaaaaa agcgacttcg agtttgctcc cctttgcttg aagagacccc 2580
ctcccccttc caacgagctt ccggacttgt ctgcacccca agcaagaagg cgagttagtt 2640
ttctagagac ttgaaggagt ctcccccttc ctgcatcacc accttggttt tgttttattt 2700
tgcttcttgg tcaagaaagg aggggagaac ccagcgcacc cctcccccca ttttttaaa 2760
cgcgtgatga agacagaagg ctccggggtg acgaatttgg ccgatggcag atgttttggg 2820
ggaacgccgg gactgagaga ctccacgcag gcgaattccc gtttggggct ttttttcct 2880
ccctcttttc cccttgcccc ctctgcagcc ggaggaggag atgttgaggg gaggaggcca 2940
gccagtgtga ccggcgctag gaaatgaccc gagaaccccg ttggaagcgc agcagcggga 3000
gctaggggcg ggggcggagg aggacacgaa ctggaagggg gttcacggtc aaactgaaat 3060
ggatttgcac gttggggagc tggcggcggc ggctgctggg cctccgcctt cttttctacg 3120
tgaaatcagt gaggtgagac ttcccagacc ccggaggcgt ggaggagagg agactgtttg 3180
atgtggtaca ggggcagtca gtggagggcg agtggtttcg gaaaaaaaaa aagaaaaaaa 3240
gaaaaaaaaa gaaaaaaaaa agatttttt cttctcttaa tcggaatcgt gatggtgttg 3300
gattatttca atggtggggt taatatagca tgttatcctg tctatctttt aaagatttct 3360
gtataagact gttgagcagt ttttaaaata gtgtaggata atataaaaag cagatagatg 3420
gcgctatgtt tgattcctac aacgaaatta tcaccagctt tttttcattc ttaactcttt 3480
aaaggattca aacgcaactc aaatctgtgc tggactttaa aaaaacaatt caggaccaaa 3540
ttttttctca gtgtgtgtgt ttattcctta taggtgtaaa tgagaagacg tgtttttttc 3600
cttcaccgat gctccatcct cgtatttctt tttccttgta aatgtaatca gatgccattt 3660
tatatgtgga cgtatttata ctggccaaac atatttttc ttttgtccct ttttttcttt 3720
cctttctttt tacttccttt atttctttat tccttccttt tccttttttt cttttttttt 3780
tctttttttt ttttttttt tggtagttgt tgttacccac gccattttac gtctccttca 3840
ctgaagggct agagttttaa cttttaattt tttatattta aatgtagact tttgacactt 3900
ttaaaaaaca aaaaaagaca agagagatga aaacgtttga ttattttctc agtgtatttt 3960
tgtaaaaaat atataaaggg ggtgttaatc ggtgtaaatc gctgtttgga tttcctgatt 4020
ttataacagg gcggctggtt aatatctcac acagtttaaa aaatcagccc ctaatttctc 4080
catgtttaca cttcaatctg caggcttctt aaagtgacag tatcccttaa cctgccacca 4140
gtgtccaccc tccggccccc gtcttgtaaa aaggggagga gaattagcca aacactgtaa 4200
gcttttaaga aaaacaaagt tttaaacgaa atactgctct gtccagaggc tttaaaactg 4260
gtgcaattac agcaaaaagg gattctgtag ctttaacttg taaaccacat ctttttgca 4320
ctttttttat aagcaaaaac gtgccgttta aaccactgga tctatctaaa tgccgatttg 4380
agttcgcgac actatgtact gcgtttttca ttcttgtatt tgactattta atcctttcta 4440
cttgtcgcta aatataattg ttttagtctt atggcatgat gatagcatat gtgttcaggt 4500
ttatagctgt tgtgtttaaa aattgaaaaa agtggaaaac atctttgtac atttaagtct 4560
gtattataat aagcaaaaag attgtgtgta tgtatgttta atataacatg acaggcacta 4620
ggacgtctgc ctttttaagg cagttccgtt aagggttttt gtttttaaac tttttttgc 4680
catccatcct gtgcaatatg ccgtgtagaa tatttgtctt aaaattcaag gccacaaaaa 4740
caatgtttgg gggaaaaaaa agaaaaaatc atgccagcta atcatgtcaa gttcactgcc 4800
tgtcagattg ttgatatata ccttctgtaa ataacttttt ttgagaagga aataaaatca 4860
gctggaactg aaccctaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 4912

<210> 28
<211> 2637
<212> DNA
<213> Homo sapiens

<400> 28
ggcacgaggc ccctgcgtgc ggcgcttctc ccaggcccca ccttccatcc agtgccctgg 60
accctcggct gggtagcgcc accagagcga ccaaacgtcc cgcgccttcc aggccgcact 120
ccagagccaa aagagctcca tggcggcggc ggccaagccc aacaaccttt ccctggtggt 180
gcacggaccg ggggacttgc gcctggagaa ctatcctatc cctgaaccag gcccaaatga 240
ggtcttgctg aggatgcatt ctgttggaat ctgtggctca gatgtccact actgggagta 300
tggtcgaatt gggaatttta ttgtgaaaaa gcccatggtg ctgggacatg aagcttcggg 360
aacagtcgaa aaagtgggat catcggtaaa gcacctaaaa ccaggtgatc gtgttgccat 420
cgagcctggt gctccccgag aaaatgatga attctgcaag atgggccgat acaatctgtc 480
accttccatc ttcttctgtg ccacgccccc cgatgacggg aacctctgcc ggttctataa 540
gcacaatgca gccttttgtt acaagcttcc tgacaatgtc acctttgagg aaggcgccct 600
gatcgagcca ctttctgtgg ggatccatgc ctgcaggaga ggcggagtta ccctgggaca 660
caaggtcctt gtgtgtggag ctgggccaat cgggatggtc actttgctcg tggccaaagc 720
aatgggagca gctcaagtag tggtgactga tctgtctgct acccgattgt ccaaagccaa 780
ggagattggg gctgatttag tcctccagat ctccaaggag agccctcagg aaatcgccag 840
gaaagtagaa ggtcagctgg ggtgcaagcc ggaagtcacc atcgagtgca cgggggcaga 900
ggcctccatc caggcgggca tctacgccac tcgctctggt gggaccctcg tgcttgtggg 960
gctgggctct gagatgacca ccgtacccct actgcatgca gccatccggg aggtggatat 1020
caagggcgtg tttcgatact gcaacacgtg gccagtggcg atttcgatgc ttgcgtccaa 1080
gtctgtgaat gtaaaacccc tcgtcaccca taggtttcct ctggagaaag ctctggaggc 1140
ctttgaaaca tttaaaaagg gattggggtt gaaaatcatg ctcaagtgtg accccagtga 1200

ccagaatccc tgatgttaat gggctctgcc ctcatcccca cagtcttggg atctcagggc 1260
acaatggctg gacatgggtg ggctctgatg cagaactttc tcttttgaat gttaagaata 1320
actaatacaa ttcattgtga acagaagtcc ttaagcagag gaattggtgt gccttaaaga 1380
tacaatctgg gatagtttgg gggaacttgt agccagaatg ccctgttcat gctgagcaaa 1440
gttcagcaag tagagcagag tttggcaggc aggtgccagg aactcccctt cttcctggag 1500
tgccttcatt gaggaaggaa atctggccct tgggtttcct ggttccactg ctactgaccc 1560
agaggggaat gagggctgag ttatgaaaag ataacttcat gaagacttaa ctggcccaga 1620
agctgatttt catgaaaatc tgccactcag ggtctgggat gaaggcttgt cagcacttcc 1680
agtttagaac gcaatgtttc tagagacata ttggctgttt gttttgatga taaaaggaga 1740
ataagaaaag gcatcacttt cctggatcca ggataatttt taaaccaatc aaatgaaaaa 1800
aacaaacaaa caaaaaagga aatgtcatgt gaggttaaac cagtttgcat tcccctaatg 1860
tggaaaaagt aagaggacta ctcagcactg tttgaagatt gcctcttcta cagcttctga 1920
gaattgtgtt atttcacttg ccaagtgaag gacccctcc ccaacatgcc ccagcccacc 1980
cctaagcatg gtcccttgtc accaggcaac caggaaactg ctacttgtgg acctcaccag 2040
agaccaggag ggtttggtta gctcacagga cttcccccac cccagaagat tagcatccca 2100
tactagactc atactcaact caactaggct catactcaat tgatggttat tagacaattc 2160
catttctttc tggttattat aaacagaaaa tctttcctct tctcattacc agtaaaggct 2220
cttggtatct ttctgttgga atgatttcta tgaacttgtc ttattttaat ggtgggtttt 2280
ttttctggta agatttagac ctaaatcgca tcatgccaac ttgtgacttt gagactattc 2340
atcaagaatg aggatatagt agccatgaca tagcttgagc tatagccttt aattccttac 2400
tttggctatg ggtggagggt gagtttgaag aggttctgat tttcttgtaa cctgggaaag 2460
ccatgacctt gtgcccgatt ctttcagatt gctttgggta ataaatattg gtggtggtat 2520
ctgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2580
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2637

<210> 29
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 29
tagaagttta caatgaagtt tcttctaata ctgctcctgc aggccactgc ttctggagct 60
cttcccctga acagctctac aagcctggaa aaaaataatg tgctatttgg tgagagatac 120
ttagaaaaat tttatggcct tgagataaac aaacttccag tgacaaaaat gaaatatagt 180
ggaaacttaa tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc 240
gggcaactgg acacatctac cctggagatg atgcacgcac ctcgatgtgg agtccccgat 300
ctccatcatt tcagggaaat gccaggggcg cccgtatgga ggaaacatta tatcacctac 360
agaatcaata attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa 420
gctttccaag tatggagtaa tgttaccccc ttgaaattca gcaagattaa cacaggcatg 480
gctgacattt tggtggtttt tgcccgtgga gctcatggag acttccatgc ttttgatggc 540
aaaggtggaa tcctagccca tgcttttgga cctggatctg gcattggagg ggatgcacat 600
ttcgatgagg acgaattctg gactacacat tcaggaggca caaacttgtt cctcactgct 660
gttcacgaga ttggccattc cttaggtctt ggccattcta gtgatccaaa ggctgtaatg 720
ttccccacct acaaatatgt cgacatcaac acatttcgcc tctctgctga tgacatacgt 780
ggcattcagt ccctgtatgg agacccaaaa gagaaccaac gcttgccaaa tcctgacaat 840
tcagaaccag ctctctgtga ccccaatttg agttttgatg ctgtcactac cgtgggaaat 900
aagatctttt tcttcaaaga caggttcttc tggctgaagg tttctgagag accaaagacc 960
agtgttaatt taatttcttc cttatggcca accttgccat ctggcattga agctgcttat 1020
gaaattgaag ccagaaatca agtttttctt tttaaagatg acaaatactg gttaattagc 1080
aatttaagac cagagccaaa ttatcccaag agcatacatt cttttggttt tcctaacttt 1140
gtgaaaaaaa ttgatgcagc tgtttttaac ccacgttttt ataggaccta cttctttgta 1200
gataaccagt attggaggta tgatgaaagg agacagatga tggaccctgg ttatcccaaa 1260
ctgattacca agaacttcca aggaatcggg cctaaaattg atgcagtctt ctattctaaa 1320
aacaaatact actatttctt ccaaggatct aaccaatttg aatatgactt cctactccaa 1380
cgtatcacca aaacactgaa aagcaatagc tggtttggtt gttagaaatg gtgtaattaa 1440
tggtttttgt tagttcactt cagcttaata agtatttatt gcatatttgc tatgtcctca 1500
gtgtaccact acttagagat atgtatcata aaaataaaat ctgtaaacca taggtaatga 1560
ttatataaaa tacataatat ttttcaattt tgaaaactct aattgtccat tcttgcttga 1620
ctctactatt aagtttgaaa atagttacct tcaaagcaag ataattctat ttgaagcatg 1680
ctctgtaagt tgcttcctaa catccttgga ctgagaaatt atacttactt ctggcataac 1740
taaaattaag tatatatatt ttggctcaaa taaaattg 1778

<210> 30
<211> 777
<212> DNA
<213> Homo sapiens

<400> 30
ggccccttgt ctgcagagat ggctcccaat gcttcctgcc tctgtgtgca tgtccgttcc 60
gaggaatggg atttaatgac ctttgatgcc aacccatatg acagcgtgaa aaaaatcaaa 120
gaacatgtcc ggtctaagac caaggttcct gtgcaggacc aggttctttt gctgggctcc 180
aagatcttaa agccacggag aagcctctca tcttatggca ttgacaaaga gaagaccatc 240
caccttaccc tgaaagtggt gaagcccagt gatgaggagc tgcccttgtt tcttgtggag 300
tcaggtgatg aggcaaagag gcacctcctc caggtgcgaa ggtccagctc agtggcacaa 360
gtgaaagcaa tgatcgagac taagacgggt ataatccctg agacccagat tgtgacttgc 420
aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggcaac 480
ttactcttcc tggcatctta ttgtattgga gggtgaccac cctggggatg gggtgttggc 540
aggggtcaaa aagcttattt cttttaatct cttactcaac gaacacatct tctgatgatt 600
tcccaaaatt aatgagaatg agatgagtag agtaagattt gggtgggatg ggtaggatga 660
agtatattgc ccaactctat gtttctttga ttctaacaca attaattaag tgacatgatt 720
tttactaatg tattactgag actagtaaat aaatttttaa ggcaaaatag agcattc 777

<210> 31
<211> 9645
<212> DNA
<213> Homo sapiens

<400> 31
atgcccaagc gcgcgcactg gggggccctc tccgtggtgc tgatcctgct ttggggccat 60
ccgcgagtgg cgctggcctg cccgcatcct tgtgcctgct acgtccccag cgaggtccac 120
tgcacgttcc gatccctggc ttccgtgccc gctggcattg ctagacacgt ggaaagaatc 180
aatttggggt ttaatagcat acaggccctg tcagaaacct catttgcagg actgaccaag 240
ttggagctac ttatgattca cggcaatgag atcccaagca tccccgatgg agctttaaga 300
gacctcagct ctcttcaggt tttcaagttc agctacaaca agctgagagt gatcacagga 360
cagaccctcc agggtctctc taacttaatg aggctgcaca ttgaccacaa caagatcgag 420
tttatccacc ctcaagcttt caacggctta acgtctctga ggctactcca tttggaagga 480
aatctcctcc accagctgca ccccagcacc ttctccacgt tcacattttt ggattatttc 540
agactctcca ccataaggca cctctactta gcagagaaca tggttagaac tcttcctgcc 600
agcatgcttc ggaacatgcc gcttctggag aatctttact tgcagggaaa tccgtggacc 660
tgcgattgtg agatgagatg gtttttggaa tgggatgcaa aatccagagg aattctgaag 720
tgtaaaaagg acaaagctta tgaaggcggt cagttgtgtg caatgtgctt cagtccaaag 780
aagttgtaca aacatgagat acacaagctg aaggacatga cttgtctgaa gccttcaata 840
gagtcccctc tgagacagaa caggagcagg agtattgagg aggagcaaga acaggaagag 900
gatggtggca gccagctcat cctggagaaa ttccaactgc cccagtggag catctctttg 960
aatatgaccg acgagcacgg gaacatggtg aacttggtct gtgacatcaa gaaaccaatg 1020
gatgtgtaca agattcactt gaaccaaacg gatcctccag atattgacat aaatgcaaca 1080
gttgccttgg actttgagtg tccaatgacc cgagaaaact atgaaaagct atggaaattg 1140
atagcatact acagtgaagt tcccgtgaag ctacacagag agctcatgct cagcaaagac 1200
cccagagtca gctaccagta caggcaggat gctgatgagg aagctcttta ctacacaggt 1260
gtgagagccc agattcttgc agaaccagaa tgggtcatgc agccatccat agatatccag 1320
ctgaaccgac gtcagagtac ggccaagaag gtgctacttt cctactacac ccagtattct 1380
caaacaatat ccaccaaaga tacaaggcag gctcggggca gaagctgggt aatgattgag 1440
cctagtggag ctgtgcaaag agatcagact gtcctggaag ggggtccatg ccagttgagc 1500
tgcaacgtga aagcttctga gagtccatct atcttctggg tgcttccaga tggctccatc 1560
ctgaaagcgc ccatggatga cccagacagc aagttctcca ttctcagcag tggctggctg 1620
aggatcaagt ccatggagcc atctgactca ggcttgtacc agtgcattgc tcaagtgagg 1680
gatgaaatgg accgcatggt atatagggta cttgtgcagt ctccctccac tcagccagcc 1740
gagaaagaca cagtgacaat tggcaagaac ccaggggagt cggtgacatt gccttgcaat 1800
gctttagcaa tacccgaagc ccaccttagc tggattcttc caaacagaag gataattaat 1860
gatttggcta acacatcaca tgtatacatg ttgccaaatg gaactctttc catcccaaag 1920
gtccaagtca gtgatagtgg ttactacaga tgtgtggctg tcaaccagca aggggcagac 1980
cattttacgg tgggaatcac agtgaccaag aaagggtctg gcttgccatc caaaagaggc 2040
agacgcccag gtgcaaaggc tctttccaga gtcagagaag acatcgtgga ggatgaaggg 2100
ggctcgggca tgggagatga agagaacact tcaaggagac ttctgcatcc aaaggaccaa 2160
gaggtgttcc tcaaaacaaa ggatgatgcc atcaatggag acaagaaagc caagaaaggg 2220
agaagaaagc tgaaactctg gaagcattcg gaaaaagaac cagagaccaa tgttgcagaa 2280
ggtcgcagag tgtttgaatc tagacgaagg ataaacatgg caaacaaaca gattaatccg 2340
gagcgctggg ctgatatttt agccaaagtc cgtgggaaaa atctccctaa gggcacagaa 2400
gtacccccgt tgattaaaac cacaagtcct ccatccttga gcctagaagt cacaccacct 2460
tttcctgctg tttctccccc ctcagcatct cctgtgcaga cagtaaccag tgctgaagaa 2520
tcctcagcag atgtacctct acttggtgaa gaagagcacg ttttgggtac catttcctca 2580
gccagcatgg ggctagaaca caaccacaat ggagttattc ttgttgaacc tgaagtaaca 2640
agcacacctc tggaggaagt tgttgatgac ctttctgaga agactgagga gataacttcc 2700
actgaaggag acctgaaggg gacagcagcc cctacactta tatctgagcc ttatgaacca 2760

tctcctactc tgcacacatt agacacagtc tatgaaaagc ccacccatga agagacggca 2820
acagagggtt ggtctgcagc agatgttgga tcgtcaccag agcccacatc cagtgagtat 2880
gagcctccat tggatgctgt ctccttggct gagtctgagc ccatgcaata ctttgaccca 2940
gatttggaga ctaagtcaca accagatgag gataagatga aagaagacac ctttgcacac 3000
cttactccaa ccccccaccat ctgggttaat gactccagta catcacagtt atttgaggat 3060
tctactatag gggaaccagg tgtcccaggc caatcacatc tacaaggact gacagacaac 3120
atccaccttg tgaaaagtag tctaagcact caagacacct tactgattaa aaagggtatg 3180
aaagagatgt ctcagacact acagggagga aatatgctag agggagaccc cacacactcc 3240
agaagttctg agagtgaggg ccaagagagc aaatccatca ctttgcctga ctccacactg 3300
ggtataatga gcagtatgtc tccagttaag aagcctgcgg aaaccacagt tggtaccctc 3360
ctagacaaag acaccacaac agtaacaaca acaccaaggc aaaaagttgc tccgtcatcc 3420
accatgagca ctcacccttc tcgaaggaga cccaacggga gaaggagatt acgccccaac 3480
aaattccgcc accggcacaa gcaaacccca cccacaactt ttgccccatc agagactttt 3540
tctactcaac caactcaagc acctgacatt aagatttcaa gtcaagtgga gagttctctg 3600
gttcctacag cttgggtgga taacacagtt aatacccccа aacagttgga aatggagaag 3660
aatgcagaac ccacatccaa gggaacacca cggagaaaac acgggaagag gccaaacaaa 3720
catcgatata ccccttctac agtgagctca agagcgtccg gatccaagcc cagcccttct 3780
ccagaaaata aacatagaaa cattgttact cccagttcag aaactatact tttgcctaga 3840
actgtttctc tgaaaactga gggcccttat gattccttag attacatgac aaccaccaga 3900
aaaatatatt catcttaccc taaagtccaa gagacacttc cagtcacata taaacccaca 3960
tcagatggaa aagaaattaa ggatgatgtt gccacaaatg ttgacaaaca taaaagtgac 4020
attttagtca ctggtgaatc aattactaat gccataccaa cttctcgctc cttggtctcc 4080
actatgggag aatttaagga agaatcctct cctgtaggct ttccaggaac tccaacctgg 4140
aatccctcaa ggacggccca gcctgggagg ctacagacag acatacctgt taccacttct 4200
ggggaaaatc ttacagaccc tccccttctt aaagagcttg aggatgtgga tttcacttcc 4260
gagtttttgt cctctttgac agtctccaca ccatttcacc aggaagaagc tggttcttcc 4320
acaactctct caagcataaa agtggaggtg gcttcaagtc aggcagaaac caccaccctt 4380
gatcaagatc atcttgaaac cactgtggct attctccttt ctgaaactag accacagaat 4440
cacaccccta ctgctgcccg gatgaaggag ccagcatcct cgtccccatc cacaattctc 4500
atgtctttgg gacaaaccac caccactaag ccagcacttc ccagtccaag aatatctcaa 4560
gcatctagag attccaagga aaatgttttc ttgaattatg tggggaatcc agaaacagaa 4620
gcaaccccag tcaacaatga aggaacacag catatgtcag ggccaaatga attatcaaca 4680
ccctcttccg accgggatgc atttaacttg tctacaaagc tggaattgga aaagcaagta 4740
tttggtagta ggagtctacc acgtggccca gatagccaac gccaggatgg aagagttcat 4800
gcttctcatc aactaaccag agtccctgcc aaacccatcc taccaacagc aacagtgagg 4860
ctacctgaaa tgtccacaca aagcgcttcc agatactttg taacttccca gtcacctcgt 4920
cactggacca acaaaccgga aataactaca tatccttctg gggctttgcc agagaacaaa 4980
cagtttacaa ctccaagatt atcaagtaca acaattcctc tcccattgca catgtccaaa 5040
cccagcattc ctagtaagtt tactgaccga agaactgacc aattcaatgg ttactccaaa 5100
gtgtttggaa ataacaacat ccctgaggca agaaacccag ttggaaagcc tcccagtcca 5160
agaattcctc attattccaa tggaagactc cctttcttta ccaacaagac tctttctttt 5220
ccacagttgg gagtcacccg gagaccccag atacccactt ctcctgcccc agtaatgaga 5280
gagagaaaag ttattccagg ttcctacaac aggatacatt cccatagcac cttccatctg 5340
gactttggcc ctccggcacc tccgttgttg cacactccgc agaccacggg atcaccctca 5400
actaacttac agaatatccc tatggtctct tccacccaga gttctatctc ctttataaca 5460
tcttctgtcc agtcctcagg aagcttccac cagagcagct caaagttctt tgcaggagga 5520
cctcctgcat ccaaattctg gtctcttggg gaaaagcccc aaatcctcac caagtcccca 5580
cagactgtgt ccgtcaccgc tgagacagac actgtgttcc cctgtgaggc aacaggaaaa 5640
ccaaagcctt tcgttacttg gacaaaggtt tccacaggag ctcttatgac tccgaatacc 5700
aggatacaac ggtttgaggt tctcaagaac ggtaccttag tgatacggaa ggttcaagta 5760
caagatcgag gccagtatat gtgcaccgcc agcaacctgc acggcctgga caggatggtg 5820
gtcttgcttt cggtcaccgt gcagcaacct caaatcctag cctcccacta ccaggacgtc 5880
actgtctacc tgggagacac cattgcaatg gagtgtctgg ccaaagggac cccagccccc 5940
caaatttcct ggatcttccc tgacaggagg gtgtggcaaa ctgtgtcccc cgtggagagc 6000
cgcatcaccc tgcacgaaaa ccggaccctt tccatcaagg aggcgtcctt ctcagacaga 6060
ggcgtctata agtgcgtggc cagcaatgca gccggggcgg acagcctggc catccgcctg 6120
cacgtggcgg cactgccccc cgttatccac caggagaagc tggagaacat ctcgctgccc 6180
ccggggctca gcattcacat tcactgcact gccaaggctg cgcccctgcc cagcgtgcgc 6240
tgggtgctcg gggacggtac ccagatccgc ccctcgcagt tcctccacgg gaacttgttt 6300
gttttcccca acgggacgct ctacatccgc aacctcgcgc ccaaggacag cgggcgctat 6360
gagtgcgtgg ccgccaacct ggtaggctcc gcgcgcagga cggtgcagct gaacgtgcag 6420
cgtgcagcag ccaacgcgcg catcacgggc acctccccgc ggaggacgga cgtcaggtac 6480
ggaggaaccc tcaagctgga ctgcagcgcc tcgggggacc cctggccgcg catcctctgg 6540
aggctgccgt ccaagaggat gatcgacgcg ctcttcagtt ttgatagcag aatcaaggtg 6600
tttgccaatg ggaccctggt ggtgaaatca gtgacggaca aagatgccgg agattacctg 6660
tgcgtagctc gaaataaggt tggtgatgac tacgtggtgc tcaaagtgga tgtggtgatg 6720
aaaccggcca agattgaaca caaggaggag aacgaccaca aagtcttcta cgggggtgac 6780

ctgaaagtgg actgtgtggc caccgggctt cccaatcccg agatctcctg gagcctccca 6840
gacgggagtc tggtgaactc cttcatgcag tcggatgaca gcggtggacg caccaagcgc 6900
tatgtcgtct tcaacaatgg gacactctac tttaacgaag tggggatgag ggaggaagga 6960
gactacacct gctttgctga aaatcaggtc gggaaggacg agatgagagt cagagtcaag 7020
gtggtgacag cgcccgccac catccggaac aagacttact tggcggttca ggtgccctat 7080
ggagacgtgg tcactgtagc ctgtgaggcc aaaggagaac ccatgcccaa ggtgacttgg 7140
ttgtccccaa ccaacaaggt gatccccacc tcctctgaga agtatcagat ataccaagat 7200
ggcactctcc ttattcagaa agcccagcgt tctgacagcg gcaactacac ctgcctggtc 7260
aggaacagcg cgggagagga taggaagacg gtgtggattc acgtcaacgt ccagccaccc 7320
aagatcaacg gtaaccccaa ccccatcacc accgtgcggg agatagcagc cgggggcagt 7380
cggaaactga ttgactgcaa agctgaaggc atccccaccc cgagggtgtt atgggctttt 7440
cccgagggtg tggttctgcc agctccatac tatggaaacc ggatcactgt ccatggcaac 7500
ggttccctgg acatcaggag tttgaggaag agcgactccg tccagctggt atgcatggca 7560
cgcaacgagg gaggggaggc gaggttgatc gtgcagctca ctgtcctgga gcccatggag 7620
aaacccatct tccacgaccc gatcagcgag aagatcacgg ccatggcggg ccacaccatc 7680
agcctcaact gctctgccgc ggggacccca acacccagcc tggtgtgggt ccttcccaat 7740
ggcaccgatc tgcagagtgg acagcagctg cagcgcttct accacaaggc tgacggcatg 7800
ctacacatta gcggtctctc ctcggtggac gctggggcct accgctgcgt ggcccgcaat 7860
gccgctggcc acacggagag gctggtctcc ctgaaggtgg gactgaagcc agaagcaaac 7920
aagcagtatc ataacctggt cagcatcatc aatggtgaga ccctgaagct cccctgcacc 7980
cctcccgggg ctgggcaggg acgtttctcc tggacgctcc ccaatggcat gcatctggag 8040
ggcccccaaa ccctgggacg cgtttctctt ctggacaatg gcaccctcac ggttcgtgag 8100
gcctcggtgt ttgacagggg tacctatgta tgcaggatgg agacggagta cggcccttcg 8160
gtcaccagca tccccgtgat tgtgatcgcc tatcctcccc ggatcaccag cgagcccacc 8220
ccggtcatct acacccggcc cgggaacacc gtgaaactga actgcatggc tatggggatt 8280
cccaaagctg acatcacgtg ggagttaccg gataagtcgc atctgaaggc aggggttcag 8340
gctcgtctgt atggaaacag atttcttcac ccccagggat cactgaccat ccagcatgcc 8400
acacagagag atgccggctt ctacaagtgc atggcaaaaa acattctcgg cagtgactcc 8460
aaaacaactt acatccacgt cttctgaaat gtggattcca gaatgattgc ttaggaactg 8520
acaacaaagc ggggtttgta agggaagcca ggttggggaa taggagctct taaataatgt 8580
gtcacagtgc atggtggcct ctggtgggtt tcaagttgag gttgatcttg atctacaatt 8640
gttgggaaaa ggaagcaatg cagacacgag aaggagggct cagccttgct gagacacttt 8700
cttttgtgtt tacatcatgc caggggcttc attcagggtg tctgtgctct gactgcaatt 8760
tttcttcttt tgcaaatgcc actcgactgc cttcataagc gtccatagga tatctgagga 8820
acattcatca aaaataagcc atagacatga acaacacctc actaccccat tgaagacgca 8880
tcacctagtt aacctgctgc agttttaca tgatagactt tgttccagat tgacaagtca 8940
tctttcagtt atttcctctg tcacttcaaa actccagctt gcccaataag gatttagaac 9000
cagagtgact gatatatata tatatatttt aattcagagt tacatacata cagctaccat 9060
tttatatgaa aaaagaaaaa catttcttcc tggaactcac tttttatata atgttttata 9120
tatatatttt ttcctttcaa atcagacgat gagactagaa ggagaaatac tttctgtctt 9180
attaaaatta ataaattatt ggtctttaca agacttggat acattacagc agacatggaa 9240
atataatttt aaaaaatttc tctccaacct ccttcaaatt cagtcaccac tgttatatta 9300
ccttctccag gaaccctcca gtggggaagg ctgcgatatt agatttcctt gtatgcaaag 9360
tttttgttga aagctgtgct cagaggaggt gagaggagag gaaggagaaa actgcatcat 9420
aactttacag aattgaatct agagtcttcc ccgaaaagcc cagaaacttc tctgcagtat 9480
ctggcttgtc catctggtct aaggtggctg cttcttcccc agccatgagt cagtttgtgc 9540
ccatgaataa tacacgacct gttatttcca tgactgcttt actgtatttt taaggtcaat 9600
atactgtaca tttgataata aaataatatt ctcccaaaaa aaaaa 9645

<210> 32
<211> 5921
<212> DNA
<213> Homo sapiens

<400> 32
agcagacggg agtttctcct cggggtcgga gcaggaggca cgcggagtgt gaggccacgc 60
atgagcggac gctaacccccc tccccagcca caaagagtct acatgtctag ggtctagaca 120
tgttcagctt tgtggacctc cggctcctgc tcctcttagc ggccaccgcc ctcctgacgc 180
acggccaaga ggaaggccaa gtcgagggcc aagacgaaga catcccacca atcacctgcg 240
tacagaacgg cctcaggtac catgaccgag acgtgtggaa acccgagccc tgccggatct 300
gcgtctgcga caacggcaag gtgttgtgcg atgacgtgat ctgtgacgag accaagaact 360
gccccggcgc cgaagtcccc gagggcgagt gctgtcccgt ctgccccgac ggctcagagt 420
cacccaccga ccaagaaacc accggcgtcg agggacccaa gggagacact ggcccccgag 480
gcccaagggg acccgcaggc ccccctggcc gagatggcat ccctggacag cctggacttc 540
ccggaccccc cggaccccca ggacctcccg gacccctgg cctcggagga aactttgctc 600
cccagctgtc ttatggctat gatgagaaat caaccggagg aatttccgtg cctggcccca 660
tgggtccctc tggtcctcgt ggtctccctg gccccctgg tgcacctggt ccccaaggct 720

tccaaggtcc ccctggtgag cctggcgagc ctggagcttc aggtcccatg ggtccccgag 780
gtcccccagg tccccctgga aagaatggag atgatgggga agctggaaaa cctggtcgtc 840
ctggtgagcg tgggcctcct gggcctcagg gtgctcgagg attgcccgga acagctggcc 900
tccctggaat gaagggacac agaggtttca gtggtttgga tggtgccaag ggagatgctg 960
gtcctgctgg tcctaagggt gagcctggca gccctggtga aaatggagct cctggtcaga 1020
tgggcccccg tggcctgcct ggtgagagag gtcgccctgg agcccctggc cctgctggtg 1080
ctcgtggaaa tgatggtgct actggtgctg ccgggccccc tggtcccacc ggccccgctg 1140
gtcctcctgg cttccctggt gctgttggtg ctaagggtga agctggtccc caagggcccc 1200
gaggctctga aggtccccag ggtgtgcgtg gtgagcctgg ccccccctggc cctgctggtg 1260
ctgctggccc tgctggaaac cctggtgctg atggacagcc tggtgctaaa ggtgccaatg 1320
gtgctcctgg tattgctggt gctcctggct tccctggtgc ccgaggcccc tctggacccc 1380
agggccccgg cggccctcct ggtcccaagg gtaacagcgg tgaacctggt gctcctggca 1440
gcaaaggaga cactggtgct aagggagagc ctggccctgt tggtgttcaa ggacccccctg 1500
gccctgctgg agaggaagga aagcgaggag ctcgaggtga acccggaccc actggcctgc 1560
ccggaccccc tggcgagcgt ggtggacctg gtagccgtgg tttccctggc gcagatggtg 1620
ttgctggtcc caagggtccc gctggtgaac gtggttctcc tggccccgct ggccccaaag 1680
gatctcctgg tgaagctggt cgtcccggtg aagctggtct gcctggtgcc aagggtctga 1740
ctggaagccc tggcagccct ggtcctgatg gcaaaactgg ccccccctggt cccgccggtc 1800
aagatggtcg ccccggaccc ccaggcccac ctggtgcccg tggtcaggct ggtgtgatgg 1860
gattccctgg acctaaaggt gctgctggag agcccggcaa ggctggagag cgaggtgttc 1920
ccggaccccc tggcgctgtc ggtcctgctg gcaaagatgg agaggctgga gctcagggac 1980
cccctggccc tgctggtccc gctggcgaga gaggtgaaca aggccctgct ggctcccccg 2040
gattccaggg tctccctggt cctgctggtc ctccaggtga agcaggcaaa cctggtgaac 2100
agggtgttcc tggagacctt ggcgcccctg gcccctctgg agcaagaggc gagagaggtt 2160
tccctggcga gcgtggtgtg caaggtcccc ctggtcctgc tggaccccga ggggccaacg 2220
gtgctcccgg caacgatggt gctaagggtg atgctggtgc ccctggagct cccggtagcc 2280
agggcgcccc tggccttcag ggaatgcctg gtgaacgtgg tgcagctggt cttccagggc 2340
ctaagggtga cagaggtgat gctggtccca aaggtgctga tggctctcct ggcaaagatg 2400
gcgtccgtgg tctgaccggc cccattggtc ctcctggccc tgctggtgcc cctggtgaca 2460
agggtgaaag tggtcccagc ggccctgctg gtcccactgg agctcgtggt gccccggag 2520
accgtggtga gcctggtccc cccggccctg ctggctttgc tggcccccct ggtgctgacg 2580
gccaacctgg tgctaaaggc gaacctggtg atgctggtgc caaaggcgat gctggtcccc 2640
ctgggcctgc cggacccgct ggacccccctg gccccattgg taatgttggt gctcctggag 2700
ccaaaggtgc tcgcggcagc gctggtcccc ctggtgctac tggtttccct ggtgctgctg 2760
gccgagtcgg tcctcctggc ccctctggaa atgctggacc ccctggccct cctggtcctg 2820
ctggcaaaga aggcggcaaa ggtccccgtg gtgagactgg ccctgctgga cgtcctggtg 2880
aagttggtcc ccctggtccc cctggccctg ctggcgagaa aggatcccct ggtgctgatg 2940
gtcctgctgg tgctcctggt actcccgggc ctcaaggtat tgctggacag cgtggtgtgg 3000
tcggcctgcc tggtcagaga ggagagagag gcttccctgg tcttcctggc ccctctggtg 3060
aacctggcaa acaaggtccc tctggagcaa gtggtgaacg tggtcccccc ggtcccatgg 3120
gccccccctgg attggctgga cccccctggtg aatctggacg tgaggggct cctgctgccg 3180
aaggttcccc tggacgagac ggttctcctg gcgccaaggg tgaccgtggt gagaccggcc 3240
ccgctggacc ccctggtgct cctggtgctc ctggtgcccc tggccccgtt ggccctgctg 3300
gcaagagtgg tgatcgtggt gagactggtc ctgctggtcc cgccggtccc gtcggccccg 3360
tcggcgcccg tggccccgcc ggaccccaag gcccccgtgg tgacaagggt gagacaggcg 3420
aacagggcga cagaggcata aagggtcacc gtggcttctc tggcctccag ggtcccccctg 3480
gccctcctgg ctctcctggt gaacaaggtc cctctggagc ctctggtcct gctggtcccc 3540
gaggtccccc tggctctgct ggtgctcctg gcaaagatgg actcaacggt ctccctggcc 3600
ccattgggcc ccctggtcct cgcggtcgca ctggtgatgc tggtcctgtt ggtcccccccg 3660
gccctcctgg acctcctggt cccccctggtc ctcccagcgc tggtttcgac ttcagcttcc 3720
tgccccagcc acctcaagag aaggctcacg atggtggccg ctactaccgg gctgatgatg 3780
ccaatgtggt tcgtgaccgt gacctcgagg tggacaccac cctcaagagc ctgagccagc 3840
agatcgagaa catccggagc ccagagggaa gccgcaagaa ccccgcccgc acctgccgtg 3900
acctcaagat gtgccactct gactggaaga gtggagagta ctggattgac cccaaccaag 3960
gctgcaacct ggatgccatc aaagtcttct gcaacatgga gactggtgag acctgcgtgt 4020
accccactca gcccagtgtg gcccagaaga actggtacat cagcaagaac cccaaggaca 4080
agaggcatgt ctggttcggc gagagcatga ccgatggatt ccagttcgag tatggcggcc 4140
agggctccga ccctgccgat gtggccatcc agctgacctt cctgcgcctg atgtccaccg 4200
aggcctccca gaacatcacc taccactgca agaacagcgt ggcctacatg gaccagcaga 4260
ctggcaacct caagaaggcc ctgctcctca agggctccaa cgagatcgag atccgcgccg 4320
agggcaacag ccgcttcacc tacagcgtca ctgtcgatgg ctgcacgagt cacaccggag 4380
cctggggcaa gacagtgatt gaatacaaaa ccaccaagtc ctcccgcctg cccatcatcg 4440
atgtggcccc cttggacgtt ggtgccccag accaggaatt cggcttcgac gttggccctg 4500
tctgcttcct gtaaactccc tccatcccaa cctggctccc tcccacccaa ccaactttcc 4560
ccccaacccg gaaacagaca agcaacccaa actgaacccc cccaaaagcc aaaaaatggg 4620
agacaatttc acatggactt tggaaaatat ttttttcctt tgcattcatc tctcaaactt 4680
agtttttatc tttgaccaac cgaacatgac caaaaaccaa aagtgcattc aaccttacca 4740

aaaaaaaaaa aaaaaaaaaa agaataaata aataagtttt taaaaaagga agcttggtcc 4800
acttgcttga agacccatgc gggggtaagt ccctttctgc ccgttgggtt atgaaacccc 4860
aatgctgccc tttctgctcc tttctccaca ccccccttgg cctcccctcc actccttccc 4920
aaatctgtct ccccagaaga cacaggaaac aatgtattgt ctgcccagca atcaaaggca 4980
atgctcaaac acccaagtgg cccccaccct cagcccgctc ctgcccgccc agcaccccca 5040
ggccctgggg acctggggtt ctcagactgc caaagaagcc ttgccatctg gcgctcccat 5100
ggctcttgca acatctcccc ttcgtttttg agggggtcat gccgggggag ccaccagccc 5160
ctcactgggt tcggaggaga gtcaggaagg gccacgacaa agcagaaaca tcggatttgg 5220
ggaacgcgtg tcatcccttg tgccgcaggc tgggcgggag agactgttct gttctgttcc 5280
ttgtgtaact gtgttgctga aagactacct cgttcttgtc ttgatgtgtc accggggcaa 5340
ctgcctgggg gcggggatgg gggcagggtg gaagcggctc cccatttta taccaaaggt 5400
gctacatcta tgtgatgggt ggggtgggga gggaatcact ggtgctatag aaattgagat 5460
gccccccag gccagcaaat gttccttttt gttcaaagtc tatttttatt ccttgatatt 5520
ttttctttct ttttttttt ttttgtggat ggggacttgt gaatttttct aaaggtgcta 5580
tttaacatgg gaggagagcg tgtgcgctcc agcccagccc gctgctcact ttccaccctc 5640
tctccacctg cctctggctt ctcaggcctc tgctctccga cctctctcct ctgaaaccct 5700
cctccacagc tgcagcccat cctcccggct ccctcctagt ctgtcctgcg tcctctgtcc 5760
ccgggtttca gagacaactt cccaaagcac aaagcagttt ttccctaggg gtgggaggaa 5820
gcaaaagact ctgtacctat tttgtatgtg tataataatt tgagatgttt ttaattattt 5880
tgattgctgg aataaagcat gtggaaatga cccaaacata a 5921

<210> 33
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 33
cggaacgagg gcaacctgca cagccatgcc cgggcaagaa ctcaggacgg tgaatggctc 60
tcagatgctc ctggtgttgc tggtgctctc gtggctgccg catgggggcg ccctgtctct 120
ggccgaggcg agccgcgcaa gtttcccggg accctcagag ttgcactccg aagactccag 180
attccgagag ttgcggaaac gctacgagga cctgctaacc aggctgcggg ccaaccagag 240
ctgggaagat tcgaacaccg acctcgtccc ggcccctgca gtccggatac tcacgccaga 300
agtgcggctg ggatccggcg gccacctgca cctgcgtatc tctcgggccg cccttcccga 360
ggggctcccc gaggcctccc gccttcaccg ggctctgttc cggctgtccc cgacggcgtc 420
aaggtcgtgg gacgtgacac gaccgctgcg gcgtcagctc agccttgcaa gaccccaagc 480
gcccgcgctg cacctgcgac tgtcgccgcc gccgtcgcag tcggaccaac tgctggcaga 540
atcttcgtcc gcacggcccc agctggagtt gcacttgcgg ccgcaagccg ccaggggcg 600
ccgcagagcg cgtgcgcgca acggggacga ctgtccgctc gggcccgggc gttgctgccg 660
tctgcacacg gtccgcgcgt cgctggaaga cctgggctgg gccgattggg tgctgtcgcc 720
acgggaggtg caagtgacca tgtgcatcgg cgcgtgcccg agccagttcc gggcggcaaa 780
catgcacgcg cagatcaaga cgagcctgca ccgcctgaag cccgacacgg agccagcgcc 840
ctgctgcgtg cccgccagct acaatcccat ggtgctcatt caaaagaccg acaccggggt 900
gtcgctccag acctatgatg acttgttagc caaagactgc cactgcatat gagcagtcct 960
ggtccttcca ctgtgcacct gcgcggggga ggcgacctca gttgtcctgc cctgtggaat 1020
gggctcaagg ttcctgagac acccgattcc tgcccaaaca gctgtattta tataagtctg 1080
ttatttatta ttaatttatt ggggtgacct tcttggggac tcgggggctg gtctgatgga 1140
actgtgtatt tatttaaaac tctggtgata aaaataaagc tgtctgaact gttaaaaaaa 1200
aaaa 1204

<210> 34
<211> 5221
<212> DNA
<213> Homo sapiens

<400> 34
ataaaagggg gctgaggaaa taccggacac ggtcacccgt tgccagctct agcctttaaa 60
ttcccggctc ggggacctcc acgcaccgcg gctagcgccg acaaccagct agcgtgcaag 120
gcgccgcggc tcagcgcgta ccggcgggct tcgaaaccgc agtcctccgg cgaccccgaa 180
ctccgctccg gagcctcagc cccctggaaa gtgatcccgg catccgagag ccaagatgcc 240
ggcccacttg ctgcaggacg atatctctag ctcctatacc accaccacca ccattacagc 300
gcctccctcc agggtcctgc agaatggagg agataagttg gagacgatgc ccctctactt 360
ggaagacgac attcgccctg atataaaaga tgatatatat gaccccacct acaaggataa 420
ggaaggccca agccccaagg ttgaatatgt ctggagaaac atcatcctta tgtctctgct 480
acacttggga gccctgtatg ggatcacttt gattcctacc tgcaagttct acacctggct 540
ttgggggta ttctactatt ttgtcagtgc cctgggcata acagcaggag ctcatcgtct 600
gtggagccac cgctcttaca aagctcggct gcccctacgg ctctttctga tcattgccaa 660
cacaatggca ttccagaatg atgtctatga atgggctcgt gaccaccgtg cccaccacaa 720

gttttcagaa acacatgctg atcctcataa ttcccgacgt ggctttttct tctctcacgt 780
gggttggctg cttgtgcgca aacacccagc tgtcaaagag aaggggagta cgctagactt 840
gtctgaccta gaagctgaga aactggtgat gttccagagg aggtactaca aacctggctt 900
gctgctgatg tgcttcatcc tgcccacgct tgtgccctgg tatttctggg gtgaaacttt 960
tcaaaacagt gtgttcgttg ccactttctt gcgatatgct gtggtgctta atgccacctg 1020
gctggtgaac agtgctgccc acctcttcgg atatcgtcct tatgacaaga acattagccc 1080
ccgggagaat atcctggttt cacttggagc tgtgggtgag ggcttccaca actaccacca 1140
ctccttccc tatgactact ctgccagtga gtaccgctgg cacatcaact tcaccacatt 1200
cttcattgat tgcatggccg ccctcggtct ggcctatgac cggaagaaag tctccaaggc 1260
cgccatcttg gccaggatta aaagaaccgg agatggaaac tacaagagtg gctgagtttg 1320
gggtccctca ggtttccttt ttcaaaaacc agccaggcag aggttttaat gtctgtttat 1380
taactactga ataatgctac caggatgcta aagatgatga tgttaaccca ttccagtaca 1440
gtattctttt aaaattcaaa agtattgaaa gccaacaact ctgcctttat gatgctaagc 1500
tgatattatt tcttctctta tcctctctct cttctaggcc cattgtcctc cttttcactt 1560
tattgctatc gccctccttt cccttattgc ctcccaggca agcagctggt cagtctttgc 1620
tcagtgtcca gcttccaaag cctagacaac ctttctgtag cctaaaacga atggtctttg 1680
ctccagataa ctctctttcc ttgagctgtt gtgagctttg aagtaggtgg cttgagctag 1740
agataaaaca gaatcttctg ggtagtcccc tgttgattat cttcagccca ggcttttgct 1800
agatggaatg gaaaagcaac ttcatttgac acaaagcttc taaagcaggt aaattgtcgg 1860
gggagagagt tagcatgtat gaatgtaagg atgagggaag cgaagcaaga ggaacctctc 1920
gccatgatca gacatacagc tgcctaccta atgaggactt caagccccac cacatagcat 1980
gcttcctttc tctcctggct cggggtaaaa agtggctgcg gtgtttggca atgctaattc 2040
aatgccgcaa catatagttg aggccgagga taaagaaaag acattttaag tttgtagtaa 2100
aagtggtctc tgctggggaa gggttttctt ttctttttt ctttaataac aaggagattt 2160
cttagttcat atatcaagaa gtcttgaagt tgggtgtttc cagaattggt aaaaacagca 2220
gctcatggaa ttttgagtat tccatgagct gctcattaca gttctttcct ctttctgctc 2280
tgccatcttc aggatattgg ttcttcccct catagtaata agatggctgt ggcatttcca 2340
aacatccaaa aaaagggaag gatttaagga ggtgaagtcg ggtcaaaaat aaaatatata 2400
tacatatata cattgcttag aacgttaaac tattagagta tttcccttcc aaagagggat 2460
gtttggaaaa aactctgaag gagaggagga attagttggg atgccaattt cctctccact 2520
gctggacatg agatggagag gctgagggac aggatctata ggcagcttct aagagcgaac 2580
ttcacatagg aagggatctg agaacacgtt gccaggggct tgagaaggtt actgagtgag 2640
ttattgggag tcttaataaa ataaactaga tattaggtcc attcattaat tagttccagt 2700
ttctccttga aatgagtaaa aactagaagg cttctctcca cagtgttgtg ccccttcact 2760
cattttttt tgaggagaag ggggtctctg ttaacatcta gcctaaagta tacaactgcc 2820
tgggggcag ggttaggaat ctcttcacta ccctgattct tgattcctgg ctctaccctg 2880
tctgtccctt ttctttgacc agatctttct cttccctgaa cgttttcttc tttccctgga 2940
caggcagcct cctttgtgtg tattcagagg cagtgatgac ttgctgtcca ggcagctccc 3000
tcctgcacac agaatgctca gggtcactga accactgctt ctcttttgaa agtagagcta 3060
gctgccactt tcacgtggcc tccgcagtgt ctccacctac acccctgtgc tcccctgcca 3120
cactgatggc tcaagacaag gctggcaaac cctcccagaa acatctctgg cccagaaagc 3180
ctctctctcc ctccctctct catgaggcac agccaagcca agcgctcatg ttgagccagt 3240
gggccagcca cagagcaaaa gagggtttat ttttcagtccc ctctctctgg gtcagaacca 3300
gagggcatgc tgaatgcccc ctgcttactt ggtgagggtg ccccgcctga gtcagtgctc 3360
tcagctggca gtgcaatgct tgtagaagta ggaggaaaca gttctcactg ggaagaagca 3420
agggcaagaa cccaagtgcc tcacctcgaa aggaggccct gttccctgga gtcagggtga 3480
actgcaaagc tttggctgag acctgggatt tgagatacca caaaccctgc tgaacacagt 3540
gtctgttcag caaactaacc agcattccct acagcctagg gcagacaata gtatagaagt 3600
ctggaaaaaa acaaaaacag aatttgagaa ccttggacca ctcctgtccc tgtagctcag 3660
tcatcaaagc agaagtctgg ctttgctcta ttaagattgg aaatgtacac taccaaacac 3720
tcagtccact gttgagcccc agtgctggaa gggaggaagg cctttcttct gtgttaattg 3780
cgtagaggct acaggggtta gcctggacta aaggcatcct tgtcttttga gctattcacc 3840
tcagtagaaa aggatctaag ggaagatcac tgtagtttag ttctgttgac ctgtgcacct 3900
acccccttgga aatgtctgct ggtatttcta attccacagg tcatcagatg cctgcttgat 3960
aatatataaa caataaaaac aactttcact tcttcctatt gtaatcgtgt gccatggatc 4020
tgatctgtac catgacccta cataaggctg gatggcacct caggctgagg gccccaatgt 4080
atgtgtggct gtgggtgtgg gtgggagtgt gtctgctgag taaggaacac gattttcaag 4140
attctaaagc tcaattcaag tgacacatta atgataaact cagatctgat caagagtccg 4200
gatttctaac agtccctgct ttgggggtg tgctgacaac ttagctcagg tgccttacat 4260
cttttctaat cacagtgttg catatgagcc tgccctcact ccctctgcag aatccctttg 4320
cacctgagac cctactgaag tggctggtag aaaaaggggc ctgagtggag gattatcagt 4380
atcacgattt gcaggattcc cttctgggct tcattctgga aacttttgtt agggctgctt 4440
ttcttaagtg cccacatttg atggagggtg gaaataattt gaatgtattt gatttataag 4500
tttttttttt tttttgggtt aaaagatggt tgtagcattt aaaatggaaa attttctcct 4560
tggtttgcta gtatcttggg tgtattctct gtaagtgtag ctcaaatagg tcatcatgaa 4620
aggttaaaaa agcgaggtgg ccatgttatg ctggtggtta aggccagggc ctctccaacc 4680
actgtgccac tgacttgctg tgtgaccctg ggcaagtcac ttaactataa ggtgcctcag 4740

ttttccttct gttaaaatgg ggataataat actgacctac ctcaaagggc agttttgagg 4800
catgactaat gctttttaga aagcattttg ggatccttca gcacaggaat tctcaagacc 4860
tgagtatttt ttataatagg aatgtccacc atgaacttga tacgtccgtg tgtcccagat 4920
gctgtcatta gtctatatgg ttctccaaga aactgaatga atccattgga gaagcggtgg 4980
ataactagcc agacaaaatt tgagaataca taaacaacgc attgccacgg aaacatacag 5040
aggatgcctt ttctgtgatt gggtgggatt ttttcccttt ttatgtggga tatagtagtt 5100
acttgtgaca aaaataattt tggaataatt tctattaata tcaactctga agctaattgt 5160
actaatctga gattgtgttt gttcataata aaagtgaagt gaatctaaaa aaaaaaaaaa 5220
a 5221

<210> 35
<211> 799
<212> DNA
<213> Homo sapiens

<400> 35
cactcccaaa gaactgggta ctcaacactg agcagatctg ttctttgagc taaaaaccat 60
gtgctgtacc aagagtttgc tcctggctgc tttgatgtca gtgctgctac tccacctctg 120
cggcgaatca gaagcagcaa gcaactttga ctgctgtctt ggatacacag accgtattct 180
tcatcctaaa tttattgtgg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa 240
tgctatcatc tttcacacaa agaaaaagtt gtctgtgtgc gcaaatccaa aacagacttg 300
ggtgaaatat attgtgcgtc tcctcagtaa aaaagtcaag aacatgtaaa aactgtggct 360
tttctggaat ggaattggac atagcccaag aacagaaaga accttgctgg ggttggaggt 420
ttcacttgca catcatggag ggtttagtgc ttatctaatt tgtgcctcac tggacttgtc 480
caattaatga agttgattca tattgcatca tagtttgctt tgtttaagca tcacattaaa 540
gttaaactgt attttatgtt atttatagct gtaggttttc tgtgtttagc tatttaatac 600
taattttcca taagctattt tggtttagtg caaagtataa aattatattt ggggggaat 660
aagattatat ggactttctt gcaagcaaca agctattttt taaaaaaact atttaacatt 720
cttttgttta tattgttttg tctcctaaat tgttgtaatt gcattataaa ataagaaaaa 780
cattaataag acaaatatt 799

<210> 36
<211> 2993
<212> DNA
<213> Homo sapiens

<400> 36
cgctggggcg ctttccgagg aaattcggga ctcgagtttc ccggggaaga ggcgcggcct 60
gagcccggcg agggtgggga gggcaggcgc aggtggaccc cggcgccccc cgagccccgc 120
tgtgaccttg gccgcggggg aggggctggg ccgctgcggg gcagtcgcgg ccgccagagg 180
gggcagcgga gaagaacttg cccaacttgg cggcgcgggc tggggcggct ctgcgcctcc 240
gcgcccgcct ccccggcctc cgccttctcc cctcccgcga gcctcctccc ctcccgcgag 300
cctcctcccc tgggccctcc tcccgtcctc cccgccgccg ccggtcccgg tgcgcgccca 360
tccctgcccg cagccccgcg cgccggccga gtcgctgagc cgcggctgcc ggacgggacg 420
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg cactggcccg 480
ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc gccgcccccgg agctggcccc 540
cgcgcccttc acgctgcccc tccgggtggc cgcggccacg aaccgcgtag ttgcgcccac 600
cccgggaccc gggacccctg ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc 660
tgccctggcg tcccccgcgg gcgccgccaa cttcttggcc atggtagaca acctgcaggg 720
ggactctggc cgcggctact acctggagat gctgatcggg acccccccgc agaagctaca 780
gattctcgtt gacactggaa gcagtaactt tgccgtggca ggaaccccgc actcctacat 840
agacacgtac tttgacacag agaggtctag cacataccgc tccaagggct ttgacgtcac 900
agtgaagtac acacaaggaa gctggacggg cttcgttggg gaagacctcg tcaccatccc 960
caaaggcttc aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 1020
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca cacttgccaa 1080
gccatcaagt tctctggaga ccttcttcga ctccctggtg acacaagcaa acatccccaa 1140
cgttttctcc atgcagatgt gtggagccgg cttgcccgtt gctggatctg ggaccaacgg 1200
aggtagtctt gtcttgggtg gaattgaacc aagtttgtat aaaggagaca tctggtatac 1260
ccctattaag gaagagtggt actaccagat agaaattctg aaattggaaa ttggaggcca 1320
aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg acagtggcac 1380
cacgctgctg cgcctgcccc agaaggtgtt tgatgcggtg gtggaagctg tggcccgcgc 1440
atctctgatt ccagaattct ctgatggttt ctggactggg tcccagctgg cgtgctggac 1500
gaattcggaa acaccttggt cttacttccc taaaatctcc atctacctga gagacgagaa 1560
ctccagcagg tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1620
ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa atgcgctggt 1680
gatcggtgcc acggtgatgg agggcttcta cgtcatcttc gacagagccc agaagagggt 1740
gggcttcgca gcgagcccct gtgcagaaat tgcaggtgct gcagtgtctg aaatttccgg 1800

gcctttctca acagaggatg tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc 1860
cattttgtgg attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1920
aatcgtcctg ctgctgctgc cgttccggtg tcagcgtcgc ccccgtgacc ctgaggtcgt 1980
caatgatgag tcctctctgg tcagacatcg ctggaaatga atagccaggc ctgacctcaa 2040
gcaaccatga actcagctat taagaaaatc acatttccag ggcagcagcc gggatcgatg 2100
gtggcgcttt ctcctgtgcc cacccgtctt caatctctgt tctgctccca gatgccttct 2160
agattcactg tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 2220
aaataattaa aaaaaaaact tcattctaaa ccaaaacaga gtggattggg ctgcaggctc 2280
tatggggttc gttatgccaa agtgtctaca tgtgccacca acataaaaca aaaccaagcc 2340
ttggctcgtt ctcttctctc ttcaatctct ggaaaaataa gtacatatag ttgataaccc 2400
ctcttagctt acaggaagct ttttgtatta attgcctttg aggttatttt ccgccagacc 2460
tcaacctggg tcaaagtggt acaggaaggc ttgcagtatg atggcaggag aatcagcctg 2520
gggcctgggg atgtaaccaa gctgtaccct tgagacctgg aaccagagcc acaggcccct 2580
tttgtgggtt tctctgtgct ctgaatggga gccagaattc actaggaggt catcaaccga 2640
tggtcctcac aagcctcttc tgaagatgga aggccttttg cccgttgagg tagaggggaa 2700
ggaaatctcc tcttttgtac ccaatactta tgttgtattg ttggtgcgaa agtaaaaaca 2760
ctacctcttt tgagactttg cccagggtcc tgtgcctgga tgggggtgca ggcagccttg 2820
accacggctg ttcccctcac ccaaaagaat tatcatccca acagccaaga cccaacaggt 2880
gctgaactgt gcatcaacca ggaagagttc tatccccaag ctggccacta tcacatatgc 2940
ttactcttgc ttaaaattaa taaatcatgt tttgatgaga aaaaactatt cta 2993

<210> 37
<211> 1381
<212> DNA
<213> Homo sapiens

<400> 37
atgcgcgatc tcccggagca tgcgcagcag cggcgccgac gcggggcggt gcctggtgac 60
cgcgcgcgct cccggaagtg tgccggcgtc gcgcgaaggt tcagcaggga gccgtgggcc 120
gggcgcgcgg ttcccggcac gtgtctcggc acgtggcagc gcgcctggcc ctgggcttgg 180
aggcgccggc gccctggatc cgccggccgt ggtcgccgag tcggtgtcgt ccttgaccat 240
cgccgacgcg ttcattgcag ccggcgagag ctcagctccg accccgccgc gccccgcgct 300
tcccaggagg ttcatctgct ccttccctga ctgcagcgcc aattacagca aagcctggaa 360
gcttgacgcg cacctgtgca agcacacggg ggagagacca tttgtttgtg actatgaagg 420
gtgtggcaag gccttcatca gggactacca tctgagccgc cacattctga ctcacacagg 480
agaaaagccg tttgtttgtg cagccaatgg ctgtgatcaa aaattcaaca caaaatcaaa 540
cttgaagaaa cattttgaac gcaaacatga aaatcaacaa aaacaatata tatgcagttt 600
tgaagactgt aagaagacct ttaagaaaca tcagcagctg aaaatccatc agtgccagaa 660
taccaatgaa cctctattca agtgtaccca ggaaggatgt gggaaacact ttgcatcacc 720
cagcaagctg aaacgacatg ccaaggccca cgagggctat gtatgtcaaa aaggatgttc 780
ctttgtggca aaaacatgga cggaacttct gaaacatgtg agagaaaccc ataaagagga 840
aatactatgt gaagtatgcc ggaaaacatt taaacgcaaa gattacctta agcaacacat 900
gaaaactcat gccccagaaa gggatgtatg tcgctgtcca agagaaggct gtggaagaac 960
ctatacaact gtgtttaatc tccaaagcca tatcctctcc ttccatgagg aaagccgccc 1020
ttttgtgtgt gaacatgctg gctgtggcaa aacatttgca atgaaacaaa gtctcactag 1080
gcatgctgtt gtacatgatc ctgacaagaa gaaaatgaag ctcaaagtca aaaaatctcg 1140
tgaaaaacgg gagtttggcc tctcatctca gtggatatat cctcccaaaa ggaaacaagg 1200
gcaaggctta tctttgtgtc aaaacggaga gtcacccaac tgtgtggaag acaagatgct 1260
ctcgacagtt gcagtactta cccttggcta agaactgcac tgctttgttt aaaggactgc 1320
agaccaagga gtcgagcttt ctctcagagc atgcttttct ttattaaaat tactgatgca 1380
g 1381

<210> 38
<211> 4720
<212> DNA
<213> Homo sapiens

<400> 38
gcgagaccta gcaggcccgg ggctgggcgt gccctcgcct gccacgctgc gcgctgccct 60
cagccgggcc gctggggccg tgcagtgcac cgggcacgcc gcgccaggct gggggcaggc 120
accgagcctc cgtgggaggt cccgaggcag cttcgcctgc tcgccctggc tccagccctc 180
acctgccgca gccttagctg agcagccgcc gccactgggc gccccccgct ccccacttcg 240
ccagcgcccg ctcctcggct cggcccgggg tagtttgtag ggacgcagct ctccacgtgc 300
gcgactgcga ggctggacgc tacgggctcc tggaaaggag acaccagcat ttgccacaat 360
gctgtcatcc actgacttta catttgcttc ctgggagctt gtggtccgcg ttgaccatcc 420
caatgaagag cagcagaaag acgtcacact gagagtatct ggagaccttc atgttggagg 480
agtgatgctc aagttagtag aacagatcaa tatatcccaa gactggtcag actttgctct 540

ttggtgggaa cagaagcatt gctggcttct gaaaacccac tggaccctgg acaaatatgg 600
ggtccaggca gatgcaaagc ttctcttcac ccctcagcat aaaatgctgc gccttcgtct 660
gccgaatttg aagatggtga ggttgcgagt cagcttctca gctgtggttt ttaaagctgt 720
cagtgatatc tgcaaaatcc tgaatattag aagatcagaa gagctttcct tgttaaagcc 780
gtctggtgac tattttaaga agaagaagaa aaaagacaaa aataataagg aacccataat 840
tgaagatatt ctaaacctgg agagttctcc aacagcttca ggttcatcag taagtcctgg 900
tttatacagt aaaaccatga cccctatata tgaccccatc aatggaacac cagcatcatc 960
caccatgact tggttcagtg acagcccttt gacggaacaa aactgcagca tcctcgcatt 1020
cagccaaccc ccccagtccc cagaagcact tgcggatatg taccagcctc ggtctctggt 1080
tgataaagcc aagctcaatg caggttggct agactcctca cgctccctta tggaacaagg 1140
catccaagag gatgagcagc tgctcttacg atttaaatat tattctttct tcgacttgaa 1200
tcctaaatat gatgctgtcc gaataaacca actctatgag caagccaggt gggccattct 1260
cttagaagaa attgattgca cagaggaaga aatgttgatc tttgcagctc tacagtacca 1320
cattagcaaa ctgtcgttgt ctgctgaaac acaggatttt gcaggcgagt ccgaggttga 1380
tgaaatagaa gcggcgcttt ctaatttgga agtaacccta gaaggtggaa aagcggacag 1440
ccttttggag gacattactg atatccctaa acttgcagat aatctcaaat tatttaggcc 1500
caagaagtta ctaccaaaag ctttcaaaca atattggttt atctttaaag acacatccat 1560
agcatacttt aaaaataagg aacttgaaca aggagaacca ctagaaaaac taaatcttag 1620
aggctgcgaa gttgtgcccg atgtaaatgt agcaggaaga aaatttggaa tcaagttact 1680
aatccctgtt gccgatggta tgaatgaaat gtatttgaga tgtgaccatg agaatcaata 1740
cgcccaatgg atggctgcct gcatgttggc atcgaagggc aaaaccatgg cagacagctc 1800
ctaccagcca gaggtcctca acatcctttc atttctgagg atgaaaaaca ggaactctgc 1860
atctcaggtg gcttccagtc tcgaaaacat ggatatgaac ccagaatgtt ttgtgtcacc 1920
acggtgtgca aagaaacaca aatccaaaca gctggccgcc cggatcctgg aggcgcacca 1980
gaacgtggcc cagatgcccc tggtcgaagc caagctgcgg ttcatccagg cgtggcagtc 2040
actgcctgag tttggcctca cctactacct tgtcagattt aaaggaagca aaaaagatga 2100
cattctggga gtttcatata acaggttgat taaaattgat gcagccaccg ggattccagt 2160
gacaacatgg agattcacaa atatcaaaca gtggaatgta aactgggaaa cccggcaggt 2220
ggtcatcgag tttgaccaaa acgtctttac tgctttcacc tgcctgagtg cagattgcaa 2280
gattgtgcac gagtacattg gcggctacat tttcttgtcc acccgctcca aggaccagaa 2340
tgaaacactc gatgaggact tgttccacaa attgaccggc ggtcaggatt gaaacaagca 2400
cgcgtgctcg gctcacacca acaaggcaag ccaaaggcgc ccctccccag agggatccct 2460
aacgtgccca gcatgtagat tctggactaa cagacaacat acattcaccg ctggtcaccc 2520
agatcctcat tcaaacccac tgctggcaca tccctttcct tactttgccc tgtgctacca 2580
gccacggaag gagcctctct tgtttttttct ataaaatggg taggcaggag aaaagcaggt 2640
gccctaagat tgctctaagg cccagcatgt ggttacagtt ctctgacttg cagaacctgc 2700
caggtgtatg gctacaagtt atcctcgtgc tgatctgtct cattactaag tcaatggaga 2760
agacagaaag gtaaaaatca cgtgtagcaa gaacaactct tatttcacaa actcaggtat 2820
gaaacgaaac gcctgtcctt catggaactg cttttagctc ctgtcttttc aaaatggcag 2880
agggagttcc tacacacact ttttccctgg aggccaaggt ctaggggtag aaaggggagg 2940
ggtggggcta ccaggtagca gttgacaacc caaggtcaga ggagtggccc tcagtgtcat 3000
ctgtccacag tgatacctgc caagatgacc actgacccac atctggtctt agtcattggt 3060
ctcctcagat ttctggggcc acctgcaagc cccattccat tcctacagat ctctcagcca 3120
cctgtaagtc ctttgtgaag atgtgggtga cacaggggga caggaaaacc catttctcaa 3180
cccagatcca tgtctccact gcttctactc tgggttggga ttcaggaaga caggcacagt 3240
cctctctgtt catagaaaca cctgccagtg tcaaggattc cagtcaggtg tctatcccaa 3300
ctggtcaggg agagaagggc agacccattc tcaaagacca ccatgtccaa ggtctgacag 3360
ctccccactg gctgccccca caggggcttt aggctggtct gggtcatggg gaagcgtccc 3420
tcttatcgct ggtctgtgtt ctcctggatt tggtatctat gttggtacga ctcctggcct 3480
tttatctaaa ggactttggc ttttgtaaat cacaagccaa taatagactt ttttctcccc 3540
ctctgttttt tgctgtgtca tctctgcctt gagactgcct tgagacagtg cttgccttga 3600
gagagtgagc caattaacag ctgcctgaat tgtcattttc cattttggtt tgttagaggt 3660
gggaggggtg ggttttgaga aggtcaaaag caataccaga agtaaaggga aatatcagac 3720
aatattttat tatttttca tagatgttct gccacacaaa gaacttgggg tgtaaggata 3780
aggcaaaagc tccaatccca tttttcagtt ctcctaggat gcacccctca gggagcctgg 3840
ccagagttcc gaggctcgtg agcgtcagct gttgctttat tttccatcaa agccctctga 3900
gaagtgagac ctcagcaatt ccgggagcca catagagaca gacttggcaa gggacccccc 3960
ggttctgagc cagtagctgc catctggaaa ttcctctttt agcctctcct tagaggtgaa 4020
tgtgaatgaa gcctcccagg cacccgctga atttctgagg ccttgcttaa agctcagaag 4080
tggtttaggc atttggaaaa tctggttcac atcataaaga acttgatttg aaatgttttc 4140
tatagaaaca agtgctaagt gtaccgtatt atacttgatg ttggtcattt ctcagtccta 4200
tttctcagtt ctattatttt agaacctagt cagttcttta agattataac tggtcctaca 4260
ttaaaataat gcttctcgat gtcagatttt acctgtttgc tgctgagaac atctctgcct 4320
aatttaccaa agccagacct tcagttcaac atgcttcctt agcttttcat agttgtctga 4380
catttccatg aaaacaaagg aaccaacttt gttttaacca aactttgttt ggttacagtt 4440
ttcaggggag cgtttcttcc atgacacaca gcaacatccc aaagaaataa acaagtgtga 4500
caaaaaaaaa aaaaaacaaa cctaaatgct actgttccaa agagcaactt gatggttttt 4560

tttaatactg agtgcaaaag gtcacccaaa ttcctatgat gaaattttaa attaatgggc 4620
acctttcaac atcatttgct tccttatcta cagttgattc agaaatctgc atttttttatt 4680
cttttatatg acttttaagt aaaagattta tatggatttg 4720

<210> 39
<211> 3213
<212> DNA
<213> Homo sapiens

<400> 39
agagactcaa gatgattccc tttttaccca tgttttctct actattgctg cttattgtta 60
accctataaa cgccaacaat cattatgaca agatcttggc tcatagtcgt atcaggggtc 120
gggaccaagg cccaaatgtc tgtgcccttc aacagatttt gggcaccaaa aagaaatact 180
tcagcacttg taagaactgg tataaaaagt ccatctgtgg acagaaaacg actgttttat 240
atgaatgttg ccctggttat atgagaatgg aaggaatgaa aggctgccca gcagttttgc 300
ccattgacca tgtttatggc actctgggca tcgtgggagc caccacaacg cagcgctatt 360
ctgacgcctc aaaactgagg gaggagatcg agggaaaggg atccttcact tactttgcac 420
cgagtaatga ggcttgggac aacttggatt ctgatatccg tagaggtttg gagagcaacg 480
tgaatgttga attactgaat gctttacata gtcacatgat taataagaga atgttgacca 540
aggacttaaa aaatggcatg attattcctt caatgtataa caatttgggg cttttcatta 600
accattatcc taatggggtt gtcactgtta attgtgctcg aatcatccat gggaaccaga 660
ttgcaacaaa tggtgttgtc catgtcattg accgtgtgct tacacaaatt ggtacctcaa 720
ttcaagactt cattgaagca gaagatgacc tttcatcttt tagagcagct gccatcacat 780
cggacatatt ggaggccctt ggaagagacg gtcacttcac actctttgct cccaccaatg 840
aggcttttga gaaacttcca cgaggtgtcc tagaaaggtt catgggagac aaagtggctt 900
ccgaagctct tatgaagtac cacatcttaa atactctcca gtgttctgag tctattatgg 960
gaggagcagt ctttgagacg ctggaaggaa atacaattga gataggatgt gacggtgaca 1020
gtataacagt aaatggaatc aaaatggtga acaaaaagga tattgtgaca aataatggtg 1080
tgatccattt gattgatcag gtcctaattc ctgattctgc caaacaagtt attgagctgg 1140
ctggaaaaca gcaaaccacc ttcacggatc ttgtggccca attaggcttg gcatctgctc 1200
tgaggccaga tggagaatac actttgctgg cacctgtgaa taatgcattt tctgatgata 1260
ctctcagcat ggttcagcgc ctccttaaat taattctgca gaatcacata ttgaaagtaa 1320
aagttggcct taatgagctt tacaacgggc aaatactgga aaccatcgga ggcaaacagc 1380
tcagagtctt cgtatatcgt acagctgtct gcattgaaaa ttcatgcatg gagaaaggga 1440
gtaagcaagg gagaaacggt gcgattcaca tattccgcga gatcatcaag ccagcagaga 1500
aatccctcca tgaaaagtta aaacaagata agcgctttag caccttcctc agcctacttg 1560
aagctgcaga cttgaaagag ctcctgacac aacctggaga ctggacatta tttgtgccaa 1620
ccaatgatgc ttttaaggga atgactagtg aagaaaaaga aattctgata cgggacaaaa 1680
atgctcttca aaacatcatt ctttatcacc tgacaccagg agttttcatt ggaaaaggat 1740
ttgaacctgg tgttactaac attttaaaga ccacacaagg aagcaaaatc tttctgaaag 1800
aagtaaatga tacacttctg gtgaatgaat tgaaatcaaa agaatctgac atcatgacaa 1860
caaatggtgt aattcatgtt gtagataaac tcctctatcc agcagacaca cctgttggaa 1920
atgatcaact gctggaaata cttaataaat taatcaaata catccaaatt aagtttgttc 1980
gtggtagcac cttcaaagaa atccccgtga ctgtctatac aactaaaatt ataaccaaag 2040
ttgtggaacc aaaaattaaa gtgattgaag gcagtcttca gcctattatc aaaactgaag 2100
gacccacact aacaaaagtc aaaattgaag gtgaacctga attcagactg attaaagaag 2160
gtgaaacaat aactgaagtg atccatggag agccaattat taaaaaatac accaaaatca 2220
ttgatggagt gcctgtggaa ataactgaaa aagagacacg agaagaacga atcattacag 2280
gtcctgaaat aaaatacact aggatttcta ctggaggtgg agaaacagaa gaaactctga 2340
agaaattgtt acaagaagag gtcaccaagg tcaccaaatt cattgaaggt ggtgatggtc 2400
atttatttga agatgaagaa attaaaagac tgcttcaggg agacacaccc gtgaggaagt 2460
tgcaagccaa caaaaaagtt caaggttcta gaagacgatt aagggaaggt cgttctcagt 2520
gaaaatccaa aaaccagaaa aaaatgttta tacaacccta agtcaataac ctgaccttag 2580
aaaattgtga gagccaagtt gacttcagga actgaaacat cagcacaaag aagcaatcat 2640
caaataattc tgaacacaaa tttaatattt ttttttctga atgagaaaca tgagggaaat 2700
tgtggagtta gcctcctgtg gtaaaggaat tgaagaaaat ataacacctt acacccttt 2760
tcatcttgac attaaaagtt ctggctaact ttggaatcca ttagagaaaa atccttgtca 2820
ccagattcat tacaattcaa atcgaagagt tgtgaactgt tatcccattg aaaagaccga 2880
gccttgtatg tatgttatgg atacataaaa tgcacgcaag ccattatctc tccatgggaa 2940
gctaagttat aaaaataggt gcttggtgta caaaactttt tatatcaaaa ggctttgcac 3000
atttctatat gagtgggttt actggtaaat tatgttattt tttacaacta attttgtact 3060
ctcagaatgt ttgtcatatg cttcttgcaa tgcatatttt ttaatctcaa acgtttcaat 3120
aaaaccattt ttcagatata aagagaatta cttcaaattg agtaattcag aaaaactcaa 3180
gatttaagtt aaaaagtggt ttggacttgg gaa 3213

<210> 40
<211> 2133

<212> DNA
<213> Homo sapiens

<400> 40
cgggagagcg cgctctgcct gccgcctgcc tgcctgccac tgagggttcc cagcaccatg 60
agggcctgga tcttctttct cctttgcctg gccgggaggg ccttggcagc ccctcagcaa 120
gaagccctgc ctgatgagac agaggtggtg gaagaaactg tggcagaggt gactgaggta 180
tctgtgggag ctaatcctgt ccaggtggaa gtaggagaat ttgatgatgg tgcagaggaa 240
accgaagagg aggtggtggc ggaaaatccc tgccagaacc accactgcaa acacggcaag 300
gtgtgcgagc tggatgagaa caacaccccc atgtgcgtgt gccaggaccc caccagctgc 360
ccagccccca ttggcgagtt tgagaaggtg tgcagcaatg acaacaagac cttcgactct 420
tcctgccact tctttgccac aaagtgcacc ctggagggca ccaagaaggg ccacaagctc 480
cacctggact acatcgggcc ttgcaaatac atccccccct gcctggactc tgagctgacc 540
gaattccccc tgcgcatgcg ggactggctc aagaacgtcc tggtcaccct gtatgagagg 600
gatgaggaca acaaccttct gactgagaag cagaagctgc gggtgaagaa gatccatgag 660
aatgagaagc gcctggaggc aggagaccac cccgtggagc tgctggcccg ggacttcgag 720
aagaactata acatgtacat cttccctgta cactggcagt tcggccagct ggaccagcac 780
cccattgacg ggtacctctc ccacaccgag ctggctccac tgcgtgctcc cctcatcccc 840
atggagcatt gcaccacccg ctttttcgag acctgtgacc tggacaatga caagtacatc 900
gccctggatg agtgggccgg ctgcttcggc atcaagcaga aggatatcga caaggatctt 960
gtgatctaaa tccactcctt ccacagtacc ggattctctc tttaaccctc cccttcgtgt 1020
ttcccccaat gtttaaaatg tttggatggt ttgttgttct gcctggagac aaggtgctaa 1080
catagattta agtgaataca ttaacggtgc taaaaatgaa aattctaacc caagacatga 1140
cattcttagc tgtaacttaa ctattaaggc cttttccaca cgcattaata gtcccatttt 1200
tctcttgcca tttgtagctt tgcccattgt cttattggca catgggtgga cacggatctg 1260
ctgggctctg ccttaaacac acattgcagc ttcaactttt ctctttagtg ttctgtttga 1320
aactaatact taccgagtca gactttgtgt tcatttcatt tcagggtctt ggctgcctgt 1380
gggcttcccc aggtggcctg gaggtgggca aagggaagta acagacacac gatgttgtca 1440
aggatggttt tgggactaga ggctcagtgg tgggagagat ccctgcagaa tccaccaacc 1500
agaacgtggt ttgcctgagg ctgtaactga gagaaagatt ctggggctgt cttatgaaaa 1560
tatagacatt ctcacataag cccagttcat caccatttcc tcctttacct ttcagtgcag 1620
tttcttttca cattaggctg ttggttcaaa cttttgggag cacggactgt cagttctctg 1680
ggaagtggtc agcgcatcct gcagggcttc tcctcctctg tcttttggag aaccagggct 1740
cttctcaggg gctctaggga ctgccaggct gtttcagcca ggaaggccaa aatcaagagt 1800
gagatgtaga aagttgtaaa atagaaaaag tggagttggt gaatcggttg ttctttcctc 1860
acatttggat gattgtcata aggtttttag catgttcctc cttttcttca ccctcccctt 1920
tgttcttcta ttaatcaaga gaaacttcaa agttaatggg atggtcggat ctcacaggct 1980
gagaactcgt tcacctccaa gcatttcatg aaaaagctgc ttcttattaa tcatacaaac 2040
tctcaccatg atgtgaagag tttcacaaat ctttcaaaat aaaaagtaat gacttagaaa 2100
ctgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2133

<210> 41
<211> 2691
<212> DNA
<213> Homo sapiens

<400> 41
gcttgcccgt cggtcgctag ctcgctcggt gcgcgtcgtc ccgctccatg gcgctcttcg 60
tgcggctgct ggctctcgcc ctggctctgg ccctgggccc cgccgcgacc ctggcgggtc 120
ccgccaagtc gccctaccag ctggtgctgc agcacagcag gctccggggc cgccagcacg 180
gccccaacgt gtgtgctgtg cagaaggtta ttggcactaa taggaagtac ttcaccaact 240
gcaagcagtg gtaccaaagg aaaatctgtg gcaaatcaac agtcatcagc tacgagtgct 300
gtcctggata tgaaaaggtc cctggggaga agggctgtcc agcagcccta ccactctcaa 360
acctttacga gaccctggga gtcgttggat ccaccaccac tcagctgtac acggaccgca 420
cggagaagct gaggcctgag atggaggggc ccggcagctt caccatcttc gcccctagca 480
acgaggcctg ggcctccttg ccagctgaag tgctggactc cctggtcagc aatgtcaaca 540
ttgagctgct caatgccctc cgctaccata tggtgggcag gcgagtcctg actgatgagc 600
tgaaacacgg catgaccctc acctctatgt accagaattc caacatccag atccaccact 660
atcctaatgg gattgtaact gtgaactgtg cccggctcct gaaagccgac caccatgcaa 720
ccaacggggt ggtgcacctc atcgataagg tcatctccac catcaccaac aacatccagc 780
agatcattga gatcgaggac acctttgaga cccttcgggc tgctgtggct gcatcagggc 840
tcaacacgat gcttgaaggt aacggccagt acacgctttt ggccccgacc aatgaggcct 900
tcgagaagat ccctagtgag actttgaacc gtatcctggg cgacccagaa gccctgagag 960
acctgctgaa caaccacatc ttgaagtcag ctatgtgtgc tgaagccatc gttgcggggc 1020
tgtctgtaga gaccctggag ggcacgacac tggaggtggg ctgcagcggg gacatgctca 1080
ctatcaacgg gaaggcgatc atctccaata aagacatcct agccaccaac ggggtgatcc 1140
actacattga tgagctactc atcccagact cagccaagac actatttgaa ttggctgcag 1200

agtctgatgt gtccacagcc attgaccttt tcagacaagc cggcctcggc aatcatctct 1260
ctggaagtga gcggttgacc ctcctggctc ccctgaattc tgtattcaaa gatggaaccc 1320
ctccaattga tgcccataca aggaatttgc ttcggaacca cataattaaa gaccagctgg 1380
cctctaagta tctgtaccat ggacagaccc tggaaactct gggcggcaaa aaactgagag 1440
tttttgttta tcgtaatagc ctctgcattg agaacagctg catcgcggcc cacgacaaga 1500
gggggaggta cgggaccctg ttcacgatgg accgggtgct gacccccca atggggactg 1560
tcatggatgt cctgaaggga gacaatcgct ttagcatgct ggtagctgcc atccagtctg 1620
caggactgac ggagaccctc aaccgggaag gagtctacac agtctttgct cccacaaatg 1680
aagccttccg agccctgcca ccaagagaac ggagcagact cttgggagat gccaaggaac 1740
ttgccaacat cctgaaatac cacattggtg atgaaatcct ggttagcgga ggcatcgggg 1800
ccctggtgcg gctaaagtct ctccaaggtg acaagctgga agtcagcttg aaaaacaatg 1860
tggtgagtgt caacaaggag cctgttgccg agcctgacat catggccaca aatggcgtgg 1920
tccatgtcat caccaatgtt ctgcagcctc cagccaacag acctcaggaa agaggggatg 1980
aacttgcaga ctctgcgctt gagatcttca aacaagcatc agcgttttcc agggcttccc 2040
agaggtctgt gcgactagcc cctgtctatc aaaagttatt agagaggatg aagcattagc 2100
ttgaagcact acaggaggaa tgcaccacgg cagctctccg ccaatttctc tcagatttcc 2160
acagagactg tttgaatgtt ttcaaaacca agtatcacac tttaatgtac atgggccgca 2220
ccataatgag atgtgagcct tgtgcatgtg ggggaggagg gagagagatg tacttttaa 2280
atcatgttcc ccctaaacat ggctgttaac ccactgcatg cagaaacttg gatgtcactg 2340
cctgacattc acttccagag aggacctatc ccaaatgtgg aattgactgc ctatgccaag 2400
tccctggaaa aggagcttca gtattgtggg gctcataaaa catgaatcaa gcaatccagc 2460
ctcatgggaa gtcctggcac agtttttgta aagcccttgc acagctggag aaatggcatc 2520
attataagct atgagttgaa atgttctgtc aaatgtgtct cacatctaca cgtggcttgg 2580
aggcttttat ggggccctgt ccaggtagaa aagaaatggt atgtagagct tagatttccc 2640
tattgtgaca gagccatggt gtgtttgtaa taataaaacc aaagaaacat a 2691

<210> 42
<211> 8027
<212> DNA
<213> Homo sapiens

<400> 42
acgcccgcgc cggctgtgct gcacaggggg aggagaggga accccaggcg cgagcgggaa 60
gaggggacct gcagccacaa cttctctggt cctctgcatc ccttctgtcc ctccacccgt 120
ccccttcccc accctctggc ccccaccttc ttggaggcga caacccccgg gaggcattag 180
aagggatttt tcccgcagtt gcgaagggaa gcaaacttgg tggcaacttg cctcccggtg 240
cgggcgtctc tcccccaccg tctcaacatg cttaggggtc cggggcccgg gctgctgctg 300
ctggccgtcc agtgcctggg gacagcggtg ccctccacgg gagcctcgaa gagcaagagg 360
caggctcagc aaatggttca gccccagtcc ccggtggctg tcagtcaaag caagcccggt 420
tgttatgaca atggaaaaca ctatcagata aatcaacagt gggagcggac ctacctaggc 480
aatgcgttgg tttgtacttg ttatggagga agccgaggtt ttaactgcga gagtaaacct 540
gaagctgaag agacttgctt tgacaagtac actgggaaca cttaccgagt gggtgacact 600
tatgagcgtc ctaaagactc catgatctgg gactgtacct gcatcggggc tgggcgaggg 660
agaataagct gtaccatcgc aaaccgctgc catgaagggg gtcagtccta caagattggt 720
gacacctgga ggagaccaca tgagactggt ggttacatgt tagagtgtgt gtgtcttggt 780
aatggaaaag gagaatggac ctgcaagccc atagctgaga agtgttttga tcatgctgct 840
gggacttcct atgtggtcgg agaaacgtgg gagaagccct accaaggctg gatgatggta 900
gattgtactt gcctgggaga aggcagcgga cgcatcactt gcacttctag aaatagatgc 960
aacgatcagg acacaaggac atcctataga attggagaca cctggagcaa gaaggataat 1020
cgaggaaacc tgctccagtg catctgcaca ggcaacggcc gaggagagtg gaagtgtgag 1080
aggcacacct ctgtgcagac cacatcgagc ggatctggcc ccttcaccga tgttcgtgca 1140
gctgtttacc aaccgcagcc tcacccccag cctcctccct atggccactg tgtcacagac 1200
agtggtgtgg tctactctgt ggggatgcag tggctgaaga cacaaggaaa taagcaaatg 1260
ctttgcacgt gcctgggcaa cggagtcagc tgccaagaga cagctgtaac ccagacttac 1320
ggtggcaact caaatggaga gccatgtgtc ttaccattca cctacaatgg caggacgttc 1380
tactcctgca ccacggaagg gcgacaggac ggacatcttt ggtgcagcac aacttcgaat 1440
tatgagcagg accagaaata ctctttctgc acagaccaca ctgttttggt tcagactcga 1500
ggaggaaatt ccaatggtgc cttgtgccac ttccccttcc tatacaacaa ccacaattac 1560
actgattgca cttctgaggg cagaagagac aacatgaagt ggtgtgggac cacacagaac 1620
tatgatgccg accagaagtt tgggttctgc cccatggctg cccacgagga aatctgcaca 1680
accaatgaag gggtcatgta ccgcattgga gatcagtggg ataagcagca tgacatgggt 1740
cacatgatga ggtgcacgtg tgttgggaat ggtcgtgggg aatggacatg cattgcctac 1800
tcgcagcttc gagatcagtg cattgttgat gacatcactt acaatgtgaa cgacacattc 1860
cacaagcgtc atgaagaggg gcacatgctg aactgtacat gcttcggtca gggtcggggc 1920
aggtggaagt gtgatcccgt cgaccaatgc caggattcag agactgggac gttttatcaa 1980
attggagatt catgggagaa gtatgtgcat ggtgtcagat accagtgcta ctgctatggc 2040
cgtggcattg gggagtggca ttgccaacct ttacagacct atccaagctc aagtggtcct 2100

gtcgaagtat ttatcactga gactccgagt cagcccaact cccaccccat ccagtggaat 2160
gcaccacagc catctcacat ttccaagtac attctcaggt ggagacctaa aaattctgta 2220
ggccgttgga aggaagctac cataccaggc cacttaaact cctacaccat caaaggcctg 2280
aagcctggtg tggtatacga gggccagctc atcagcatcc agcagtacgg ccaccaagaa 2340
gtgactcgct ttgacttcac caccaccagc accagcacac ctgtgaccag caacaccgtg 2400
acaggagaga cgactcccct ttctcctctt gtggccactt ctgaatctgt gaccgaaatc 2460
acagccagta gctttgtggt ctcctgggtc tcagcttccg acaccgtgtc gggattccgg 2520
gtggaatatg agctgagtga ggagggagat gagccacagt acctggatct tccaagcaca 2580
gccacttctg tgaacatccc tgacctgctt cctggccgaa aatacattgt aaatgtctat 2640
cagatatctg aggatgggga gcagagtttg atcctgtcta cttcacaaac aacagcgcct 2700
gatgcccctc ctgacccgac tgtggaccaa gttgatgaca cctcaattgt tgttcgctgg 2760
agcagacccc aggctcccat cacagggtac agaatagtct attcgccatc agtagaaggt 2820
agcagcacag aactcaacct tcctgaaact gcaaactccg tcaccctcag tgacttgcaa 2880
cctggtgttc agtataacat cactatctat gctgtggaag aaaatcaaga aagtacacct 2940
gttgtcattc aacaagaaac cactggcacc ccacgctcag atacagtgcc ctctcccagg 3000
gacctgcagt ttgtggaagt gacagacgtg aaggtcacca tcatgtggac accgcctgag 3060
agtgcagtga ccggctaccg tgtggatgtg atccccgtca acctgcctgg cgagcacggg 3120
cagaggctgc ccatcagcag gaacaccttt gcagaagtca ccgggctgtc ccctggggtc 3180
acctattact tcaaagtctt tgcagtgagc catgggaggg agagcaagcc tctgactgct 3240
caacagacaa ccaaactgga tgctcccact aacctccagt ttgtcaatga aactgattct 3300
actgtcctgg tgagatggac tccacctcgg gcccagataa caggataccg actgaccgtg 3360
ggccttaccc gaagaggcca gcccaggcag tacaatgtgg gtccctctgt ctccaagtac 3420
cccctgagga atctgcagcc tgcatctgag tacaccgtat ccctcgtggc cataaagggc 3480
aaccaagaga gccccaaagc cactggagtc tttaccacac tgcagcctgg gagctctatt 3540
ccaccttaca acaccgaggt gactgagacc accatcgtga tcacatggac gcctgctcca 3600
agaattggtt ttaagctggg tgtacgacca agccagggag gagaggcacc acgagaagtg 3660
acttcagact caggaagcat cgttgtgtcc ggcttgactc caggagtaga atacgtctac 3720
accatccaag tcctgagaga tggacaggaa agagatgcgc caattgtaaa caaagtggtg 3780
acaccattgt ctccaccaac aaacttgcat ctggaggcaa accctgacac tggagtgctc 3840
acagtctcct gggagaggag caccacccca gacattactg gttatagaat taccacaacc 3900
cctacaaacg gccagcaggg aaattctttg gaagaagtgg tccatgctga tcagagctcc 3960
tgcacttttg ataacctgag tcccggcctg gagtacaatg tcagtgttta cactgtcaag 4020
gatgacaagg aaagtgtccc tatctctgat accatcatcc cagctgttcc tcctcccact 4080
gacctgcgat tcaccaacat tggtccagac accatgcgtg tcacctgggc tccacccca 4140
tccattgatt taaccaactt cctggtgcgt tactcacctg tgaaaaatga ggaagatgtt 4200
gcagagttgt caatttctcc ttcagacaat gcagtggtct taacaaatct cctgcctggt 4260
acagaatatg tagtgagtgt ctccagtgtc tacgaacaac atgagagcac acctcttaga 4320
ggaagacaga aaacaggtct tgattcccca actggcattg acttttctga tattactgcc 4380
aactctttta ctgtgcactg gattgctcct cgagccacca tcactggcta caggatccgc 4440
catcatcccg agcacttcag tgggagacct cgagaagatc gggtgcccca ctctcggaat 4500
tccatcaccc tcaccaacct cactccaggc acagagtatg tggtcagcat cgttgctctt 4560
aatggcagag aggaaagtcc cttattgatt ggccaacaat caacagtttc tgatgttccg 4620
agggacctgg aagttgttgc tgcgacccca accagcctac tgatcagctg ggatgctcct 4680
gctgtcacag tgagatatta caggatcact tacggagaaa caggaggaaa tagccctgtc 4740
caggagttca ctgtgcctgg gagcaagtct acagctacca tcagcggcct taaacctgga 4800
gttgattata ccatcactgt gtatgctgtc actggccgtg gagacagccc cgcaagcagc 4860
aagccaattt ccattaatta ccgaacagaa attgacaaac catcccagat gcaagtgacc 4920
gatgttcagg acaacagcat tagtgtcaag tggctgcctt caagttcccc tgttactggt 4980
tacagagtaa ccaccactcc caaaaatgga ccaggaccaa caaaaactaa aactgcaggt 5040
ccagatcaaa cagaaatgac tattgaaggc ttgcagccca cagtggagta tgtggttagt 5100
gtctatgctc agaatccaag cggagagagt cagcctctgg ttcagactgc agtaaccaac 5160
attgatcgcc ctaaaggact ggcattcact gatgtggatg tcgattccat caaaattgct 5220
tgggaaagcc cacaggggca agtttccagg tacagggtga cctactcgag ccctgaggat 5280
ggaatccatg agctattccc tgcacctgat ggtgaagaag acactgcaga gctgcaaggc 5340
ctcagaccgg gttctgagta cacagtcagt gtggttgcct tgcacgatga tatggagagc 5400
cagcccctga ttggaaccca gtccacagct attcctgcac caactgacct gaagttcact 5460
caggtcacac ccacaagcct gagcgcccag tggacaccac ccaatgttca gctcactgga 5520
tatcgagtgc gggtgacccc caaggagaag accggaccaa tgaaagaaat caaccttgct 5580
cctgacagct catccgtggt tgtatcagga cttatggtgg ccaccaaata tgaagtgagt 5640
gtctatgctc ttaaggacac tttgacaagc agaccagctc agggtgttgt caccactctg 5700
gagaatgtca gcccaccaag aagggctcgt gtgacagatg ctactgagac caccatcacc 5760
attagctgga gaaccaagac tgagacgatc actggcttcc aagttgatgc cgttccagcc 5820
aatggccaga ctccaatcca gagaaccatc aagccagatg tcagaagcta caccatcaca 5880
ggtttacaac caggcactga ctacaagatc tacctgtaca ccttgaatga caatgctcgg 5940
agctcccctg tggtcatcga cgcctccact gccattgatg caccatccaa cctgcgtttc 6000
ctggccacca cacccaattc cttgctggta tcatggcagc cgccacgtgc caggattacc 6060
ggctacatca tcaagtatga gaagcctggg tctcctccca gagaagtggt ccctcggccc 6120

cgccctggtg tcacagaggc tactattact ggcctggaac cgggaaccga atatacaatt 6180
tatgtcattg ccctgaagaa taatcagaag agcgagcccc tgattggaag gaaaaagaca 6240
gacgagcttc cccaactggt aacccttcca caccccaatc ttcatggacc agagatcttg 6300
gatgttcctt ccacagttca aaagacccct ttcgtcaccc accctgggta tgacactgga 6360
aatggtattc agcttcctgg cacttctggt cagcaaccca gtgttgggca acaaatgatc 6420
tttgaggaac atggttttag gcggaccaca ccgcccacaa cggccacccc cataaggcat 6480
aggccaagac catacccgcc gaatgtagga caagaagctc tctctcagac aaccatctca 6540
tgggccccat tccaggacac ttctgagtac atcatttcat gtcatcctgt tggcactgat 6600
gaagaaccct tacagttcag ggttcctgga acttctacca gtgccactct gacaggcctc 6660
accagaggtg ccacctacaa catcatagtg gaggcactga aagaccagca gaggcataag 6720
gttcgggaag aggttgttac cgtgggcaac tctgtcaacg aaggcttgaa ccaacctacg 6780
gatgactcgt gctttgaccc ctacacagtt tcccattatg ccgttggaga tgagtgggaa 6840
cgaatgtctg aatcaggctt taaactgttg tgccagtgct taggctttgg aagtggtcat 6900
ttcagatgtg attcatctag atggtgccat gacaatggtg tgaactacaa gattggagag 6960
aagtgggacc gtcagggaga aaatggccag atgatgagct gcacatgtct tgggaacgga 7020
aaaggagaat tcaagtgtga ccctcatgag gcaacgtgtt acgatgatgg gaagacatac 7080
cacgtaggag aacagtggca gaaggaatat ctcggtgcca tttgctcctg cacatgcttt 7140
ggaggccagc ggggctggcg ctgtgacaac tgccgcagac ctgggggtga acccagtccc 7200
gaaggcacta ctggccagtc ctacaaccag tattctcaga gataccatca gagaacaaac 7260
actaatgtta attgcccaat tgagtgcttc atgcctttag atgtacaggc tgacagagaa 7320
gattcccgag agtaaatcat ctttccaatc cagaggaaca agcatgtctc tctgccaaga 7380
tccatctaaa ctggagtgat gttagcagac ccagcttaga gttcttcttt ctttcttaag 7440
ccctttgctc tggaggaagt tctccagctt cagctcaact cacagcttct ccaagcatca 7500
ccctgggagt ttcctgaggg ttttctcata aatgagggct gcacattgcc tgttctgctt 7560
cgaagtattc aataccgctc agtattttaa atgaagtgat tctaagattt ggtttgggat 7620
caataggaaa gcatatgcag ccaaccaaga tgcaaatgtt ttgaaatgat atgaccaaaa 7680
ttttaagtag gaaagtcacc caaacacttc tgctttcact taagtgtctg gcccgcaata 7740
ctgtaggaac aagcatgatc ttgttactgt gatattttaa atatccacag tactcacttt 7800
ttccaaatga tcctagtaat tgcctagaaa tatctttctc ttacctgtta tttatcaatt 7860
tttcccagta tttttatacg gaaaaaattg tattgaaaac acttagtatg cagttgataa 7920
gaggaatttg gtataattat ggtgggtgat tatttttat actgtatgtg ccaaagcttt 7980
actactgtgg aaagacaact gttttaataa aagatttaca ttccaca 8027

<210> 43
<211> 5084
<212> DNA
<213> Homo sapiens

<400> 43
agcaccacgg cagcaggagg tttcggctaa gttggaggta ctggccacga ctgcatgccc 60
gcgcccgcca ggtgatacct ccgccggtga cccaggggct ctgcgacaca aggagtctgc 120
atgtctaagt gctagacatg ctcagctttg tggatacgcg gactttgttg ctgcttgcag 180
taaccttatg cctagcaaca tgccaatctt tacaagagga aactgtaaga aagggcccag 240
ccggagatag aggaccacgt ggagaaaggg gtccaccagg ccccccaggc agagatggtg 300
aagatggtcc cacaggccct cctggtccac ctggtcctcc tggcccccct ggtctcggtg 360
ggaactttgc tgctcagtat gatggaaaag gagttggact tggccctgga ccaatgggct 420
taatgggacc tagaggccca cctggtgcag ctggagcccc aggccctcaa ggtttccaag 480
gacctgctgg tgagcctggt gaacctggtc aaactggtcc tgcaggtgct cgtggtccag 540
ctggccctcc tggcaaggct ggtgaagatg gtcaccctgg aaaacccgga cgacctggtg 600
agagaggagt tgttggacca cagggtgctc gtggtttccc tggaactcct ggacttcctg 660
gcttcaaagg cattagggga cacaatggtc tggatggatt gaagggacag cccggtgctc 720
ctggtgtgaa gggtgaacct ggtgcccctg gtgaaaatgg aactccaggt caaacaggag 780
cccgtgggct tcctggtgag agaggacgtg ttggtgcccc tggcccagct ggtgcccgtg 840
gcagtgatgg aagtgtgggt cccgtgggtc ctgctggtcc cattgggtct gctggccctc 900
caggcttccc aggtgccctt ggccccaagg gtgaaattgg agctgttggt aacgctggtc 960
ctgctggtcc cgccggtccc cgtggtgaag tgggtcttcc aggcctctcc ggccccgttg 1020
gacctcctgg taatcctgga gcaaacggcc ttactggtgc caagggtgct gctggccttc 1080
ccggcgttgc tggggctccc ggcctccctg gaccccgcgg tattcctggc cctgttggtg 1140
ctgccggtgc tactggtgcc agaggacttg ttggtgagcc tggtccagct ggctccaaag 1200
gagagagcgg taacaagggt gagcccggct ctgctgggcc ccaaggtcct cctggtccca 1260
gtggtgaaga aggaaagaga ggccctaatg gggaagctgg atctgccggc cctccaggac 1320
ctcctgggct gagaggtagt cctggttctc gtggtcttcc tggagctgat ggcagagctg 1380
gcgtcatggg ccctcctggt agtcgtggtg caagtggccc tgctggagtc cgaggaccta 1440
atggagatgc tggtcgccct ggggagcctg gtctcatggg acccagaggt cttcctggtt 1500
cccctggaaa tatcggcccc gctggaaaag aaggtcctgt cggcctccct ggcatcgacg 1560
gcaggcctgg cccaattggc ccagctggag caagaggaga gcctggcaac attggattcc 1620
ctggacccaa aggccccact ggtgatcctg gcaaaaacgg tgataaaggt catgctggtc 1680

ttgctggtgc tcggggtgct ccaggtcctg atggaaacaa tggtgctcag ggacctcctg 1740
gaccacaggg tgttcaaggt ggaaaaggtg aacagggtcc cgctggtcct ccaggcttcc 1800
agggtctgcc tggcccctca ggtcccgctg gtgaagttgg caaaccagga gaaaggggtc 1860
tccatggtga gtttggtctc cctggtcctg ctggtccaag aggggaacgc ggtcccccag 1920
gtgagagtgg tgctgccggt cctactggtc ctattggaag ccgaggtcct tctggacccc 1980
cagggcctga tggaaacaag ggtgaacctg gtgtggttgg tgctgtgggc actgctggtc 2040
catctggtcc tagtggactc ccaggagaga ggggtgctgc tggcatacct ggaggcaagg 2100
gagaaaaggg tgaacctggt ctcagaggtg aaattggtaa ccctggcaga gatggtgctc 2160
gtggtgctca tggtgctgta ggtgcccctg gtcctgctgg agccacaggt gaccggggcg 2220
aagctggggc tgctggtcct gctggtcctg ctggtcctcg gggaagccct ggtgaacgtg 2280
gcgaggtcgg tcctgctggc cccaacggat ttgctggtcc ggctggtgct gctggtcaac 2340
cgggtgctaa aggagaaaga ggagccaaag ggcctaaggg tgaaaacggt gttgttggtc 2400
ccacaggccc cgttggagct gctggcccag ctggtccaaa tggtcccccc ggtcctgctg 2460
gaagtcgtgg tgatggaggc ccccctggta tgactggttt ccctggtgct gctggacgga 2520
ctggtccccc aggaccctct ggtatttctg gccctcctgg tccccctggt cctgctggga 2580
aagaagggct tcgtggtcct cgtggtgacc aaggtccagt tggccgaact ggagaagtag 2640
gtgcagttgg tccccctggc ttcgctggtg agaagggtcc ctctggagag gctggtactg 2700
ctggacctcc tggcactcca ggtcctcagg gtcttcttgg tgctcctggt attctgggtc 2760
tccctggctc gagaggtgaa cgtggtctac ctggtgttgc tggtgctgtg ggtgaacctg 2820
gtcctcttgg cattgccggc cctcctgggg cccgtggtcc tcctggtgct gtgggtagtc 2880
ctggagtcaa cggtgctcct ggtgaagctg gtcgtgatgg caaccctggg aacgatggtc 2940
ccccaggtcg cgatggtcaa cccggacaca agggagagcg cggttaccct ggcaatattg 3000
gtcccgttgg tgctgcaggt gcacctggtc ctcatggccc cgtgggtcct gctggcaaac 3060
atggaaaccg tggtgaaact ggtccttctg gtcctgttgg tcctgctggt gctgttggcc 3120
caagaggtcc tagtggccca caaggcattc gtggcgataa gggagagccc ggtgaaaagg 3180
ggcccagagg tcttcctggc ttaaagggac acaatggatt gcaaggtctg cctggtatcg 3240
ctggtcacca tggtgatcaa ggtgctcctg gctccgtggg tcctgctggt cctaggggcc 3300
ctgctggtcc ttctggccct gctggaaaag atggtcgcac tggacatcct ggtacggttg 3360
gacctgctgg cattcgaggc cctcagggtc accaaggccc tgctggcccc cctggtcccc 3420
ctggccctcc tggacctcca ggtgtaagcg gtggtggtta tgactttggt tacgatggag 3480
acttctacag ggctgaccag cctcgctcag caccttctct cagacccaag gactatgaag 3540
ttgatgctac tctgaagtct ctcaacaacc agattgagac ccttcttact cctgaaggct 3600
ctagaaagaa cccagctcgc acatgccgtg acttgagact cagccaccca gagtggagca 3660
gtggttacta ctggattgac cctaaccaag gatgcactat ggatgctatc aaagtatact 3720
gtgatttctc tactggcgaa acctgtatcc gggcccaacc tgaaaacatc ccagccaaga 3780
actggtatag gagctccaag gacaagaaac acgtctggct aggagaaact atcaatgctg 3840
gcagccagtt tgaatataat gtagaaggag tgacttccaa ggaaatggct acccaacttg 3900
ccttcatgcg cctgctggcc aactatgcct ctcagaacat cacctaccac tgcaagaaca 3960
gcattgcata catggatgag gagactggca acctgaaaaa ggctgtcatt ctacagggct 4020
ctaatgatgt tgaacttgtt gctgagggca acagcaggtt cacttacact gttcttgtag 4080
atggctgctc taaaaagaca aatgaatggg gaaagacaat cattgaatac aaaacaaata 4140
agccatcacg cctgcccttc cttgatattg caccttgga catcggtggt gctgaccatg 4200
aattctttgt ggacattggc ccagtctgtt tcaaataaat gaactcaatc taaattaaaa 4260
aagaaagaaa tttgaaaaaa ctttctcttt gccatttctt cttcttcttt tttaactgaa 4320
agctgaatcc ttccatttct tctgcacatc tacttgctta aattgtgggc aaaagagaaa 4380
aagaaggatt gatcagagca ttgtgcaata cagtttcatt aactccttcc cccgctcccc 4440
caaaaatttg aatttttttt tcaacactct tacacctgtt atggaaaatg tcaacctttg 4500
taagaaaacc aaaataaaaa ttgaaaaata aaaaccataa acatttgcac cacttgtggc 4560
ttttgaatat cttccacaga gggaagttta aaacccaaac ttccaaaggt ttaaactacc 4620
tcaaaacact ttcccatgag tgtgatccac attgttaggt gctgacctag acagagatga 4680
actgaggtcc ttgttttgtt ttgttcataa tacaaaggtg ctaattaata gtatttcaga 4740
tacttgaaga atgttgatgg tgctagaaga atttgagaag aaatactcct gtattgagtt 4800
gtatcgtgtg gtgtattttt taaaaaattt gatttagcat tcatattttc catcttattc 4860
ccaattaaaa gtatgcagat tatttgccca aagttgtcct cttcttcaga ttcagcattt 4920
gttctttgcc agtctcattt tcatcttctt ccatggttcc acagaagctt tgtttcttgg 4980
gcaagcagaa aaattaaatt gtacctattt tgtatatgtg agatgtttaa ataaattgtg 5040
aaaaaaatga aataaagcat gtttggtttt ccaaaagaac atat 5084

<210> 44
<211> 595
<212> DNA
<213> Homo sapiens

<400> 44
gggcaaggct gggccgggaa gggcgtgggt tgaggagagg ctccagaccc gcacgccgcg 60
cgcacagagc tctcagcgcc gctcccagcc acagcctccc gcgcctcgct cagctccaac 120
atggcaaaaa tctccagccc tacagagact gagcggtgca tcgagtccct gattgctgtc 180

ttccagaagt atgctggaaa ggatggttat aactacactc tctccaagac agagttccta 240
agcttcatga atacagaact agctgccttc acaaagaacc agaaggaccc tggtgtcctt 300
gaccgcatga tgaagaaact ggacaccaac agtgatggtc agctagattt ctcagaattt 360
cttaatctga ttggtggcct agctatggct tgccatgact ccttcctcaa ggctgtccct 420
tcccagaagc ggacctgagg acccccttggc cctggccttc aaacccaccc cctttccttc 480
cagcctttct gtcatcatct ccacagccca cccatccccc gagcacacta accacctcat 540
gcaggcccca cctgccaata gtaataaagc aatgtcactt ttttaaaaca tgaaa 595

<210> 45
<211> 647
<212> DNA
<213> Homo sapiens

<400> 45
gctcactgag caccgtccca gcatccggac accacagcgg cccttcgctc cacgcagaaa 60
accacacttc tcataccttc actcaacact tccttcccca aagccagaag atgcacaagg 120
aggaacatga ggtggctgtg ctgggggcac cccccagcac catccttcca aggtccaccg 180
tgattaacat ccacagcgag acctccgtgc ccgaccatgt cgtctggtcc ctgttcaaca 240
ccctcttctt gaactggtgc tgtctgggct tcatagcatt cgcctactcc gtaaagtcta 300
gggacaggaa gatggttggc gacgtgaccg gggcccaggc ctatgcctcc accgccaagt 360
gcctgaacat ctgggccctg attctgggca tcctcatgac cattggattc atcctgttac 420
tggtattcgg ctctgtaaca gtctaccata ttatgttaca gataatacag gaaaaacggg 480
gttactagta gccgcccata gcctgcaacc tttgcactcc actgtgcaat gctggccctg 540
cacgctgggg ctgttgcccc tgcccccttg gtcctgcccc tagatacagc agtttatacc 600
cacacacctg tctacagtgt cattcaataa agtgcacgtg cttgtga 647

<210> 46
<211> 2067
<212> DNA
<213> Homo sapiens

<400> 46
cgctttttt ttttttttt atgaataaat tgtatgtgtt tctagctgaa actactcacc 60
aatatgcatg ttaaattcaa tcctctctta cctattcttt gatataactc cttgaagttt 120
tcccattctc ctacatcatc tcccccaccc ccactgagtc atttctataa tacaaacata 180
ttatcttttt attaaattaa aaatctacct gtacaccttg aatgacaatg ctcggagctc 240
ccctgtggtc atcgacgcct ccactgccat tgatgcacca tccaacctgc gtttcctggc 300
caccacaccc aattccttgc tggtatcatg gcagccgcca cgtgccagga ttaccggcta 360
catcatcaag tatgagaagc ctgggtctcc tcccagagaa gtggtccctc ggccccgccc 420
tggtgtcaca gaggctacta ttactggcct ggaaccggga accgaatata caatttatgt 480
cattgccctg aagaataatc agaagagcga gcccctgatt ggaaggaaaa agacaggaca 540
agaagctctc tctcagacaa ccatctcatg ggcccattc caggacactt ctgagtacat 600
catttcatgt catcctgttg gcactgatga agaaccctta cagttcaggg ttcctggaac 660
ttctaccagt gccactctga caggcctcac cagaggtgcc acctacaaca tcatagtgga 720
ggcactgaaa gaccagcaga ggcataaggt tcgggaagag gttgttaccg tgggcaactc 780
tgtcaacgaa ggcttgaacc aacctacgga tgactcgtgc tttgacccct acacagtttc 840
ccattatgcc gttggagatg agtgggaacg aatgtctgaa tcaggcttta aactgttgtg 900
ccagtgctta ggctttggaa gtggtcattt cagatgtgat tcatctagat ggtgccatga 960
caatggtgtg aactacaaga ttggagagaa gtgggaccgt cagggagaaa atggccagat 1020
gatgagctgc acatgtcttg ggaacggaaa aggagaattc aagtgtgacc ctcatgaggc 1080
aacgtgttat gatgatggga agacatacca cgtaggagaa cagtggcaga aggaatatct 1140
cggtgccatt tgctcctgca catgctttgg aggccagcgg ggctggcgct gtgacaactg 1200
ccgcagacct gggggtgaac ccagtcccga aggcactact ggccagtcct acaaccagta 1260
ttctcagaga taccatcaga gaacaaacac taatgttaat tgcccaattg agtgcttcat 1320
gcctttagat gtacaggctg acagagaaga ttcccgagag taaatcatct ttccaatcca 1380
gaggaacaag catgtctctc tgccaagatc catctaaact ggagtgatgt tagcagaccc 1440
agcttagagt tcttctttct ttcttaagcc ctttgctctg gaggaagttc tccagcttca 1500
gctcaactca cagcttctcc aagcatcacc ctgggagttt cctgagggtt ttctcataaa 1560
tgagggctgc acattgcctg ttctgcttcg aagtattcaa taccgctcag tattttaaat 1620
gaagtgattc taagatttgg tttgggatca ataggaaagc atatgcagcc aaccaagatg 1680
caaatgtttt gaaatgatat gaccaaaatt ttaagtagga aagtcaccca aacacttctg 1740
ctttcactta agtgtctggc ccgcaatact gtaggaacaa gcatgatctt gttactgtga 1800
tattttaaat atccacagta ctcacttttt ccaaatgatc ctagtaattg cctagaaata 1860
tctttctctt acctgttatt tatcaatttt tcccagtatt tttatacgga aaaaattgta 1920
ttgaaaacac ttagtatgca gttgataaga ggaatttggt ataattatgg tgggtgatta 1980
ttttttatac tgtatgtgcc aaagctttac tactgtggaa agacaactgt tttaataaaa 2040
gatttacatt ccaaaaaaaa aaaaaaa 2067

<210> 47
<211> 5489
<212> DNA
<213> Homo sapiens

<400> 47
ggctgagttt tatgacgggc ccggtgctga agggcaggga acaacttgat ggtgctactt 60
tgaactgctt ttcttttctc ctttttgcac aaagagtctc atgtctgata tttagacatg 120
atgagctttg tgcaaaaggg gagctggcta cttctcgctc tgcttcatcc cactattatt 180
ttggcacaac aggaagctgt tgaaggagga tgttcccatc ttggtcagtc ctatgcggat 240
agagatgtct ggaagccaga accatgccaa atatgtgtct gtgactcagg atccgttctc 300
tgcgatgaca taatatgtga cgatcaagaa ttagactgcc ccaacccaga aattccattt 360
ggagaatgtt gtgcagtttg cccacagcct ccaactgctc ctactcgccc tcctaatggt 420
caaggacctc aaggccccaa gggagatcca ggccctcctg gtattcctgg gagaaatggt 480
gaccctggta ttccaggaca accagggtcc cctggttctc ctggcccccc tggaatctgt 540
gaatcatgcc ctactggtcc tcagaactat tctccccagt atgattcata tgatgtcaag 600
tctggagtag cagtaggagg actcgcaggc tatcctggac cagctggccc cccaggccct 660
cccggtcccc ctggtacatc tggtcatcct ggttcccctg gatctccagg ataccaagga 720
ccccctggtg aacctgggca agctggtcct tcaggccctc caggacctcc tggtgctata 780
ggtccatctg gtcctgctgg aaaagatgga gaatcaggta gacccggacg acctggagag 840
cgaggattgc ctggacctcc aggtatcaaa ggtccagctg ggatacctgg attccctggt 900
atgaaaggac acagaggctt cgatggacga aatggagaaa agggtgaaac aggtgctcct 960
ggattaaagg gtgaaaatgg tcttccaggc gaaaatggag ctcctggacc catgggtcca 1020
agaggggctc ctggtgagcg aggacggcca ggacttcctg gggctgcagg tgctcggggt 1080
aatgacggtg ctcgaggcag tgatggtcaa ccaggccctc ctggtcctcc tggaactgcc 1140
ggattccctg gatcccctgg tgctaagggt gaagttggac ctgcagggtc tcctggttca 1200
aatggtgccc ctggacaaag aggagaacct ggacctcagg gacacgctgg tgctcaaggt 1260
cctcctggcc ctcctgggat taatggtagt cctggtggta aaggcgaaat gggtcccgct 1320
ggcattcctg gagctcctgg actgatggga gcccggggtc ctccaggacc agccggtgct 1380
aatggtgctc ctggactgcg aggtggtgca ggtgagcctg gtaagaatgg tgccaaagga 1440
gagcccggac cacgtggtga acgcggtgag gctggtattc caggtgttcc aggagctaaa 1500
ggcgaagatg gcaaggatgg atcacctgga gaacctggtg caaatgggct tccaggagct 1560
gcaggagaaa ggggtgcccc tgggttccga ggacctgctg gaccaaatgg catcccagga 1620
gaaaagggtc ctgctggaga gcgtggtgct ccaggccctg cagggcccag aggagctgct 1680
ggagaacctg gcagagatgg cgtccctgga ggtccaggaa tgaggggcat gcccggaagt 1740
ccaggaggac caggaagtga tgggaaacca gggcctcccg gaagtcaagg agaaagtggt 1800
cgaccaggtc ctcctgggcc atctggtccc cgaggtcagc ctggtgtcat gggcttcccc 1860
ggtcctaaag gaaatgatgg tgctcctggt aagaatggag aacgaggtgg ccctggagga 1920
cctggccctc agggtcctcc tggaaagaat ggtgaaactg gacctcaagg acccccaggg 1980
cctactgggc ctggtggtga caaaggagac acaggacccc ctggtccaca aggattacaa 2040
ggcttgcctg gtacaggtgg tcctccagga gaaaatggaa aacctgggga accaggtcca 2100
aagggtgatg ccggtgcacc tggagctcca ggaggcaagg gtgatgctgg tgcccctggt 2160
gaacgtggac ctcctggatt ggcaggggcc ccaggactta gaggtggagc tggtcccctc 2220
ggtcccgaag gaggaaaggg tgctgctggt cctcctgggc cacctggtgc tgctggtact 2280
cctggtctgc aaggaatgcc tggagaaaga ggaggtcttg gaagtcctgg tccaaagggt 2340
gacaagggtg aaccaggcgg cccaggtgct gatggtgtcc cagggaaaga tggcccaagg 2400
ggtcctactg gtcctattgg tcctcctggc ccagctggcc agcctggaga taagggtgaa 2460
ggtggtgccc ccggacttcc aggtatagct ggacctcgtg gtagccctgg tgagagaggt 2520
gaaactggcc ctccaggacc tgctggtttc cctggtgctc ctggacagaa tggtgaacct 2580
ggtggtaaag gagaaagagg ggctccgggt gagaaaggtg aaggaggccc tcctggagtt 2640
gcaggacccc ctggaggttc tggacctgct ggtcctcctg gtccccaagg tgtcaaaggt 2700
gaacgtggca gtcctggtgg acctggtgct gctggcttcc ctggtgctcg tggtcttcct 2760
ggtcctcctg gtagtaatgg taacccagga cccccaggtc ccagcggttc tccaggcaag 2820
gatgggcccc caggtcctgc gggtaacact ggtgctcctg gcagccctgg agtgtctgga 2880
ccaaaaggtg atgctggcca accaggagag aagggatcgc ctggtgccca gggcccacca 2940
ggagctccag gcccacttgg gattgctggg atcactggag cacggggtct tgcaggacca 3000
ccaggcatgc caggtcctag gggaagccct ggccctcagg gtgtcaaggg tgaaagtggg 3060
aaaccaggag ctaacggtct cagtggagaa cgtggtcccc ctggacccca gggtcttcct 3120
ggtctggctg gtacagctgg tgaacctgga agagatggaa accctggatc agatggtctt 3180
ccaggccgag atggatctcc tggtggcaag ggtgatcgtg gtgaaaatgg ctctcctggt 3240
gcccctggcg ctcctggtca tccaggccca cctggtcctg tcggtccagc tggaaagagt 3300
ggtgacagag gagaaagtgg ccctgctggc cctgctggtg ctcccggtcc tgctggttcc 3360
cgaggtgctc ctggtcctca aggcccacgt ggtgacaaag gtgaaacagg tgaacgtgga 3420
gctgctggca tcaaaggaca tcgaggattc cctggtaatc caggtgcccc aggttctcca 3480
ggccctgctg gtcagcaggg tgcaatcggc agtccaggac ctgcaggccc cagaggacct 3540
gttggaccca gtggacctcc tggcaaagat ggaaccagtg gacatccagg tcccattgga 3600

ccaccagggc ctcgaggtaa cagaggtgaa agaggatctg agggctcccc aggccaccca 3660
gggcaaccag gccctcctgg acctcctggt gcccctggtc cttgctgtgg tggtgttgga 3720
gccgctgcca ttgctgggat tggaggtgaa aaagctggcg gttttgcccc gtattatgga 3780
gatgaaccaa tggatttcaa aatcaacacc gatgagatta tgacttcact caagtctgtt 3840
aatggacaaa tagaaagcct cattagtcct gatggttctc gtaaaaaccc cgctagaaac 3900
tgcagagacc tgaaattctg ccatcctgaa ctcaagagtg gagaatactg ggttgaccct 3960
aaccaaggat gcaaattgga tgctatcaag gtattctgta atatggaaac tggggaaaca 4020
tgcataagtg ccaatccttt gaatgttcca cggaaacact ggtggacaga ttctagtgct 4080
gagaagaaac acgtttggtt tggagagtcc atggatggtg gttttcagtt tagctacggc 4140
aatcctgaac ttcctgaaga tgtccttgat gtgcagctgg cattccttcg acttctctcc 4200
agccgagctt cccagaacat cacatatcac tgcaaaaata gcattgcata catggatcag 4260
gccagtggaa atgtaaagaa ggccctgaag ctgatggggt caaatgaagg tgaattcaag 4320
gctgaaggaa atagcaaatt cacctacaca gttctggagg atggttgcac gaaacacact 4380
ggggaatgga gcaaaacagt ctttgaatat cgaacacgca aggctgtgag actacctatt 4440
gtagatattg caccctatga cattggtggt cctgatcaag aatttggtgt ggacgttggc 4500
cctgtttgct ttttataaac caaactctat ctgaaatccc aacaaaaaaa atttaactcc 4560
atatgtgttc ctcttgttct aatcttgtca accagtgcaa gtgaccgaca aaattccagt 4620
tatttatttc caaaatgttt ggaaacagta taatttgaca aagaaaaatg atacttctct 4680
ttttttgctg ttccaccaaa tacaattcaa atgctttttg ttttatttttt ttaccaattc 4740
caatttcaaa atgtctcaat ggtgctataa taaataaact tcaacactct ttatgataac 4800
aacactgtgt tatattcttt gaatcctagc ccatctgcag agcaatgact gtgctcacca 4860
gtaaaagata acctttcttt ctgaaatagt caaatacgaa attagaaaag ccctccctat 4920
tttaactacc tcaactggtc agaaacacag attgtattct atgagtccca gaagatgaaa 4980
aaaattttat acgttgataa aacttataaa tttcattgat taatctcctg gaagattggt 5040
ttaaaaagaa aagtgtaatg caagaattta aagaaatatt tttaaagcca caattatttt 5100
aatattggat atcaactgct tgtaaaggtg ctcctctttt ttcttgtcat tgctggtcaa 5160
gattactaat atttgggaag gctttaaaga cgcatgttat ggtgctaatg tactttcact 5220
tttaaactct agatcagaat tgttgacttg cattcagaac ataaatgcac aaaatctgta 5280
catgtctccc atcagaaaga ttcattggca tgccacaggg attctcctcc ttcatcctgt 5340
aaaggtcaac aataaaaacc aaattatggg gctgcttttg tcacactagc atagagaatg 5400
tgttgaaatt taactttgta agcttgtatg tggttgttga tctttttttt ccttacagac 5460
acccataata aaatatcata ttaaaattc 5489

<210> 48
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 48
acagagctta ggacacagag cacatcaaaa gttcccaaag agggcttgct ctctcttcac 60
ctgctctgtt ctacagcaca ctaccagaag acagcagaaa tgaaaagcat ttactttgtg 120
gctggattat ttgtaatgct ggtacaaggc agctggcaac gttcccttca agacacagag 180
gagaaatcca gatcattctc agcttcccag gcagacccac tcagtgatcc tgatcagatg 240
aacgaggaca agcgccattc acagggcaca ttcaccagtg actacagcaa gtatctggac 300
tccaggcgtg cccaagattt tgtgcagtgg ttgatgaata ccaagaggaa caggaataac 360
attgccaaac gtcacgatga atttgagaga catgctgaag ggacctttac cagtgatgta 420
agttcttatt tggaaggcca agctgccaag gaattcattg cttggctggt gaaaggccga 480
ggaaggcgag atttcccaga agaggtcgcc attgttgaag aacttggccg cagacatgct 540
gatggttctt tctctgatga gatgaacacc attcttgata atcttgccgc cagggacttt 600
ataaactggt tgattcagac caaaatcact gacaggaaat aactatatca ctattcaaga 660
tcatcttcac aacatcacct gctagccacg tgggatgttt gaaatgttaa gtcctgtaaa 720
tttaagaggt gtattctgag gccacattgc tttgcatgcc aataaataaa ttttctttta 780
gtgttgtgta gccaaaaatt acaaatggaa taaagtttta tcaaaatatt gctaaaatat 840
cagctttaaa atatgaaagt gctagattct gttatttttct tcttattttg gatgaagtac 900
cccaacctgt ttacatttag cgataaaatt atttttctat gatataattt gtaaatgtaa 960
attattccga tctgacatat ctgcattata ataataggag aatagaagaa ctggtagcca 1020
cagtggtgaa attggaaaga gaactttctt cctgaaacct ttgtcttaaa aatactcagc 1080
tttcaatgta tcaaagatac aattaaataa aattttcaag cttcttta 1128

<210> 49
<211> 3528
<212> DNA
<213> Homo sapiens

<400> 49
tatgcatgga gtggacctgt aggcgacttg catcgtcttc aacatgaaga tagccacagt 60
gtcagtgctt ctgcccttgg ctctttgcct catacaagat gctgccagta agaatgaaga 120

tcaggaaatg tgccatgaat ttcaggcatt tatgaaaaat ggaaaactgt tctgtcccca 180
ggataagaaa ttttttcaaa gtcttgatgg aataatgttc atcaataaat gtgccacgtg 240
caaaatgata ctggaaaaag aagcaaaatc acagaagagg gccaggcatt tagcaagagc 300
tcccaaggct actgccccaa cagagctgaa ttgtgatgat tttaaaaaag gagaaagaga 360
tggggatttt atctgtcctg attattatga agctgtttgt ggcacagatg ggaaaacata 420
tgacaacaga tgtgcactgt gtgctgagaa tgcgaaaacc gggtcccaaa ttggtgtaaa 480
aagtgaaggg gaatgtaaga gcagtaatcc agagcaggat gtatgcagtg cttttcggcc 540
ctttgttaga gatggaagac ttggatgcac aagggaaaat gatcctgttc ttggtcctga 600
tgggaagacg catggcaata agtgtgcaat gtgtgctgag ctgtttttaa aagaagctga 660
aaatgccaag cgagagggtg aaactagaat tcgacgaaat gctgaaaagg atttttgcaa 720
ggaatatgaa aaacaagtga gaaatggaag gctttttttgt acacgggaga gtgatccagt 780
ccgtggccct gacggcagga tgcatggcaa caaatgtgcc ctgtgtgctg aaattttcaa 840
gcggcgtttt tcagaggaaa acagtaaaac agatcaaaat ttgggaaaag ctgaagaaaa 900
aactaaagtt aaaagagaaa ttgtgaaact ctgcagtcaa tatcaaaatc aggcaaagaa 960
tggaatactt ttctgtacca gagaaaatga ccctattcgt ggtccagatg ggaaaatgca 1020
tggcaacttg tgttccatgt gtcaagtcta cttccaagca gaaaatgaag aaaagaaaaa 1080
ggctgaagca cgagctagaa acaaaagaga atctggaaaa gcaacctcat atgcagagct 1140
ttgcaatgaa tatcgaaagc ttgtgaggaa cggaaaactt gcttgcacca gagagaacga 1200
tcctatccag ggcccagatg ggaaagtgca cggcaacacc tgctccatgt gtgaggtctt 1260
cttccaagca gaagaagaag aaaagaaaaa gaaggaaggc gaatcaagaa acaaaagaca 1320
atctaagagt acagcttcct ttgaggagtt gtgtagtgaa taccgcaaat ccaggaaaaa 1380
cggacggctt ttttgcacca gagagaatga ccccatccag ggcccagatg ggaaaatgca 1440
tggcaacacc tgctccatgt gtgaggcctt ctttcaacaa gaagaaagag caagagcaaa 1500
ggctaaaaga gaagctgcaa aggaaatctg cagtgaattt cgggaccaag tgaggaatgg 1560
aacacttata tgcaccaggg agcataatcc tgtccgtgga ccagatggca aaatgcatgg 1620
aaacaagtgt gccatgtgtg ccagtgtgtt caaacttgaa gaagaagaga agaaaaatga 1680
taaagaagaa aaagggaaag ttgaggctga aaaagttaag agagaagcag ttcaggagct 1740
gtgcagtgaa tatcgtcatt atgtgaggaa tggacgactc ccctgtacca gagagaatga 1800
tcctattgag ggtctagatg ggaaaatcca cggcaacacc tgctccatgt gtgaagcctt 1860
cttccagcaa gaagcaaaag aaaaagaaag agctgaaccc agagcaaaag tcaaaagaga 1920
agctgaaaag gagacatgcg atgaatttcg gagactttg caaaatggaa aacttttctg 1980
cacaagagaa aatgatcctg tgcgtggccc agatggcaag acccatggca acaagtgtgc 2040
catgtgtaag gcagtcttcc agaaagaaaa tgaggaaaga aagaggaaag aagaggaaga 2100
tcagagaaat gctgcaggac atggttccag tggtggtgga ggaggaaaca ctcaggacga 2160
atgtgctgag tatcaggaac aaatgaaaaa tggaagactc agctgtactc gggagagtga 2220
tcctgtacgt gatgctgatg gcaaatcgta caacaatcag tgtaccatgt gtaaagcaaa 2280
attggaaaga gaagcagaga gaaaaaatga gtattctcgc tccagatcaa atgggactgg 2340
atcagaatca gggaaggata catgtgatga gtttagaagc caaatgaaaa atggaaaact 2400
tatctgcact cgagaaagtg accctgtccg gggtccagat ggcaagacac atggtaataa 2460
gtgtactatg tgtaaggaaa aactggaaag ggaagcagct gaaaaaaaaa agaaagagga 2520
tgaagacagg agcaatacag gagaaaggag caatacagga gaaaggagca atgacaaaga 2580
ggatctgtgt cgtgaatttc gaagcatgca gagaaatgga aagcttatct gcaccagaga 2640
aaataaccct gttcgaggcc catatggcaa gatgcacatc aataaatgtg ctatgtgtca 2700
gagcatcttt gatcgagaag ctaatgaaag aaaaaagaaa gatgaagaga aatcaagtag 2760
caagccctca aataatgcaa aggatgagtg cagtgaattt cgaaactata taaggaacaa 2820
tgaactcatc tgccctagag agaatgaccc agtgcacggt gctgatggaa agttctatac 2880
aaacaagtgc tacatgtgca gagctgtctt tctaacagaa gctttggaaa gggcaaagct 2940
tcaagaaaag ccatcccatg ttagagcttc tcaagaggaa gacagcccag actctttcag 3000
ttctctggat tctgagatgt gcaaagacta ccgagtattg cccaggatag gctatctttg 3060
tccaaaggat ttaaagcctg tctgtggtga cgatggccaa acctacaaca atccttgcat 3120
gctctgtcat gaaaacctga tacgccaaac aaatacacac atccgcagta cagggaagtg 3180
tgaggagagc agcaccccag gaaccaccgc agccagcatg cccccgtctg acgaatgaca 3240
ggaagattgt tgaaagccat gagggaaaaa ataaacccca gttctgaatc acctaccttc 3300
accatctgta tatacaaaga attcttcgga gcttgtctta tttgctatag aaaacaatac 3360
agagcttttg ggaatggaat cactgatttt cagtcttttc catttctttc ctcctagaat 3420
ctgtgatctg agggtataaa gacatttcca ccaagtttga gccctcaaaa tgtcctgatt 3480
acaatgctgt ctgtccaact gcctgttcaa taaaagtaaa ctcagcag 3528

<210> 50
<211> 3494
<212> DNA
<213> Homo sapiens

<400> 50
taatttttgc ccagtctgcc tgttgtgggg ctcctcccct ttggggatat aagcccggcc 60
tggggctgct ccgttctctg cctggcctga ggctccctga gccgcctccc caccatcacc 120
atggccaagg gcttctatat ttccaagtcc ctgggcatcc tggggatcct cctgggcgtg 180

gcagccgtgt gcacaatcat cgcactgtca gtggtgtact cccaggagaa gaacaagaac 240
gccaacagct cccccgtggc ctccaccacc ccgtccgcct cagccaccac caaccccgcc 300
tcggccacca ccttggacca aagtaaagcg tggaatcgtt accgcctccc caacacgctg 360
aaacccgatt cctaccaggt gacgctgaga ccgtacctca cccccaatga caggggcctg 420
tacgttttta agggctccag caccgtccgt ttcacctgca aggaggccac tgacgtcatc 480
atcatccaca gcaagaagct caactacacc ctcagccagg ggcacagggt ggtcctgcgt 540
ggtgtgggag gctcccagcc ccccgacatt gacaagactg agctggtgga gcccaccgag 600
tacctggtgg tgcacctcaa gggctccctg gtgaaggaca gccagtatga gatggacagc 660
gagttcgagg gggagttggc agatgacctg gcgggcttct accgcagcga gtacatggag 720
ggcaatgtca gaaaggtggt ggccactaca cagatgcagg ctgcagatgc ccggaagtcc 780
ttcccatgct tcgatgagcc ggccatgaag gccgagttca acatcacgct tatccacccc 840
aaggacctga cagccctgtc caacatgctt cccaaaggtc ccagcacccc acttccagaa 900
gaccccaact ggaatgtcac tgagttccac accacgccca agatgtccac gtacttgctg 960
gccttcattg tcagtgagtt cgactacgtg gagaagcagg catccaatgg tgtcttgatc 1020
cggatctggg cccggcccag tgccattgcg gcgggccacg gcgattatgc cctgaacgtg 1080
acgggcccca tccttaactt ctttgctggt cattatgaca caccctaccc actcccaaaa 1140
tcagaccaga ttggcctgcc agacttcaac gccggcgcca tggagaactg gggactggtg 1200
acctaccggg agaactccct gctgttcgac cccctgtcct cctccagcag caacaaggag 1260
cgggtggtca ctgtgattgc tcatgagctg gcccaccagt ggttcgggaa cctggtgacc 1320
atagagtggt ggaatgacct gtggctgaac gagggcttcg cctcctacgt ggagtacctg 1380
ggtgctgact atgcggagcc cacctggaac ttgaaagacc tcatggtgct gaatgatgtg 1440
taccgcgtga tggcagtgga tgcactggcc tcctcccacc cgctgtccac acccgcctcg 1500
gagatcaaca cgccggccca gatcagtgag ctgtttgacg ccatctccta cagcaagggc 1560
gcctcagtcc tcaggatgct ctccagcttc ctgtccgagg acgtattcaa gcagggcctg 1620
gcgtcctacc tccacacctt tgcctaccag aacaccatct acctgaacct gtgggaccac 1680
ctgcaggagg ctgtgaacaa ccggtccatc caactcccca ccaccgtgcg ggacatcatg 1740
aaccgctgga ccctgcagat gggcttcccg gtcatcacgg tggataccag cacggggacc 1800
ctttcccagg agcacttcct ccttgacccc gattccaatg ttacccgccc ctcagaattc 1860
aactacgtgt ggattgtgcc catcacatcc atcagagatg gcagacagca gcaggactac 1920
tggctgatag atgtaagagc ccagaacgat ctcttcagca catcaggcaa tgagtgggtc 1980
ctgctgaacc tcaatgtgac gggctattac cgggtgaact acgacgaaga gaactggagg 2040
aagattcaga ctcagctgca gagagaccac tcggccatcc ctgtcatcaa tcgggcacag 2100
atcattaatg acgccttcaa cctggccagt gcccataagg tccctgtcac tctggcgctg 2160
aacaacaccc tcttcctgat tgaagagaga cagtacatgc cctgggaggc cgccctgagc 2220
agcctgagct acttcaagct catgtttgac cgctccgagg tctatggccc catgaagaac 2280
tacctgaaga agcaggtcac acccctcttc attcacttca gaaataatac caacaactgg 2340
agggagatcc cagaaaacct gatggaccag tacagcgagg ttaatgccat cagcaccgcc 2400
tgctccaacg gagttccaga gtgtgaggag atggtctctg gccttttcaa gcagtggatg 2460
gagaacccca ataataaccc gatccacccc aacctgcggt ccaccgtcta ctgcaacgct 2520
atcgcccagg gcggggagga ggagtgggac ttcgcctggg agcagttccg aaatgccaca 2580
ctggtcaatg aggctgacaa gctccgggca gccctggcct gcagcaaaga gttgtggatc 2640
ctgaacaggt acctgagcta caccctgaac ccggacttaa tccggaagca ggacgccacc 2700
tctaccatca tcagcattac caacaacgtc attgggcaag gtctggtctg ggactttgtc 2760
cagagcaact ggaagaagct ttttaacgat tatggtggtg gctcgttctc cttctccaac 2820
ctcatccagg cagtgacacg acgattctcc accgagtatg agctgcagca gctggagcag 2880
ttcaagaagg acaacgagga aacaggcttc ggctcaggca cccgggccct ggagcaagcc 2940
ctggagaaga cgaaagccaa catcaagtgg gtgaaggaga acaaggaggt ggtgctccag 3000
tggttcacag aaaacagcaa atagtcccca gcccttgaag tcacccggcc ccgatgcaag 3060
gtgcccacat gtgtccatcc cagcggctgg tgcagggcct ccattcctgg agcccgaggc 3120
accagtgtcc tcccctcaag gacaaagtct ccagcccacg ttctctctgc ctgtgagcca 3180
gtctagttcc tgatgaccca ggctgcctga gcacctccca gcccctgccc ctcatgccaa 3240
ccccgcccta ggcctggcat ggcacctgtc gcccagtgcc ctggggctga tctcagggaa 3300
gcccagctcc agggccagat gagcagaagc tctcgatgga caatgaacgg ccttgctggg 3360
ggccgccctg taccctcttt caccttttccc taaagaccct aaatctgagg aatcaacagg 3420
gcagcagatc tgtatatttt tttctaagag aaaatgtaaa taaaggattt ctagatgaaa 3480
aaaaaaaaaa aaaa 3494

<210> 51
<211> 1309
<212> DNA
<213> Homo sapiens

<400> 51
taggagataa gagtatcttg cacagcaggt gcaggtttcc cagcagctca ggcaagagtc 60
cgatgtttgt gccatctgat cctgatgtct ggagagatag ccatgtgtga gcctgaattt 120
ggcaatgaca aggccaggga gccgagcgtg ggtggcaggt ggcgagtgtc ctggtacgaa 180
cggtttgtgc agccatgtct ggtcgaactg ctgggctctg ctctcttcat cttcatcggg 240

tgcctgtcgg tcattgagaa tgggacggac actgggctgc tgcagccggc cctggcccac 300
gggctggctt tggggctcgt gattgccacg ctggggaata tcagtggtgg acacttcaac 360
cctgcggtgt ccctggcagc catgctgatc ggaggcctca acctggtgat gctcctcccg 420
tactgggtct cacagctgct cgggggggatg ctcggggctg ccttggccaa ggtggtgagt 480
cctgaggaga ggttctggaa tgcatctggg gcggcctttg tgacagtcca ggagcagggg 540
caggtggcag gggcgttggt ggcagagatc atcctgacga cgctgctggc cctggctgta 600
tgcatgggtg ccatcaatga gaagacaaag ggccctctgg ccccgttctc catcggcttt 660
gccgtcaccg tggatatcct ggctgggggc cctgtgtctg gaggctgcat gaatcccgcc 720
cgtgcttttg gacctgcggt ggtggccaac cactggaact tccactggat ctactggctg 780
ggcccactcc tggctggcct gcttgttgga ctgctcatta ggtgcttcat tggagatggg 840
aagacccgcc tcatcctgaa ggctcggtga gcagagctcg tgggattcct gctgctccag 900
gtgtcctcag ctcacctgtc ccagactgag gacaggggag ttcctgcatt tcctgccagg 960
gcagaggccc agaggagcga ccccctgctt ccactgcttg ggcctgcttt ctcagataga 1020
ctgactgctg aggaggctct aggttcttgg aattcctttg tgctcatcag agaccccagc 1080
ctggggaaca cgctgcccgc actgcccaga gagcagtgca aacaccacaa cacgagcgtg 1140
tttcttgaga ggaatgtccc cgagttggac aaggaggctg tttctgcaca tcagctcatt 1200
tcccgcaccc catttcttgc ttgattgctt tgttgggggc ctggccactt ccttgcttct 1260
caagctgaca attctcactt tgcaataaat agtccagtgt ttccttcat 1309

<210> 52
<211> 596
<212> DNA
<213> Homo sapiens

<400> 52
gacagcgcag ggggaaccca gggagcgcga tgggctgcag ggctgcgtca gggctcctgc 60
caggagtggc cgtggtcctc ctgctgctgc tgcagagcac acagtcagtc tacatccagt 120
accaaggctt ccgggtccag ctggaatcca tgaagaagct gagtgacctg gaggcacagt 180
gggcacccag cccccgcctg caggcccaga gcctcctgcc cgccgtgtgc caccaccctg 240
ctctgcctca ggaccttcag cctgtctgcg cctcgcagga ggcttccagc atcttcaaga 300
ccctgaggac catcgctaac gacgactgtg agctgtgtgt gaacgttgcg tgtaccggct 360
gcctctgaga tagccctggg taccctgagc ccaccaggga cacctcgccc ttcagcccac 420
caccctggca ggcttccatc cccgtccatg ctcaagatgg gtccctggcc accatggtca 480
tcaccaccct tccagggcct gagcagctgg atctggtaca aagcaatcgg acatagagtt 540
ggagggggag gcccctgagg cagcccagct cctgaataaa gattctacaa cacacg 596

<210> 53
<211> 3218
<212> DNA
<213> Homo sapiens

<400> 53
gaacaaacca acatttgagc caggaataac tagagaggaa caatggggtt attcagaggt 60
tttgttttcc tcttagttct gtgcctgctg caccagtcaa atacttcctt cattaagctg 120
aataataatg gctttgaaga tattgtcatt gttatagatc ctagtgtgcc agaagatgaa 180
aaaataattg aacaaataga ggatatggtg actacagctt ctacgtacct gtttgaagcc 240
acagaaaaaa gatttttttt caaaaatgta tctatattaa ttcctgagaa ttggaaggaa 300
aatcctcagt acaaaaggcc aaaacatgaa aaccataaac atgctgatgt tatagttgca 360
ccacctacac tcccaggtag agatgaacca tacaccaagc agttcacaga atgtggagag 420
aaaggcgaat acattcactt caccctgac cttctacttg gaaaaaaaca aaatgaatat 480
ggaccaccag gcaaactgtt tgtccatgag tgggctcacc tccggtgggg agtgtttgat 540
gagtacaatg aagatcagcc tttctaccgt gctaagtcaa aaaaaatcga agcaacaagg 600
tgttccgcag gtatctctgg tagaaataga gtttataagt gtcaaggagg cagctgtctt 660
agtagagcat gcagaattga ttctacaaca aaactgtatg gaaaagattg tcaattcttt 720
cctgataaag tacaaacaga aaaagcatcc ataatgttta tgcaaagtat tgattctgtt 780
gttgaatttt gtaacgaaaa aacccataat caagaagctc caagcctaca aaacataaag 840
tgcaatttta gaagtacatg ggaggtgatt agcaattctg aggattttaa aaacaccata 900
cccatggtga caccacctcc tccacctgtc ttctcattgc tgaagatccg tcaaagaatt 960
gtgtgcttag ttcttgataa gtctggaagc atgggggta aggaccgcct aaatcgaatg 1020
aatcaagcag caaaacattt cctgctgcag actgttgaaa atggatcctg ggtggggatg 1080
gttcactttg atagtactgc cactattgta aataagctaa tccaaataaa aagcagtgat 1140
gaaagaaaca cactcatggc aggattacct acatatcctc tgggaggaac ttccatctgc 1200
tctggaatta aatatgcatt tcaggtgatt ggagagctac attcccaact cgatggatcc 1260
gaagtactgc tgctgactga tggggaggat aacactgcaa gttcttgtat tgatgaagtg 1320
aaacaaagtg gggccattgt tcattttatt gctttgggaa gagctgctga tgaagcagta 1380
atagagatga gcaagataac aggaggaagt cattttatg tttcagatga agctcagaac 1440
aatggcctca ttgatgcttt tggggctctt acatcaggaa atactgatct ctcccagaag 1500

tcccttcagc tcgaaagtaa gggattaaca ctgaatagta atgcctggat gaacgacact 1560
gtcataattg atagtacagt gggaaaggac acgttctttc tcatcacatg gaacagtctg 1620
cctcccagta tttctctctg ggatcccagt ggaacaataa tggaaaattt cacagtggat 1680
gcaacttcca aaatggccta tctcagtatt ccaggaactg caaaggtggg cacttgggca 1740
tacaatcttc aagccaaagc gaacccagaa acattaacta ttacagtaac ttctcgagca 1800
gcaaattctt ctgtgcctcc aatcacagtg aatgctaaaa tgaataagga cgtaaacagt 1860
ttccccagcc caatgattgt ttacgcagaa attctacaag gatatgtacc tgttcttgga 1920
gccaatgtga ctgctttcat tgaatcacag aatggacata cagaagtttt ggaacttttg 1980
gataatggtg caggcgctga ttctttcaag aatgatggag tctactccag gtattttaca 2040
gcatatacag aaaatggcag atatagctta aaagttcggg ctcatggagg agcaaacact 2100
gccaggctaa aattacggcc tccactgaat agagccgcgt acataccagg ctgggtagtg 2160
aacggggaaa ttgaagcaaa cccgccaaga cctgaaattg atgaggatac tcagaccacc 2220
ttggaggatt tcagccgaac agcatccgga ggtgcatttg tggtatcaca agtcccaagc 2280
cttcccttgc ctgaccaata cccaccaagt caaatcacag accttgatgc cacagttcat 2340
gaggataaga ttattcttac atggacagca ccaggagata attttgatgt tggaaaagtt 2400
caacgttata tcataagaat aagtgcaagt attcttgatc taagagacag ttttgatgat 2460
gctcttcaag taaatactac tgatctgtca ccaaaggagg ccaactccaa ggaaagcttt 2520
gcatttaaac cagaaaatat ctcagaagaa aatgcaaccc acatatttat tgccattaaa 2580
agtatagata aaagcaattt gacatcaaaa gtatccaaca ttgcacaagt aactttgttt 2640
atccctcaag caaatcctga tgacattgat cctactccta ctcctactcc tactcctgat 2700
aaaagtcata attctggagt taatatttct acgctggtat tgtctgtgat tgggtctgtt 2760
gtaattgtta actttatttt aagtaccacc atttgaacct taacgaagaa aaaaatcttc 2820
aagtagacct agaagagagt tttaaaaaac aaaacaatgt aagtaaagga tatttctgaa 2880
tcttaaaatt catcccatgt gtgatcataa actcataaaa ataatttaa gatgtcggaa 2940
aaggatactt tgattaaata aaaacactca tggatatgta aaaactgtca agattaaaat 3000
ttaatagttt catttatttg ttatttttatt tgtaagaaat agtgatgaac aaagatcctt 3060
tttcatactg atacctggtt gtatattatt tgatgcaaca gttttctgaa atgatatttc 3120
aaattgcatc aagaaattaa aatcatctat ctgagtagtc aaaatacaag taaaggagag 3180
caaataaaca acatttggaa aaaaaaaaaa aaaaaaaa 3218

<210> 54
<211> 1630
<212> DNA
<213> Homo sapiens

<400> 54
aaaagcagaa agagattacc agccacagac gggtcatgag cgcggtatta ctgctggccc 60
tcctggggtt catcctccca ctgccaggag tgcaggcgct gctctgccag tttgggacag 120
ttcagcatgt gtggaaggtg tccgacctgc cccggcaatg gacccctaag aacaccagct 180
gcgacagcgg cttggggtgc caggacacgt tgatgctcat tgagagcgga ccccaagtga 240
gcctggtgct ctccaagggc tgcacggagg ccaaggacca ggagccccgc gtcactgagc 300
accggatggg ccccggcctc tccctgatct cctacacctt cgtgtgccgc caggaggact 360
tctgcaacaa cctcgttaac tccctcccgc tttgggcccc acagccccca gcagacccag 420
gatccttgag gtgcccagtc tgcttgtcta tggaaggctg tctggagggg acaacagaag 480
agatctgccc caaggggacc acacactgtt atgatggcct cctcaggctc aggggaggag 540
gcatcttctc caatctgaga gtccagggat gcatgcccca gccaggttgc aacctgctca 600
atgggacaca ggaaattggg cccgtgggta tgactgagaa ctgcaatagg aaagattttc 660
tgacctgtca tcgggggacc accattatga cacacggaaa cttggctcaa gaacccactg 720
attggaccac atcgaatacc gagatgtgcg aggtggggca ggtgtgtcag gagacgctgc 780
tgctcataga tgtaggactc acatcaaccc tggtggggac aaaaggctgc agcactgttg 840
gggctcaaaa ttcccagaag accaccatcc actcagcccc tcctggggtg cttgtggcct 900
cctataccca cttctgctcc tcggacctgt gcaatagtgc cagcagcagc agcgttctgc 960
tgaactccct ccctcctcaa gctgcccctg tcccaggaga ccggcagtgt cctacctgtg 1020
tgcagccccc tggaacctgt tcaagtggct ccccccgaat gacctgcccc aggggcgcca 1080
ctcattgtta tgatgggtac attcatctct caggaggtgg gctgtccacc aaaatgagca 1140
ttcagggctg cgtggcccaa ccttccagct tcttgttgaa ccacaccaga caaatcggga 1200
tcttctctgc gcgtgagaag cgtgatgtgc agcctcctgc ctctcagcat gagggaggtg 1260
gggctgaggg cctggagtct ctcacttggg gggtggggct ggcactggcc ccagcgctgt 1320
ggtggggagt ggtttgccct tcctgctaac tctattaccc ccacgattct tcaccgctgc 1380
tgaccaccca cactcaacct ccctctgacc tcataaccta atggccttgg acaccagatt 1440
ctttcccatt ctgtccatga atcatcttcc ccacacacaa tcattcatat ctactcacct 1500
aacagcaaca ctggggagag cctggagcat ccggacttgc cctatgggag aggggacgct 1560
ggaggartgg ctgcatgtat ctgataatac agaccctgtc ctttcaaaaa aaaaaaaaaa 1620
aaaaaaaaaa 1630

<210> 55
<211> 2221

<212> DNA
<213> Homo sapiens

<400> 55
gtgaccggag gcgagaaacc ccgcctcggc accctgacgc agcgcaggac ccgccccgcg 60
cgtgacgcca gcgtcaggcc agccccggca tgctctgcgg ccgcccgcgg tccagctccg 120
acaacaggaa ttttctccga gagcgggccg ggctcagttc agctgctgtc cagacccgga 180
tcggcaacag tgccgcctcc agacgttctc ctgccgctcg cccgcccgtc ccagcgcccc 240
cagccctccc gcgagggcgc cccgggacgg aaggatccac cagtctgtcg gcgcccgccg 300
ttctcgtggt cgccgtcgcc gtcgtcgtgg tggtagtctc cgccgtcgcc tgggccatgg 360
ccaattacat ccacgtccct cccggctccc cggaggtgcc caagctgaac gtcaccgttc 420
aggatcagga ggagcatcgc tgccgggagg gggccctgag cctcctgcaa cacctgcggc 480
ctcactggga cccccaggag gtgaccctgc agctcttcac agatggaatc acaaataaac 540
ttattggctg ttacgtggga aacaccatgg aggatgtagt cctggtgaga atttatggca 600
ataagactga gttattagtc gatcgagatg aggaagtaaa gagttttcga gtgttgcagg 660
ctcatgggtg tgcaccacaa ctctactgta ccttcaataa tggactatgc tatgaattta 720
tacaaggaga agcactggat ccaaagcatg tctgcaaccc agccattttc aggctaatag 780
ctcgtcagct tgctaaaatc catgctattc atgcacacaa tggctggatc cccaaatcta 840
atctttggct aaagatggga aagtatttct ctctcattcc cacaggattt gcagatgaag 900
acattaataa aaggttccta agtgatatcc caagctctca gattctccag gaagagatga 960
cttggatgaa ggagattctt tccaacctgg gctcacctgt tgtgctttgc cataatgacc 1020
tattgtgtaa gaatataatc tacaatgaga aacaaggtga tgtacagttc attgattatg 1080
aatattctgg atacaactac ctggcatatg atattggaaa tcatttcaat gaatttgcag 1140
gtgtgagtga tgtagactat agtctgtatc cagatagaga actacagagt cagtggctgc 1200
gtgcttacct tgaagcctac aaagaattta agggctttgg gactgaagtt actgaaaagg 1260
aggtagaaat actcttcatt caagtcaatc agtttgcatt ggcttctcat ttcttttggg 1320
gattgtgggc tttgattcaa gccaaatact ccactattga gtttgatttc cttgggtatg 1380
caattgttcg ttttaaccag tactttaaaa tgaagcctga ggttactgca ttaaaagtgc 1440
ctgagtaaag aagagattta attattctcc agtagctgag caatgcttgt gaatcttttc 1500
ttaagaaatc ccaaaaagcc aatattagtt aaaattctgt tgtttaattt ggttatcttg 1560
ctttataaat tatgcctcta aacaatcaaa tctatttttg aaatagactg aatgatgtca 1620
agaaatatac ctactgctat ccgtatgtgg tggattagaa atgtgttaaa tctgcaaaag 1680
gtataaagat gtcagtttaa tttctttgat aatttaacct atgttgtatg tgaattattt 1740
attataaact tagcacgatt ctgtgactgt ttttctctgt ttcacgttcg ttgagtgtaa 1800
gcaatgaaaa tgtcccaaat aagtttttta agttttactt taataagatt aatttcagta 1860
aacattctag ttgttcagtg taacctttt atcttgatgc attgtaagta aaatgaatca 1920
tttactcttg aaatgccagt cattgactga tgtagataat ttaggatttt catataaaaa 1980
tagctgttta ggaaggtgaa atacattcac tgtctctgtt ggtggtacat cttgttgaat 2040
tcaatattag aaagtatttc tttttggggt aatataactt agaattaaat ccctgtttct 2100
ctatgtagtc tggcagtata aatataaata tttaccatat aatcttggaa taagtattag 2160
ttaatgttac caaaatctgt attaaataat gttttcaaat gctaaaaaaa aaaaaaaaaa 2220
a 2221

<210> 56
<211> 1306
<212> DNA
<213> Homo sapiens

<400> 56
tgataagcta caacataaac acatctaggt tcttgttctt agaatacagc atgaagaatt 60
tgctttcttc tttcttccta acattttcat gtgagatcca gaaaggacac attgtctctg 120
gccattcgaa gagagaaaga aagaaagaaa aaaaaggtat ttagagacag agagagaaaa 180
aggctgaaat gggttcgctg ggttctaaaa atccgcaaac caaacaagcc caagttcttc 240
ttttgggact tgactcagct gggaagtcta ctctccttta taaattaaag cttgctaagg 300
atattaccac catccctaca ataggtttca atgtggaaat gatcgagttg gaaaggaatc 360
tttcactcac agtctgggat gttggaggac aggaaaaaat gagaactgtt tggggctgtt 420
actgtgagaa caccgatggg ctggtgtatg ttgtggacag tacagacaaa cagcgactgg 480
aagagtctca gagacagttt gagcacattt tgaagaatga acacattaaa aatgtgcctg 540
ttgttctatt agccaacaaa caagacatgc ctggagctct gactgctgag gacatcacca 600
gaatgttcaa agtgaagaag ctttgcagtg accggaactg gtatgtgcaa ccctgctgtg 660
ccctcacagg ggaggggctg gcccaggggt tcaggaaatt aactggattt gtgaagagcc 720
acatgaaatc aagaggagac actttggcgt tcttcaagca gaactgaggc tgcgaaaaat 780
ccaagtctct acagagacac tgatgaagtt gaaagggtaa ttgtttttcc atgccaaatg 840
aggaaatcaa attaatgagt tgacaaactt ttcctgagat gttatttcat ctacatttag 900
ttaaacaact tagaatgata tctagaaaat atttattttc agccaggaac tttagcaaac 960
tgtggcaatg atcactggga atgaaaacgt ataatgttct acaatttttg ttatcacatt 1020
ggatgacttt gaatatagta gtgacacttg ggaccaaata aattatttta tatgactact 1080

agaacaaagt tttagtaagc tgtctgctaa tagagtcaga attcttccag attgtttcca 1140
gctgtaacag gtattgaatt tccaccgtgc tcctatgtaa cagctgggtg gtgtaaaaaa 1200
tgaacttcaa attatggagt ggaagaagcg taatgttaat atcttgtaaa ttcgtattcc 1260
ctattaaata aagctttctt attccctaaa aaaaaaaaaa aaaaaa 1306

<210> 57
<211> 2090
<212> DNA
<213> Homo sapiens

<400> 57
ttcggcacga gtaagaccag gatgtctctg aaatggacgt cagtctttct gctgatacag 60
ctcagttgtt actttagctc tggaagctgt ggaaaggtgc tagtgtggcc cacagaatac 120
agccattgga taaatatgaa gacaatcctg gaagagcttg ttcagagggg tcatgaggtg 180
actgtgttga catcttcggc ttctactctt gtcaatgcca gtaaatcatc tgctattaaa 240
ttagaagttt atcctacatc tttaactaaa aatgatttgg aagattctct tctgaaaatt 300
ctcgatagat ggatatatgg tgtttcaaaa aatacatttt ggtcatattt ttcacaatta 360
caagaattgt gttgggaata ttatgactac agtaacaagc tctgtaaaga tgcagttttg 420
aataagaaac ttatgatgaa actacaagag tcaaagtttg atgtcattct ggcagatgcc 480
cttaatccct gtggtgagct actggctgaa ctatttaaca tacccttttct gtacagtctt 540
cgattctctg ttggctacac atttgagaag aatggtggag gatttctgtt ccctccttcc 600
tatgtacctg ttgttatgtc agaattaagt gatcaaatga ttttcatgga gaggataaaa 660
aatatgatac atatgcttta ttttgacttt tggtttcaaa tttatgatct gaagaagtgg 720
gaccagtttt atagtgaagt tctaggaaga cccactacat tatttgagac aatggggaaa 780
gctgaaatgt ggctcattcg aacctattgg gattttgaat ttcctcgccc attcttacca 840
aatgttgatt ttgttggagg acttcactgt aaaccagcca aacccctgcc taaggaaatg 900
gaagagtttg tgcagagctc tggagaaaat ggtattgtgg tgttttctct ggggtcgatg 960
atcagtaaca tgtcagaaga aagtgccaac atgattgcat cagcccttgc ccagatccca 1020
caaaaggttc tatggagatt tgatggcaag aagccaaata cattaggttc caatactcga 1080
ctgtacaagt ggttacccca gaatgacctt cttggtcatc ccaaaaccaa agcttttata 1140
actcatggtg gaaccaatgg catctatgag gcgatctacc atgggatccc tatggtgggc 1200
attcccttgt ttgcggatca acatgataac attgctcaca tgaaagccaa gggagcagcc 1260
ctcagtgtgg acatcaggac catgtcaagt agagatttgc tcaatgcatt gaagtcagtc 1320
attaatgacc ctgtctataa agagaatgtc atgaaattat caagaattca tcatgaccaa 1380
ccaatgaagc ccctggatcg agcagtcttc tggattgagt ttgtcatgcg ccacaaagga 1440
gccaagcacc ttcgagtcgc agctcacaac ctcacctgga tccagtacca ctctttggat 1500
gtgatagcat tcctgctggc ctgcgtggca actgtgatat ttatcatcac aaaattttgc 1560
ctgttttgtt tccgaaagct tgccaaaaca ggaaagaaga agaaaagaga ttagttatat 1620
caaaagcctg aagtggaatg actgaaagat gggactcctc ctttatttca gcatggaggg 1680
ttttaaatgg aggatttcct ttttcctgtg acaaaacatc ttttcacaac ttaccttgtt 1740
aagacaaaat ttattttcca gggatttaat acgtacttta gttggaatta ttctatgtca 1800
atgattttta agctatgaaa aatacaatgg ggggaaggat agcatttgga gatataccta 1860
atgttaaatg acgagttact ggatgcagca cgcaacatgg cacatgtgta tacatatgta 1920
gctaaccctt cgttgtgcac atgtacccta aaacttaaag tataatttaa aaaaagcaaa 1980
aaaaaaaaat accaactctt ttttttaaac caggaaggaa aatgtgaaca tggaaacaac 2040
ttctagtatt ggatctgaaa ataaagtgtc atccaagcca taaaaaaaaa 2090

<210> 58
<211> 2292
<212> DNA
<213> Homo sapiens

<400> 58
ccatgggttc cccttcagcc tgtccataca gagtgtgcat tccctggcag gggctcctgc 60
tcacagcctc gcttttaacc ttctggaacc tgccaaacag tgcccagacc aatattgatg 120
tcgtgccgtt caatgtcgca gaagggaagg aggtccttct agtagtccat aatgagtccc 180
agaatcttta tggctacaac tggtacaaag gggaaagggt gcatgccaac tatcgaatta 240
taggatatgt aaaaaatata agtcaagaaa atgccccagg gcccgcacac aacggtcgag 300
agacaatata ccccaatgga accctgctga tccagaacgt tacccacaat gacgcaggat 360
tctataccct acacgttata aaagaaaatc ttgtgaatga agaagtaacc agacaattct 420
acgtattctc ggagccaccc aagccctcca tcaccagcaa caacttcaat ccggtggaga 480
acaaagatat tgtggtttta acctgtcaac ctgagactca gaacacaacc tacctgtggt 540
gggtaaacaa tcagagcctc ctggtcagtc ccaggctgct gctctccact gacaacagga 600
ccctcgttct actcagcgcc acaaagaatg acataggacc ctatgaatgt gaaatacaga 660
acccagtggg tgccagccgc agtgacccag tcaccctgaa tgtccgctat gagtcagtac 720
aagcaagttc acctgacctc tcagctggga ccgctgtcag catcatgatt ggagtactgg 780
ctgggatggc tctgatatag cagccttggt gtagtttctg catttcggga agagtgtttt 840

tattatccac ctgcagactg gactggattc ttctagctcc ttcaatccca ttttctcctg 900
tggcatcact aagtataaga cctgctctct tcctgaagac ctataagctg gaggtggaca 960
actcaatgta aatttcaagg aaaaaccctc atgcctgaga tgtgggccac tcagagctaa 1020
ccaaaatgtt caacaccata actagagaca ctcaaattgc caaccaggac aagaagttga 1080
tgacttcatg ctgtggacag tttttcccaa gatgtcccaa gcctcatcgt gacgaggctc 1140
ttatcccact ccatttttcc ctgctcatgc ctgcctcttt aatttggtaa gataatgctg 1200
taactagaat ttcacaatca gcgccttgtg caggcaattt gacagagtgt tggatgtgtc 1260
atgtcatcat gtcaaaccca aatatttgac ctaagggatc ctttattctg cccagtggct 1320
aactttaaca acatccctaa tacaactgtt tattcaaatg cacggtggtc cctgttagag 1380
ttagacctct agactcacct gttctcacgc cctgttttaa tttaacccag ctatgggatg 1440
ccagataaca gaattgctgc ctacgagctg aacagggagg agtttgtgca gttgctgaca 1500
cttcttgttg cacataaata aatacagtgg gtactataga gactcagttg caaaaattaa 1560
caaatatgct gcttgattaa aatgggtagg cttctcatgt ggctcattct ttaatctatt 1620
ctcttttatt tggtttggtt catggggtct ctgcctatgg atcatacttc aaactcttgg 1680
tgtgatcctc ctgattgtca caatattagt taccctggtg tgctgtattc tctaaaacct 1740
ttaaatgttt gcatgcagcc attcgtcaaa tgtcaaatat tctctctttg gctggaatga 1800
caaaaactca aataaatgta tgattaggag gacatcataa cctatgaatg atggaagtcc 1860
aaaatgatgg taactgacag tagtgttaat gccttatgtt tagtcaaact ctcatttagg 1920
tgacagcctg gtgactccag aatggagcca gtcatgctaa atgccatata ctcacactga 1980
aacatgagga agcaggtaga tcccagaaca gacaaaactt tcctaaaaac atgagagtcc 2040
aggctgtctg agtcagcaca gtaagaaagt cctttctgct ttaactctta gaaaaaagta 2100
atatgaagta ttctgaaatt aaccaatcag tttatttaaa tcaatttatt tatattcttc 2160
tgttcctgga ttcccatttt acaaaaccca ctgttctact gttgtattgc ccagtaggag 2220
ctatcactat attttgcaga atggaaactg ccctgactct tgaatcacaa ataaaagcca 2280
attgtatctg tt 2292

<210> 59
<211> 1994
<212> DNA
<213> Homo sapiens

<400> 59
gctgccaccg ctcctgccac tgcagtgctc gagccccgtg caggggagct tgcgggagga 60
tcgaccgaca gacggacgca cgccgaggca ctgcgccccc agccccgcgc cggtgccacc 120
gcagcccgac cccggccgcc agtccagccg cccctcgccc ggtgcctagg tgcccggccc 180
cacaccgcca gctgctcggc gcccgggtcc gccatgcgct ccgccgctgt cctggctctt 240
ctgctctgcg ccgggcaagt cactgcgctc cctgtgaaca gccctatgaa taaaggggat 300
accgaggtga tgaaatgcat cgttgaggtc atctccgaca cactttccaa gcccagcccc 360
atgcctgtca gccaggaatg ttttgagaca ctccgaggag atgaacggat cctttccatt 420
ctgagacatc agaatttact gaaggagctc caagacctcg ctctccaagg cgccaaggag 480
agggcacatc agcagaagaa acacagcggt tttgaagatg aactctcaga ggttcttgag 540
aaccagagca gccaggccga gctgaaagag gcggtggaag agccatcatc caaggatgtt 600
atggagaaaa gagaggattc caaggaggca gagaaaagtg gtgaagccac agacggagcc 660
aggccccagg ccctcccgga gcccatgcag gagtccaagg ctgaggggaa caatcaggcc 720
cctggggagg aagaggagga ggaggaggag gccaccaaca cccaccctcc agccagcctc 780
cccagccaga aatacccagg cccacaggcc gaggggaca gtgagggcct ctctcagggt 840
ctggtggaca gagagaaggg cctgagtgca gagccagggt ggcaggcaaa gagagaagag 900
gaggaggagg aggaggagga ggctgaggct ggagaggagg ctgtccccga ggaagaaggc 960
cccactgtag tgctgaaccc ccacccgagc cttggctaca aggagatccg gaaaggcgag 1020
agtcggtcgg aggctctggc tgtggatgga gctgggaagc ctggggctga ggaggctcag 1080
gaccccgaag ggaagggaga acaggagcac tcccagcaga aagaggagga ggaggagatg 1140
gcagtggtcc cgcaaggcct cttccggggt gggaagagcg gagagctgga gcaggaggag 1200
gagcggctct ccaaggagtg ggaggactcc aaacgctgga gcaagatgga ccagctggcc 1260
aaggagctga cggctgagaa gcggctggag gggcaggagg aggaggagga caaccgggac 1320
agttccatga agctctcctt ccgggcccgg gcctacggct tcaggggccc tgggccgcag 1380
ctgcgacgag gctggaggcc atcctcccgg gaggacagcc ttgaggcggg cctgcccctc 1440
caggtccgag gctaccccga ggagaagaaa gaggaggagg gcagcgcaaa ccgcagacca 1500
gaggaccagg agctggagag cctgtcggcc attgaagcag agctggagaa agtggcccac 1560
cagctgcagg cactacggcg gggctgagac accggctggc agggctggcc ccagggcacc 1620
ctgtggccct ggctctgctg tccccttggc aggtcctggc cagatggccc ggacgctgct 1680
tccggtaggg aggcagcctc cagcctgccc aagcccaggc caccctatcg ccccctacgc 1740
gccttgtctc ctactcctga ctcctacctg ccctggaaca tcctttgcag ggcagcccca 1800
caactttaaa cattgacgat tccttctctg aacacaggca gctttctaga agtttccctt 1860
cctccatcct atccactggg cacaactgca ataacttctg acctttttggt gaaagctgag 1920
aactcctgac tgtaacatat tctgtatgaa ctttatctaa agaaaaataa atctgttctg 1980
ggctctttcc tctg 1994

<210> 60
<211> 2518
<212> DNA
<213> Homo sapiens

<400> 60
ccagcagtgg ctgcaccatg cacgtgaacg gcaaagtggc gctggtgacc ggcgcggctc 60
agggcatagg cagagccttt gcagaggcgc tgctgcttaa gggcgccaag gtagcgctgg 120
tggattggaa tcttgaagca ggtgtacagt gtaaagctgc cctgcatgag caatttgaac 180
ctcagaagac tctgttcatc cagtgcgatg tggctgacca gcaacaactg agagacactt 240
ttagaaaagt tgtagaccac tttggaagac tggacatttt ggtcaataat gctggagtga 300
ataatgagaa aaactgggaa aaaactctgc aaattaattt ggtttctgtt atcagtggaa 360
cctatcttgg tttggattac atgagtaagc aaaatggagg tgaaggcggc atcattatca 420
atatgtcatc tttagcagga ctcatgcccg ttgcacagca gccggtttat tgtgcttcaa 480
agcatggcat agttggattc acacgctcag cagcgttggc tgctaatctt atgaacagtg 540
gtgtgagact gaatgccatt tgtccaggct ttgttaacac agccatcctt gaatcaattg 600
aaaaagaaga aaacatggga caatatatag aatataagga tcatatcaag gatatgatta 660
aatactatgg aattttggac ccaccattga ttgccaatgg attgataaca ctcattgaag 720
atgatgcttt aaatggtgct attatgaaga tcacaacttc taagggaatt cattttcaag 780
actatgatac aactccattt caagcaaaaa cccaatgaac agcttatgtg ttagccatag 840
ctgaaaataa gcacaaatag cttatattca gatcctatct tcatttgaat atagctttta 900
aatgaaatgt tacagtttga agttttcctt catgcacttg gtgataaacg ttttctaaat 960
ttttagttaa gtatatggat aaaaagttat gaactattaa aaatgtgatg tggaccaaag 1020
gctaggttgt aatcttgata gtctaaaaaa tgatcaaaac aaatgatttt caaggaatat 1080
tcaatattct gcctttcaga aagtgtattt atatctgtgc ttcataaata ttaatgttct 1140
tcagaacatc attttaaagg agatacttga attgttattt aaatcaaacc agatgtaaaa 1200
cactcacata caagttcata ctttaaaaga ggaaagctac ttaacaatga caaatatttc 1260
acaataataa tttttactta tataccatct ttcaactgaa catttcagtt cttccaagag 1320
cttcttagag tagtatattt tgggggcagt caaggaataa actacagtgt aaacatatcc 1380
cagatgaaaa ctgctgtatg gaaaaatgac agaaagtaac tgattgacac tgttgattca 1440
cagttcagcc tcctatctgg gaaagacatt tctttcctct gctcacttta agaactttta 1500
ccgactccaa aaatctcagg aattaaactt ttaacagtta cagcaataaa gaatagttag 1560
tactccaaaa atattatatt taagatgctc aacaagaaaa aaatgcaaat gtaatatttt 1620
tttcaaatta cttctttatt gacttgtcca aatttcaaaa gtgcctaccc ttcaataaaa 1680
ctttttttatt ctgatctcca taaattactt agtcttctat gtatagctat caaggaaata 1740
aaaccaattt tgccacagcc acaactgtaa atgtttttgt acccatgctg aaactcataa 1800
caacacagac ataaaaatag ctgtgaggtt ttgctttttt tgttgtcagc tatcttaaga 1860
atcattaaat acacctgctt tgggtaaaac tctttgcaag cagtaattaa cactagtaac 1920
agtgaaagca caagatttcc aaatcagtcg ttttctcaaa aaaatatcgt ataagtgact 1980
catcctgtct gctaactcca gacctcccag cttgaagcca aatctttcca tgtgagattg 2040
atatggattt cctagaagta ctggaatgtt gtcatatctt gccctatttt aattctgcta 2100
tagaaaacaa ttgccttcac ttttaaggag taatttgaat attaataact ctggtctaga 2160
ttttcatata atgtattaaa gacaaagtag tgaacatcaa tgaacatctg atagagataa 2220
actgtaatca ggcataagct tgtttgtatg ttctggcagt gactaatcag taaatgatgt 2280
cggtttgccc agtatcactt atcttctgta tttttcctct gtcgtgtaaa tagtataacc 2340
ttttcattta tggacaattt tttggactag tagccttcaa tatacattct gctttgaatt 2400
aatttttca aatcaataaa ttatgtagac atttaaaatc aaatatcaag tagaattgaa 2460
aaatgtgagt tacataagtt aaaaacttac tttaaatctt accttctata ggtagctc 2518

<210> 61
<211> 1510
<212> DNA
<213> Homo sapiens

<400> 61
ggcacgaggc ccaagcaggt cggcggcggc ggcaggagag cggccgggcg tcagctcctc 60
gaccccgtg tcgggctagt ccagcgaggc ggacgggcgg cgtgggccca tggccaggcc 120
cggcatggag cggtggcgcg accggctggc gctggtgacg ggggcctcgg ggggcatcgg 180
cgcggccgtg gcccgggccc tggtccagca gggactgaag gtggtgggct gcgcccgcac 240
tgtgggcaac atcgaggagc tggctgctga atgtaagagt gcaggctacc ccgggacttt 300
gatcccctac agatgtgacc tatcaaatga agaggacatc ctctccatgt tctcagctat 360
ccgttctcag cacagcggtg tagacatctg catcaacaat gctggcttgg cccggcctga 420
caccctgctc tcaggcagca ccagtggttg gaaggacatg ttcaatgtga acgtgctggc 480
cctcagcatc tgcacacggg aagcctacca gtccatgaag gagcggaatg tggacgatgg 540
gcacatcatt aacatcaata gcatgtctgg ccaccgagtg ttacccctgt ctgtgaccca 600
cttctatagt gccaccaagt atgccgtcac tgcgctgaca gagggactga ggcaagagct 660
tcgggaggcc cagacccaca tccgagccac gtgcatctct ccaggtgtgg tggagacaca 720

attcgccttc aaactccacg acaaggaccc tgagaaggca gctgccacct atgagcaaat 780
gaagtgtctc aaacccgagg atgtggccga ggctgttatc tacgtcctca gcacccccgc 840
acacatccag attggagaca tccagatgag gcccacggag caggtgacct agtgactgtg 900
ggagctcctc cttccctccc cacccttcat ggcttgcctc ctgcctctgg attttaggtg 960
ttgatttctg gatcacggga taccacttcc tgtccacacc ccgaccaggg gctagaaaat 1020
ttgtttgaga tttttatatc atcttgtcaa attgcttcag ttgtaaatgt gaaaaatggg 1080
ctggggaaag gaggtggtgt ccctaattgt tttacttgtt aacttgttct tgtgcccctg 1140
ggcacttggc ctttgtctgc tctcagtgtc ttccctttga catgggaaag gagttgtggc 1200
caaaatcccc atcttcttgc acctcaacgt ctgtggctca gggctggggt ggcagaggga 1260
ggccttcacc ttatatctgt gttgttatcc agggctccag acttcctcct ctgcctgccc 1320
cactgcaccc tctccccctt atctatctcc ttctcggctc cccagcccag tcttggcttc 1380
ttgtcccctc ctggggtcat ccctccactc tgactctgac tatggcagca gaacaccagg 1440
gcctggccca gtggatttca tggtgatcat taaaaaagaa aaatcgcaac caaaaaaaaa 1500
aaaaaaaaaa 1510

<210> 62
<211> 1104
<212> DNA
<213> Homo sapiens

<400> 62
ctcggtgcgc gaccccggct cagaggactc tttgctgtcc cgcaagatgc ggatgctgct 60
ggcgctcctg gccctctccg cggcgcggcc atcggccagt gcagagtcac actggtgcta 120
cgaggttcaa gccgagtcct ccaactaccc ctgcttggtg ccagtcaagt ggggtggaaa 180
ctgccagaag gaccgccagt cccccatcaa catcgtcacc accaaggcaa aggtggacaa 240
aaaactggga cgcttcttct tctctggcta cgataagaag caaacgtgga ctgtccaaaa 300
taacgggcac tcagtgatga tgttgctgga gaacaaggcc agcatttctg gaggaggact 360
gcctgcccca taccaggcca aacagttgca cctgcactgg tccgacttgc catataaggg 420
ctcggagcac agcctcgatg gggagcactt tgccatggag atgcacatag tacatgagaa 480
agagaagggg acatcgagga atgtgaaaga ggcccaggac cctgaagacg aaattgcggt 540
gctggccttt ctggtggagg ctggaaccca ggtgaacgag ggcttccagc cactggtgga 600
ggcactgtct aatatcccca aacctgagat gagcactacg atggcagaga gcagcctgtt 660
ggacctgctc cccaaggagg agaaactgag gcactacttc cgctacctgg gctcactcac 720
cacaccgacc tgcgatgaga aggtcgtctg gactgtgttc cgggagccca ttcagcttca 780
cagagaacag atcctggcat tctctcagaa gctgtactac gacaaggaac agacagtgag 840
catgaaggac aatgtcaggc ccctgcagca gctggggcag cgcacggtga taaagtccgg 900
ggccccgggt cggccgctgc cctgggccct gcctgccctg ctgggcccca tgctggcctg 960
cctgctggcc ggcttcctgc gatgatggct cacttctgca cgcagcctct ctgttgcctc 1020
agctctccaa gttccaggct tccggtcctt agccttccca ggtgggactt taggcatgat 1080
taaaatatgg acatattttt ggag 1104

<210> 63
<211> 1484
<212> DNA
<213> Homo sapiens

<400> 63
cccgtgagga ggaaaaggtg tgtccgctgc cacccagtgt gagcgggtga caccacccgg 60
ttaggaaatc ccagctccca agagggtata aatccctgct ttactgctga gctcctgctg 120
gaggtgaaag tctggcctgg cagccttccc caggtgagca gcaacaaggc cacgtgctgc 180
tgggtctcag tcctccactt cccgtgtcct ctggaagttg tcaggagcaa tgttgcgctt 240
gtacgtgttg gtaatgggag tttctgcctt cacccttcag cctgcggcac acacaggggc 300
tgccagaagc tgccggtttc gtgggaggca ttacaagcgg gagttcaggc tggaagggga 360
gcctgtagcc ctgaggtgcc cccaggtgcc ctactggttg tgggcctctg tcagcccccg 420
catcaacctg acatggcata aaaatgactc tgctaggacg gtcccaggag aagaagagac 480
acggatgtgg gcccaggacg gtgctctgtg gcttctgcca gccttgcagg aggactctgg 540
cacctacgtc tgcactacta gaaatgcttc ttactgtgac aaaatgtcca ttgagctcag 600
agtttttgag aatacagatg ctttcctgcc gttcatctca tacccgcaaa ttttaacctt 660
gtcaacctct ggggtattag tatgccctga cctgagtgaa ttcacccgtg acaaaactga 720
cgtgaagatt caatggtaca aggattctct tcttttggat aaagacaatg agaaatttct 780
aagtgtgagg gggaccactc acttactcgt acacgatgtg gccctggaag atgctggcta 840
ttaccgctgt gtcctgacat ttgcccatga aggccagcaa tacaacatca ctaggagtat 900
tgagctacgc atcaagaaaa aaaaagaaga gaccattcct gtgatcattt ccccctcaa 960
gaccatatca gcttctctgg ggtcaagact gacaatcccg tgtaaggtgt ttctgggaac 1020
cggcacaccc ttaaccacca tgctgtggtg gacggccaat gacacccaca tagagagcgc 1080
ctacccggga ggccgcgtga ccgaggggcc acgccaggaa tattcagaaa ataatgagaa 1140
ctacattgaa gtgccattga tttttgatcc tgtcacaaga gaggatttgc acatggattt 1200

taaatgtgtt gtccataata ccctgagttt tcagacacta cgcaccacag tcaaggaagc 1260
ctcctccacg ttctcctggg gcattgtgct ggccccactt tcactggcct tcttggtttt 1320
gggggaata tggatgcaca gacggtgcaa acacagaact ggaaaagcag atggtctgac 1380
tgtgctatgg cctcatcatc aagactttca atcctatccc aagtgaaata aatggaatga 1440
aataattcaa acacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 64
<211> 1704
<212> DNA
<213> Homo sapiens

<400> 64
atccatgcta aaggtaaaca aactgcaact tatatctgca atttattttg gtatagacaa 60
gaggtatgcc agtagcacac tggtggcttc agaagaaatt ctcaacacct agctcgccag 120
agagtctatg tatgggattg aacaatctgt aaactaaagg atcctaatca tgaaaataag 180
tatgataaat tataagtcac tattggcact gttgtttata ttagcctcct ggatcatttt 240
tacagttttc cagaactcca caaaggtttg gtctgctcta aacttatcca tctccctcca 300
ttactggaac aactccacaa agtccttatt ccctaaaaca ccactgatat cattaaagcc 360
actaacagag actgaactca gaataaagga aatcatagag aaactagatc agcagatccc 420
acccagacct ttcacccacg tgaacaccac caccagcgcc acacatagca cagccaccat 480
cctcaaccct cgagatacgt actgcagggg agaccagctg cacatcctac tggaggtcaa 540
atgtgggtgt agagattatg gaaaaattca atacaattag tgcctccaaa tgcaacaaag 600
aaacagttgc aatgaaagag aaatgcaagt ttggaatgac atccacaatc cccagtgggc 660
atgtctggag aaacacatgg aatcctgtct cctgtagttt ggctacagtc aaaatgaagg 720
aatgcctgag aggaaaactc atatacctaa tgggagattc cacgatccgc cagtggatgg 780
aatacttcaa agccagtatc aacacactga agtcagtgga tctgcatgaa tctggaaaat 840
tgcaacacca gcttgctgtg gatttggata ggaacatcaa catccagtgg caaaaatatt 900
gttatcccct gataggatca atgacctatt cagtcaaaga gatggagtac ctcacccggg 960
ccattgacag aactggagga gaaaaaaaat actgtcattg ttatttccct gggccagcat 1020
ttcagaccct ttcccattga tgtttttatc cgaagggccc tcaatgtcca caaagccatt 1080
cagcatcttc ttctgagaag cccagacact atggttatca tcaaaacaga aaacatcagg 1140
gagatgtaca atgatgcaga aagatttagt gactttcatg gttacattca atatctcatc 1200
ataaaggaca ttttccagga tctcagtgtg agtatcattg atgcctggga tataacaatt 1260
gcatatggca caaataatgt acacccacct caacatgtag tcggaaatca gattaatata 1320
ttattaaact atatttgtta aataacacaa aagtctgaaa ttcattcact taagtaaaaa 1380
aatttattga ctgtctacta gcaggccaga tgctgtgttt ggctctgaat tcccaactag 1440
caagagcaga gaatctacat tatggctgat ccataagcca ccaattcagc taaatgagat 1500
gtttctaatc tgggcttcca cttaaaaata aaactaaaaa tactcatgaa aagagcctac 1560
ccttcttgat cagagccata cccctcttca ccaatgggaa gtcaagacac ctatgggtaa 1620
aagttctctc tgatgcatga aaactcagag tgataaagta attttaaaat aaaaatttgg 1680
agaaagcaaa aaaaaaaaaa aaaa 1704

<210> 65
<211> 1182
<212> DNA
<213> Homo sapiens

<400> 65
acacaggttg gagcagagaa agaggaaaca tagaggtgcc aaaggaacaa agacataatg 60
atgtcatcca agccaacaag ccatgctgaa gtaaatgaaa ccataccaa cccttaccca 120
ccaggcagct ttatggctcc tggatttcaa cagcctctgg gttcaatcaa cttagaaaac 180
caagctcagg gtgctcagcg tgctcagccc tacggcatca catctccggg aatctttgct 240
agcagtcaac cgggtcaagg aaatatacaa atgataaatc caagtgtggg aacagcagta 300
atgaacttta aagaagaagc aaaggcacta ggggtgatcc agatcatggt tggattgatg 360
cacattggtt ttggaattgt tttgtgttta atatccttct cttttagaga agtattaggt 420
tttgcctcta ctgctgttat tggtggatac ccattctggg gtggcctttc ttttattatc 480
tctggctctc tctctgtgtc agcatccaag gagctttccc gttgtctggt gaaaggcagc 540
ctgggaatga acattgttag ttctatcttg gccttcattg gagtgattct gctgctggtg 600
gatatgtgca tcaatggggt agctggccaa gactactggg ccgtgctttc tggaaaaggc 660
atttcagcca cgctgatgat cttctccctc ttggagttct tcgtagcttg tgccacagcc 720
cattttgcca accaagcaaa caccacaacc aatatgtctg tcctggttat tccaaatatg 780
tatgaaagca accctgtgac accagcgtct tcttcagctc ctcccagatg caacaactac 840
tcagctaatg cccctaaata gtaaaagaaa aaggggtatc agtctaatct catggagaaa 900
aactacttgc aaaaacttct taagaagatg tcttttattg tctacaatga tttctagtct 960
ttaaaaactg tgtttgagat ttgtttttag gttggtcgct aatgatggct gtatctccct 1020
tcactgtctc ttcctacatt accactacta catgctggca aaggtgaagg atcagaggac 1080
tgaaaaatga ttctgcaact ctcttaaagt tagaaatgtt tctgttcata ttacttttc 1140

cttaataaaa tgtcattaga aacaaaaaaa aaaaaaaaaa aa 1182

<210> 66
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 66
agcactctcc agcctctcac cgcaaaatta cacaccccag tacaccagca gaggaaactt 60
ataacctcgg gaggcgggtc cttcccctca gtgcggtcac atacttccag aagagcggac 120
cagggctgct gccagcacct gccactcaga gcgcctctgt cgctgggacc cttcagaact 180
ctctttgctc acaagttacc aaaaaaaaaa gagccaacat gttggtattg ctggctggta 240
tctttgtggt ccacatcgct actgttatta tgctatttgt tagcaccatt gccaatgtct 300
ggttggtttc caatacggta gatgcatcag taggtctttg gaaaaactgt accaacatta 360
gctgcagtga cagcctgtca tatgccagtg aagatgccct caagacagtg caggccttca 420
tgattctctc tatcatcttc tgtgtcattg ccctcctggt cttcgtgttc cagctcttca 480
ccatggagaa gggaaaccgg ttcttcctct caggggccac cacactggtg tgctggctgt 540
gcattcttgt gggggtgtcc atctacacta gtcattatgc gaatcgtgat ggaacgcagt 600
atcaccacgg ctattcctac atcctgggct ggatctgctt ctgcttcagc ttcatcatcg 660
gcgttctcta tctggtcctg agaaagaaat aaggccggac gagttcatgg ggatctgggg 720
ggtggggagg aggaagccgt tgaatctggg agggaagtgg aggttgctgt acaggaaaaa 780
ccgagatagg ggaggggggа gggggaagca aaggggggag gtcaaatccc aaaccattac 840
tgaggggatt ctctactgcc aagcccctgc cctggggaga aagtagttgg ctagtacttt 900
gatgctccct tgatggggtc cagagagcct ccctgcagcc accagacttg gcctccagct 960
gttcttagtg acacacactg tctggggccc catcagctgc cacaacacca gccccacttc 1020
tgggtcatgc actgaggtcc acagacctac tgcactgagt taaaatagcg gtacaagttc 1080
tggcaagagc agatactgtc tttgtgctga atacgctaag cctggaagcc atcctgccct 1140
tctgacccaa agcaaaacat cacattccag tctgaagtgc ctactggggg gctttggcct 1200
gtgagccatt gtccctcttt ggaacagata tttagctctg tggaattcag tgacaaaatg 1260
ggaggaggaa agagagtttg taaggtcatg ctggtgggtt agctaaacca agaaggagac 1320
cttttcacaa tggaaaacct gggggatggt cagagcccag tcgagacctc acacacggct 1380
gtccctcatg gagacctcat gccatggtct ttgctaggcc tcttgctgaa agccaaggca 1440
gctcttctgg agtttctcta aagtcactag tgaacaattc ggtggtaaaa gtaccacaca 1500
aactatggga tccaaggggc agtcttgcaa cagtgccatg ttagggttat gtttttagga 1560
ttcccctcaa tgcagtcagt gtttctttta agtatacaac aggagagaga tggacatggc 1620
tcattgtagc acaatcctat tactcttcct ctaacatttt tgaggaagtt ttgtctaatt 1680
atcaatattg aggatcaggg ctcctaggct cagtggtagc tctggcttag acaccacctg 1740
gagtgatcac ctcttgggga ccctgcctat cccacttcac aggtgaggca tggcaattct 1800
ggaagctgat taaaacacac ataaaccaaa accaaacaac aggcccttgg gtgaaaggtg 1860
ctatataatt gtgaagtatt aagcctaccg tatttcagcc atgataagaa cagagtgcct 1920
gcattcccag gaaaatacga aaatcccatg agataaataa aaatataggt gatgggcaga 1980
tcttttcttt aaaataaaaa agcaaaaact cttgtggtac ctagtcagat ggtagacgag 2040
ctgtctgctg ccgcaggagc acctctatac aggacttaga agtagtatgt tattcctggt 2100
taagcaggca ttgctttgcc ctggagcagc tattttaagc catctcagat tctgtctaaa 2160
ggggtttttt gggaagacgt tttctttatc gccctgagaa gatctacccc agggagaatc 2220
tgagacatct tgcctacttt tctttattag ctttctcctc atccatttct tttatacctt 2280
tccttttgg ggagttgtta tgccatgatt tttggtattt atgtaaaagg attattacta 2340
attctatttc tctatgttta ttctagttaa ggaaatgttg agggcaagcc accaaattac 2400
ctaggctgag gttagagaga ttggccagca aaaactgtgg gaagatgaac tttgtcatta 2460
tgatttcatt atcacatgat tatagaaggc tgtcttagtg caaaaaacat acttacattt 2520
cagacatatc caaagggaat actcacattt tgttaagaag ttgaactatg actggagtaa 2580
accatgtatt cccttatctt ttacttttt tctgtgacat ttatgtctca tgtaatttgc 2640
attactctgg tggattgttc tagtactgta ttgggcttct tcgttaatag attatttcat 2700
atactataat tgtaaatatt ttgatacaaa tgtttataac tctagggata taaaaacaga 2760
ttctgattcc cttcaaaaaa aaaaaa 2786

<210> 67
<211> 7586
<212> DNA
<213> Homo sapiens

<400> 67
gttctttgtg acacatcaca cagaattgga gtgctgtcct tctggagagt ggtggagaac 60
caagatacag ttcagaacca aaggaataga gaagggcttt gatttctttt tggctttaga 120
ttggggattt gggaggctta gcaggaaaga tgtccactga aaatgtggaa gggaagccca 180
gtaaccttgg ggagagagga agagcccgga gctccacttt cctcagggtt gtccagccaa 240
tgtttaacca cagtattttc acttctgcag tctctcctgc tgcagaacgc atccgattca 300

tcttgggaga ggaggatgac agcccagctc cccctcagct cttcacggaa ctggatgagc 360
tgctggccgt ggatgggcag gagatggagt ggaaggaaac agccaggtgg atcaagtttg 420
aagaaaaagt ggaacagggt ggggaaagat ggagcaagcc ccatgtggcc acattgtccc 480
ttcatagttt atttgagctg aggacatgta tggagaaagg atccatcatg cttgatcggg 540
aggcttcttc tctcccacag ttggtggaga tgattgttga ccatcagatt gagacaggcc 600
tattgaaacc tgaacttaag gataaggtga cctatacttt gctccggaag caccggcatc 660
aaaccaagaa atccaacctt cggtccctgg ctgacattgg gaagacagtc tccagtgcaa 720
gtaggatgtt taccaaccct gataatggta gcccagccat gacccatagg aatctgactt 780
cctccagtct gaatgacatt tctgataaac cggagaagga ccagctgaag aataagttca 840
tgaaaaaatt gccacgtgat gcagaagctt ccaacgtgct tgttggggag gttgactttt 900
tggatactcc tttcattgcc tttgttaggc tacagcaggc tgtcatgctg ggtgccctga 960
ctgaagttcc tgtgcccaca aggttcttgt tcattctctt aggtcctaag gggaaagcca 1020
agtcctacca cgagattggc agagccattg ccaccctgat gtctgatgag gtgttccatg 1080
acattgctta taaagcaaaa gacaggcacg acctgattgc tggtattgat gagttcctag 1140
atgaagtcat cgtccttcca cctggggaat gggatccagc aattaggata gagcctccta 1200
agagtcttcc atcctctgac aaaagaaaga atatgtactc aggtggagag aatgttcaga 1260
tgaatgggga tacgccccat gatggaggtc acggaggagg aggacatggg gattgtgaag 1320
aattgcagcg aactggacgg ttctgtggtg gactaattaa agacataaag aggaaagcgc 1380
catttttgc cagtgatttt tatgatgctt taaatattca agctctttcg gcaattctct 1440
tcatttatct ggcaactgta actaatgcta tcacttttgg aggactgctt ggggatgcca 1500
ctgacaacat gcagggcgtg ttggagagtt tcctgggcac tgctgtctct ggagccatct 1560
tttgcctttt tgctggtcaa ccactcacta ttctgagcag caccggacct gtcctagttt 1620
ttgagaggct tctatttaat ttcagcaagg acaataattt tgactatttg gagtttcgcc 1680
tttggattgg cctgtggtcc gccttcctat gtctcatttt ggtagccact gatgccagct 1740
tcttggttca atacttcaca cgtttcacgg aggagggctt ttcctctctg attagcttca 1800
tctttatcta tgatgctttc aagaagatga tcaagcttgc agattactac cccatcaact 1860
ccaacttcaa agtgggctac aacactctct tttcctgtac ctgtgtgcca cctgacccag 1920
ctaatatctc aatatctaat gacaccacac tggccccaga gtatttgcca actatgtctt 1980
ctactgacat gtaccataat actacctttg actgggcatt tttgtcgaag aaggagtgtt 2040
caaaatacgg aggaaacctt gtcgggaaca actgtaattt tgttcctgat atcacactca 2100
tgtcttttat cctcttcttg ggaacctaca cctcttccat ggctctgaaa aaattcaaaa 2160
ctagtcctta ttttccaacc acagcaagaa aactgatcag tgattttgcc attatcttgt 2220
ccattctcat cttttgtgta atagatgccc tagtaggcgt ggacacccca aaactaattg 2280
tgccaagtga gttcaagcca acaagtccaa accgaggttg gttcgttcca ccgtttggag 2340
aaaaccccctg gtgggtgtgc cttgctgctg ctatcccggc tttgttggtc actatactga 2400
ttttcatgga ccaacaaatt acagctgtga ttgtaaacag gaaagaacat aaactcaaga 2460
aaggagcagg gtatcacttg gatctctttt gggtggccat cctcatggtt atatgctccc 2520
tcatggctct tccgtggtat gtagctgcta cggtcatctc cattgctcac atcgacagtt 2580
tgaagatgga gacagagact tctgcacctg gagaacaacc aaagtttcta ggagtgaggg 2640
aacaaagagt cactggaacc cttgtgttta ttctgactgg tctgtcagtc tttatggctc 2700
ccatcttgaa gtttataccc atgcctgtac tctatggtgt gttcctgtat atgggagtag 2760
catcccttaa tggtgtgcag ttcatggatc gtctgaagct gcttctgatg cctctgaagc 2820
atcagcctga cttcatctac ctgcgtcatg ttcctctgcg cagagtccac ctgttcactt 2880
tcctgcaggt gttgtgtctg gccctgcttt ggatcctcaa gtcaacggtg gctgctatca 2940
tttttccagt aatgatcttg gcacttgtag ctgtcagaaa aggcatggac tacctcttct 3000
cccagcatga cctcagcttc ctggatgatg tcattccaga aaaggacaag aaaaagaagg 3060
aggatgagaa gaaaaagaaa aagaagaagg gaagtctgga cagtgacaat gatgattctg 3120
actgcccata ctcagaaaaa gttccaagta ttaaaattcc aatggacatc atggaacagc 3180
aacctttcct aagcgatagc aaaccttctg acagagaaag atcaccaaca ttccttgaac 3240
gccacacatc atgctgataa aattcctttc cttcagtcac tcggtatgcc aagtcctcct 3300
agaactccag taaaagttgc ctcaaattag actagaactt gaacctgaag acaatgatta 3360
tttctggagg agcaagggaa cagaaactac attgtaacct gtttgtcttt cttaaaactg 3420
acatttgttg ttaatgtcat ttgtttttgt ttggctgttt gtttatttttt taacttttat 3480
ttcgtctcag tttttggtca caggccaaat aatacagcgc tctctctgct tctctcttgc 3540
atagatacaa tcaagacaat agtgcaccgt tccttaaaaa cagcatctga ggaatccccc 3600
ttttgttctt aaactttcag atgtgtcctt tgataaccaa attctgtcac tcaagacaca 3660
gacacccaca gaccctgtcc tttgcctcta ttaagcagag gatggaagta ttaaggattt 3720
tgtaacacct tttatgaaaa tgttgaagga acttaaaact ttagctttgg agctgtgctt 3780
actggcttgt ctttgtctgg tagaacaaac cttgacctcc agacagagtc ccttctcact 3840
tatagagctc tccaggactg gaaaaagtgc tgctatttta acttgctctt gcttgtaaat 3900
cctaatctta gagttatcaa aagaagaaaa aactgaaggt actttactcc ctatagagaa 3960
accattgcca tcattgtagc aagtgctgga atgtcccttt tttcctatgc aacttttta 4020
taacccttta atgaacttat ctgtggagta cattgaagaa tatttttctt cctagatttt 4080
gttgtttaaa ttatggggcc taacctgcca cttatttttt gtcaattttt aaaacttttt 4140
tttaattact gtaaagaaaa tgaatttttt cctgcagcag gaaacatagt tttcagtagt 4200
tctacctctt atttgtagct gccaggcttt ctgtaaaaat tgtattgtat ataatgtgat 4260
ttttacacat acatacacac acaaatacac aatctctagg gtaagccaga aggcaagatc 4320

agattaaaaa caccatgttt ctaagcatcc atttttccct ttctttaaaa gaaacttaac 4380
tgttctatga aggagattga gggagaagag acaaactcct atgtcatgag aataaccgat 4440
gttctgataa tagtagcatc taggtacaga tgctggttgt attaccacgt caatgtccta 4500
tgcagtattg ttagacattt tctcattttg aaatatttgt gtgtttgtgt atgtgctctg 4560
tgccatggct ggtgtatata tgtgcaatgt tagaaggcaa aagagtgatg gtaggcagag 4620
ggcaaagtca ttgaatctct tatgccagtt ttcataaaac ccaaaccaca tatgaaaaaa 4680
tccattaagg gtccaagaag tctgtccata tgaaaatgag ggtaaatata gtttatttcc 4740
caggtatcag tcattataat tgatataata gctctaacat gcaatataaa attcatagga 4800
gtattaatag cccatttaca catctataaa atgtaatggg attgcagagc tgcagagtac 4860
agtgtaacag tactctcatg caatttttt caggatgcaa aggcaattat tctttgtaag 4920
cgggacattt agatatattt gtgtacatat tatatgtatg tatatttcaa agtaccacac 4980
tgaaaattag acatttatta accaaattta acgtggtatt taaaggtaat atttttaata 5040
tgatacatta catattgtga atgtatacta aaaaaacatt ttaaatgtta aaattataat 5100
ttcagattca tataaccaca actgtgatat atcctaacta taaccagttg ttgaggggta 5160
tactagaagc agaatgaaac cacatttttt ggtttgataa tatgcactta ttgactccca 5220
ctcattgtta tgttaattaa gttattattc tgtctccttg taattttgat tacaaaaatt 5280
ttattatcct gagttagctg ttacttttac agtacctgat actcctaaaa cttttaactt 5340
atacaaatta gtcaataatg accccaattt tttcattaaa ataatagtgg tgaattatat 5400
gttattgtgt taaaacctca cttgccaaat tctggcttca catttgtatt tagggctatc 5460
cttaaaatga tgagtctata ttatctagct ttctattacc ctaatataaa ctggtataag 5520
aagactttcc ttttttcttt atgcatggaa gcatcaataa attgtttaaa aaccatgtat 5580
agtaaattca gcttaacccg tgatcttctt aagttaaagg tacttttgtt ttataaaagc 5640
tctagataaa actttctttt ctgatcatga atcaagtatc tgtggtttca tgcccctctc 5700
tatacctttc aaagaactcc tgaagcaact taactcatca tttcagcctc tgagtagagg 5760
taaaacctat gtgtacttct gtttatgatc catattgata tttatgacat gaacacagaa 5820
tagtacctta catttgctaa acagacagtt aatatcaaat cctttcaata ttctgggaac 5880
ccagggaagt ttttaaaaat gtcattactt tcaaaggaac agaagtagtt aaccaaacta 5940
acaagcaaaa cctgaggttt acctagtgac accaaattat cggtatttta actgaattta 6000
cccattgact aagaatgaac cggatttggt ggtggttttg tttctatgca aactggacac 6060
aaattacaac agtaaatttt tttataagtg cttctccctt ctccatgatg tgacttccgg 6120
agataaagga ttcaaaagat aaagacaaag tacgctcaga gttgttaacc agaaagtcct 6180
ggctgtggtt gcagaaacac tgttggaaga aaagagatga ctaagtcaag tgtctgcctt 6240
atcaaaagag caaaaatgcc tctggttttg tgtttgggag aaaaatatct tggacgcact 6300
gttttccttg ataaaagtca tcttctctac tgtgtgaaat gaatacttgg aattctaatt 6360
gttttgtgtg ccaggggcag taatgtccct gcctcttctc ccaatcaagg ttgaggagtg 6420
gggctgggga gaggacttaa ctgacttaag aagtaggaaa acaaaaacct ctctcctcag 6480
ccttccacct ccaagagagg aggaaaaaca gttgtctgct gtctgtaatt cagtttgcgt 6540
gtattttatg ctcatgcacc aacccataca gagtaaatct tttatcaact atatactggt 6600
gtttaataga gaatgattgt cttccgagtt ttttggttcc ttttttaact gtgttaaagt 6660
acttgaaatg tattgactgc tgactatatt ttaaaaacaa aatgaaataa tttgagttgt 6720
attacagagg ttgacattgt tcagggatgg gacaaagcct tcttcaatcc ttttcatact 6780
acttaatgat tttggtgcag gaacctgaga ttttctgatt tatatttcat gatatttcac 6840
atttgctctt cacagcatga gcatgaagcc cagtggcacc aaatggctgg gtacaatcaa 6900
gtgatatttt gtagcacctc actatctgaa aggccatgag ttttcagatg atttcattga 6960
gcttcattgc agcctgaaat tttaaaaaag ttgtgtaata cgccaaccag tcaagttgtg 7020
ttttggccag agatttagat atgtccaatt tcctggctca tttcattgtg ctctatgggt 7080
acgtataaaa agcaagaatt ctgtttccta ggcaaacatt gcaactcagg gctaaagtca 7140
tccagtgaaa cttttagagc cagaagtaac tttgtcccag tcctacaatg tgaaaagagt 7200
gaatagttgc ctctttttag ccatttttcat ggctggtaca tattcgtacg cattactttt 7260
cagaatcaat acgcactttc agatattctt atttttattc tcttaagtct ttattaactt 7320
tggagagaga aatgatgcat ctttttattt taaatgaagt agatcaacat ggtggaacaa 7380
aatgataaag aacagaaaac atttcaatat attactaata actttttcca atataaatcc 7440
taaaattcct ataacatagt attttacagt tttatgaagc tttctattgt gacttttatg 7500
gaattaagag atgaagaaga tgagatattt tagcatttat atttttcaaa attatatgta 7560
tacttaaaaa taaagtaact ttatgc 7586

<210> 68
<211> 1470
<212> DNA
<213> Homo sapiens

<400> 68
atgcactcaa gcagagaaga aatccacaag tactcaccag cctcctggtc tgcagagaag 60
acagaatcaa tatgagcaca gcaggaaaag taatcaaatg caaagcagct gtgctatggg 120
agttaaagaa acccttttcc attgaggagg tagaggttgc acctcctaag gctcatgaag 180
ttcgcattaa gatggtggct gcaggaatct gtcgttcaga tgagcatgtg gttagtggca 240
acctggtgac ccccttcct gtgattttag gccatgaggc agccggcatc gtggaaagtg 300

ttggagaagg ggtgactaca gtcaaaccag gtgataaagt catcccgctc tttactcctc 360
agtgtggaaa atgcagaatt tgtaaaaacc cagaaagcaa ctactgcttg aaaaatgatc 420
taggcaatcc tcgggggacc ctgcaggatg gcaccaggag gttcacctgc agcgggaagc 480
ccatccacca cttcgtcggc gtcagcacct tctcccagta cacagtggtg gatgagaatg 540
cagtggccaa aattgatgca gcctcgcccc tggagaaagt ctgcctcatt ggctgtggat 600
tttcgactgg ttatgggtct gcagtcaaag ttgccaaggt caccccaggg tctacctgtg 660
ctgtgtttgg cctgggaggg gtcggcctat ctgttgttat gggctgtaaa gcagctggag 720
cagccagaat cattgctgtg gacatcaaca aggacaaatt tgcaaaggct aaagagttgg 780
gggccactga atgcatcaac cctcaagact acaagaaacc cattcaggaa gtgctaaagg 840
aaatgactga tggaggtgtg gatttttcgt ttgaagtcat cggtcggctt gacaccatga 900
tggcttccct gttatgttgt catgaggcat gtggcacaag tgtcattgta ggggtacctc 960
ctgattccca gaacctctca ataaacccta tgctgctact gactggacgc acgtggaaag 1020
gagctatttt tggaggcttt aagagtaaag aatctgtccc gaaacttgtg gctgacttta 1080
tggctaagaa gttttcactg gatgcattaa taacaaatat tttacctttt gaaaaaataa 1140
atgaaggatt tgacctgctt cgctctggaa agagtatccg taccgtcctg acgttttgaa 1200
acaatacaga tgccttccct tgtagcagtt ttcagcctcc tctaccctac atgatctgga 1260
gcaacagcta ggaaatatca ttaattctgc tcttcagaga tgttaaaaat aaattacacg 1320
tgggagcttt ccaaagaaat ggaaattgat gggaaattat ttgtcaagca aatgtttaaa 1380
atccaaatga gaactaaata aagtgttgaa catcaactgg ggaattgaag ccaataaacc 1440
ttccttctta accattcaaa aaaaaaaaaa 1470

<210> 69
<211> 3464
<212> DNA
<213> Homo sapiens

<400> 69
cagccgtgct cgaagcgttc ctggagccca agctctcctc cacaggtgaa gacagggcca 60
gcaggagaca ccatggggca cctctcagcc ccacttcaca gagtgcgtgt accctggcag 120
gggcttctgc tcacagcctc acttctaacc ttctggaacc cgcccaccac tgcccagctc 180
actactgaat ccatgccatt caatgttgca gaggggaagg aggttcttct ccttgtccac 240
aatctgcccc agcaactttt tggctacagc tggtacaaag gggaaagagt ggatggcaac 300
cgtcaaattg taggatatgc aataggaact caacaagcta ccccagggcc cgcaaacagc 360
ggtcgagaga caatataccc caatgcatcc ctgctgatcc agaacgtcac ccagaatgac 420
acaggattct acaccctaca agtcataaag tcagatcttg tgaatgaaga agcaactgga 480
cagttccatg tatacccgga gctgcccaag ccctccatct ccagcaacaa ctccaaccct 540
gtggaggaca aggatgctgt ggccttcacc tgtgaacctg agactcagga cacaacctac 600
ctgtggtgga taaacaatca gagcctcccg gtcagtccca ggctgcagct gtccaatggc 660
aacaggaccc tcactctact cagtgtcaca aggaatgaca caggacccta tgagtgtgaa 720
atacagaacc cagtgagtgc gaaccgcagt gacccagtca ccttgaatgt cacctatggc 780
ccggacaccc ccaccatttc cccttcagac acctattacc gtccaggggc aaacctcagc 840
ctctcctgct atgcagcctc taacccacct gcacagtact cctggcttat caatggaaca 900
ttccagcaaa gcacacaaga gctctttatc cctaacatca ctgtgaataa tagtggatcc 960
tatacctgcc acgccaataa ctcagtcact ggctgcaaca ggaccacagt caagacgatc 1020
atagtcactg agctaagtcc agtagtagca aagccccaaa tcaaagccag caagaccaca 1080
gtcacaggag ataaggactc tgtgaacctg acctgctcca caaatgacac tggaatctcc 1140
atccgttggt tcttcaaaaa ccagagtctc ccgtcctcgg agaggatgaa gctgtcccag 1200
ggcaacacca ccctcagcat aaaccctgtc aagagggagg atgctgggac gtattggtgt 1260
gaggtcttca acccaatcag taagaaccaa agcgacccca tcatgctgaa cgtaaactat 1320
aatgctctac cacaagaaaa tggcctctca cctggggcca ttgctggcat tgtgattgga 1380
gtagtggccc tggttgctct gatagcagta gccctggcat gttttctgca tttcgggaag 1440
accggcaggg caagcgacca gcgtgatctc acagagcaca aaccctcagt ctccaaccac 1500
actcaggacc actccaatga cccacctaac aagatgaatg aagttactta ttctaccctg 1560
aactttgaag cccagcaacc cacacaacca acttcagcct ccccatccct aacagccaca 1620
gaaataattt attcagaagt aaaaaagcag taatgaaacc tgtcctgctc actgcagtgc 1680
tgatgtattt caagtctctc accctcatca ctaggagatt cctttccccc ctagggtaga 1740
ggggtgggga cagaaacaac tttctcctac tcttccttcc taataggcat ctccaggctg 1800
cctggtcact gcccctctct cagtgtcaat agatgaaagt acattgggag tctgtaggaa 1860
acccaacctt cttgtcattg aaatttggca aagctgactt tgggaaagag ggaccagaac 1920
ttcccctccc ttccccttct cccaacctgg acttgtttta aacttgcctg ttcagagcac 1980
tcattccttc ccacccccag tcctgtccta tcactctaat tcggatttgc catagccttg 2040
aggttatgtc cttttccatt aagtacatgt gccaggaaac agcgagagag agaaagtaaa 2100
cggcagtaat gcttctccta tttctccaaa gccttgtgtg aactagcaaa gagaagaaaa 2160
ccaaatatat aaccaatagt gaaatgccac aggtttgtcc actgtcaggg ttgtctacct 2220
gtaggatcag ggtctaagca ccttggtgct tagctagaat accacctaat ccttctggca 2280
agcctgtctt cagagaaccc actagaagca actaggaaaa atcacttgcc aaaatccaag 2340
gcaattcctg atggaaaatg caaaagcaca tatatgtttt aatatcttta tgggctctgt 2400

tcaaggcagt gctgagaggg aggggttata gcttcaggag ggaaccagct tctgataaac 2460
acaatctgct aggaacttgg gaaaggaatc agagagctgc ccttcagcga ttatttaaat 2520
tattgttaaa gaatacacaa tttggggtat tgggattttt ctccttttct ctgagacatt 2580
ccaccatttt aatttttgta actgcttatt tatgtgaaaa gggttatttt tacttagctt 2640
agctatgtca gccaatccga ttgccttagg tgaaagaaac caccgaaatc cctcaggtcc 2700
cttggtcagg agcctctcaa gatttttttt gtcagaggct ccaaatagaa aataagaaaa 2760
ggttttcttc attcatggct agagctagat ttaactcagt ttctaggcac ctcagaccaa 2820
tcatcaacta ccattctatt ccatgtttgc acctgtgcat tttctgtttg cccccattca 2880
ctttgtcagg aaaccttggc ctctgctaag gtgtatttgg tccttgagaa gtgggagcac 2940
cctacaggga cactatcact catgctggtg gcattgttta cagctagaaa gctgcactgg 3000
tgctaatgcc ccttgggaaa tggggctgtg aggaggagga ttataactta ggcctagcct 3060
cttttaacag cctctgaaat ttatcttttc ttctatgggg cttataaatg tatcttataa 3120
taaaaaggaa ggacaggagg aagacaggca aatgtacttc tcacccagtc ttctacacag 3180
atggaatctc tttggggcta agagaaaggt tttattctat attgcttacc tgatctcatg 3240
ttaggcctaa gaggctttct ccaggaggat tagcttggag ttctctatac tcaggtacct 3300
ctttcagggt tttctaaccc tgacacggac tgtgcatact ttccctcatc catgctgtgc 3360
tgtgttattt aatttttcct ggctaagatc atgtctgaat tatgtatgaa aattattcta 3420
tgtttttata ataaaaataa tatatcagac atcgaaaaaa aaaa 3464

<210> 70
<211> 2578
<212> DNA
<213> Homo sapiens

<400> 70
aagtgccttg aattccttgg taattatttc cttttaagcg tgtaactctt attattgcta 60
aactgctttt taagttaatg gtagttgttg tccaaaggaa gtctgatctg tgtttttgaa 120
acctcaatga tcgtctgttt ctaattaagg aattggatga agacatgcat cagaaaattg 180
caagggagat gaacctctct gaaactgctt ttatccgaaa actgcacccg acagacaact 240
ttgcacaaag ttcctgcttt ggactgagat ggtttacacc agcgagtgag gtcccactct 300
gtggccatgc caccctggct tctgcagctg tgctgtttca caaaataaaa aacatgaaca 360
gcacgctcac gtttgtcact ctgagtggag aactaagggc cagacgagca gaggacggca 420
tcgtcctgga cttgcctctt tatccagccc acccccagga cttccatgaa gtagaggact 480
tgataaagac tgccataggc aacacactgg tccaggacat ctgttattct ccagataccc 540
aaaagctcct cgtccgcctc agtgacgttt acaacaggtc gtttctggag aacctgaaag 600
tgaacacgga gaatctgctg caagttgaaa acacagggaa ggtgaaaggg cttattctta 660
cccttaaagg agagcctggt gggcagaccc aagcatttga cttttactca agatattttg 720
caccgtgggt tggtgtggct gaagacccag tgacagggtc tgcacacgct gttctcagca 780
gctactggtc ccagcatctg gggaagaaag aaatgcatgc ttttcagtgt tcccaccgag 840
gaggagagct gggaatttcc cttcgtccag acggaagggt tgacattaga ggaggtgcag 900
ctgttgtttt agagggcaca ctgacagcct agaggtggtt atgctgtgac gctgctgtct 960
ctaaccacca agtattttct gcttaaaaag aaatgtaagg ggctgccttt agcaaatgtg 1020
cgtagtagtc tacttaatcc tcatgttaaa aatcgaaaaa tgggccaggc gcagtggctc 1080
atgcctgtaa tcgtagcact ttgagaggcc aaggtgggtg gatcacctga ggtcaggggt 1140
tcgacaccag cctggccaac atggtgaaac ctcgtctcta ctacaaatac aaaaattagc 1200
tgggtgtggt gccacatgcc tgtaattcca gctacttggg aggctgaggc atggagaatc 1260
gcttgaaccc aggaggcaga agttgcagtg agcagagatc acaccactgc actccagcct 1320
gggcaacaga gtaagactcc atccacacac acacacacac acacaaaatt gaaaagtgaa 1380
gacattttaa tggagattta atagtgcttt ccagactaat gaactaatgg agttttggct 1440
ccactcatga gtgtatttga aatgtaagta accagctaca aagaataatg tcacttcatt 1500
tgattatgac taccaatcaa gagaaggagg aatacatttc tgaggagtga tactaaacca 1560
tttgagctta aatgagtacc tgattttgca gccattaaaa tgagtcaata actatgtgga 1620
aatatagaaa aatattttat aatataatac taagaaagag gacagtaggc cataaagtgt 1680
tagcagtgtt atgctatgtc tatataaata agcatgggcc attaaaaata gcaaactgaa 1740
aacagttcat gtgtgggggg caagtttaga agtaatttta atgtatctaa gaagtgattt 1800
cctttattgt tgtactcagg tacgaagact aaaaatcagg atgaatccag aaaattaaca 1860
caaaaaagta tgtattaggc tacttcctgt catagtgaaa ttaaacactc aaagtaatgt 1920
aatctcagct gggcgtggcg gctcatgcct gtaatcccag cactttggca ggacaaggca 1980
ggaggatcac ttgaacctag gagttcgaga ccagcctggg caacacagcg agaacttgtc 2040
tctattaaaa aaaaaaaaaa aggaatgtaa tttcaatctt tttcttgata tatggcttga 2100
gaatgataat gtaaaaggga attcttctct tacttcaata aaatgggttt taacataact 2160
ttaaattcag ttaaatatac aatattgaat acctatagtt gactttggga tggggacttt 2220
ttcaagtcat taagagtgtt tgtttaaggt gatctcattg atggtagttc tcagccgtct 2280
caaaaactgc aagctaatca gtcagacatt ctttaatgac cccaattttt tcactttaat 2340
tgttaccatg ttttctattt ttactgattt ttgctaaagc atgtaagagt gaatttatta 2400
tagcagtaat cttgtgtttc tcctgatgtg caataaatca ataattcacc agcaaaaaaa 2460
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2520

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2578

<210> 71
<211> 2657
<212> DNA
<213> Homo sapiens

<400> 71
tgggaacaca aacttgctgg cgggaagagc ccggaaagaa acctgtggat ctcccttcga 60
gatcatccaa agagaagaaa ggtgacctca cattcgtgcc ccttagcagc actctgcaga 120
aatgcctcct cagctgcaaa acggcctgaa cctctcggcc aaagttgtcc agggaagcct 180
ggacagcctg ccccaggcag tgagggagtt tctcgagaat aacgctgagc tgtgtcagcc 240
tgatcacatc cacatctgtg acggctctga ggaggagaat gggcggcttc tgggccagat 300
ggaggaagag ggcatcctca ggcggctgaa gaagtatgac aactgctggt tggctctcac 360
tgaccccagg gatgtggcca ggatcgaaag caagacggtt atcgtcaccc aagagcaaag 420
agacacagtg cccatcccca aaacaggcct cagccagctc ggtcgctgga tgtcagagga 480
ggattttgag aaagcgttca atgccaggtt cccagggtgc atgaaaggtc gcaccatgta 540
cgtcatccca ttcagcatgg ggccgctggg ctcacctctg tcgaagatcg gcatcgagct 600
gacggattcg ccctacgtgg tggccagcat gcggatcatg acgcggatgg gcacgcccgt 660
cctggaagca ctgggcgatg gggagtttgt caaatgcctc cattctgtgg ggtgccctct 720
gcctttacaa aagcctttgg tcaacaactg gccctgcaac ccggagctga cgctcatcgc 780
ccacctgcct gaccgcagag agatcatctc ctttggcagt gggtacggcg ggaactcgct 840
gctcgggaag aagtgctttg ctctcaggat ggccagccgg ctggcagagg aggaagggtg 900
gctggcagag cacatgctga ttctgggtat aaccaaccct gagggtgaga agaagtacct 960
ggcggccgca tttcccagcg cctgcgggaa gaccaacctg gccatgatga accccagcct 1020
ccccgggtgg aaggttgagt gcgtcgggga tgacattgcc tggatgaagt ttgacgcaca 1080
aggtcattta agggccatca acccagaaaa tggctttttc ggtgtcgctc ctgggacttc 1140
agtgaagacc aaccccaatg ccatcaagac catccagaag aacacaatct ttaccaatgt 1200
ggccgagacc agcgacgggg gcgtttactg ggaaggcatt gatgagccgc tagcttcagg 1260
cgtcaccatc acgtcctgga agaataagga gtggagctca gaggatgggg aaccttgtgc 1320
ccaccccaac tcgaggttct gcacccctgc cagccagtgc cccatcattg atgctgcctg 1380
ggagtctccg gaaggtgttc ccattgaagg cattatcttt ggaggccgta gacctgctgg 1440
tgtccctcta gtctatgaag ctctcagctg gcaacatgga gtctttgtgg gggcggccat 1500
gagatcagag gccacagcgg ctgcagaaca taaaggcaaa atcatcatgc atgacccctt 1560
tgccatgcgg cccttctttg gctacaactt cggcaaatac ctggcccact ggcttagcat 1620
ggcccagcac ccagcagcca aactgcccaa gatcttccat gtcaactggt tccggaagga 1680
caaggaaggc aaattcctct ggccaggctt tggagagaac tccagggtgc tggagtggat 1740
gttcaaccgg atcgatggaa aagccagcac caacgtcacg cccataggct acatccccaa 1800
ggaggatgcc ctgaacctga aaggcctggg gcacatcaac atgatggagc ttttcagcat 1860
ctccaaggaa ttctgggaca aggaggtgga agacatcgag aagtatctgg tggatcaagt 1920
caatgccgac ctcccctgtg aaatcgagag agagatcctt gccttgaagc aaagaataag 1980
ccagatgtaa tcagggcctg agaataagcc agatgtaatc agggcctgag tgctttacct 2040
ttaaaatcat taaattaaaa tccataaggt gcagtaggag caagagaggg caagtgttcc 2100
caaattgacg ccacctaata atcatcacca caccgggagc agatctgaag gcacactttg 2160
attttttaa ggataagaac cacagaacac tgggtagtag ctaatgaaat tgagaaggga 2220
aatcttagca tgcctccaaa aattcacatc caatgcatac tttgttcaaa tttaaggtta 2280
ctcaggcatt gatcttttca gtgtttttttc acttagctat gtggattagc tagaatgcac 2340
accaaaaaga tacttgagct gtatatatat atgtgtgtgt gtgtgtgtgt gtgtgtgtgt 2400
gtgcatgtat gtgcacatgt gtctgtgtga tatttggtat gtgtatttgt atgtactgtt 2460
attcaaaata tatttaatac ctttggaaaa tcttgggcaa gatgacctac tagttttcct 2520
tgaaaaaaag ttgctttgtt attaatattg tgcttaaatt atttttatac accattgttc 2580
cttaccttta cataattgca atatttcccc cttactactt cttggaaaaa aattagaaaa 2640
tgaagtttat agaaaag 2657

<210> 72
<211> 2107
<212> DNA
<213> Homo sapiens

<400> 72
ggcacgagga aagaaacaac aactggaaaa gaagcattgc ataagaccag gatgtctctg 60
aaatggatgt cagtctttct gctgatgcag ctcagttgtt actttagctc tgggagttgt 120
ggaaaggtgc tggtgtggcc cacagaatac agccattgga taaatatgaa gacaatcctg 180
gaagagcttg ttcagagggg tcatgaggtg attgtgttga catcttcggc ttctattctt 240
gtcaatgcca gtaaatcatc tgctattaaa ttagaagttt atcctacatc tttaactaaa 300
aatgatttgg aagatttttt tatgaaaatg ttcgatagat ggacatatag tatttcaaaa 360
aatacatttt ggtcatattt ttcacaacta caagaattgt gttgggaata ttctgactat 420

aatataaagc tctgtgaaga tgcagttttg aacaagaaac ttatgagaaa actacaagag 480
tcaaaatttg atgtccttct ggcagatgcc gttaatccct gtggtgagct gctggctgaa 540
ctacttaaca tacccttttct gtacagtctc cgcttctctg ttggctacac agttgagaag 600
aatggtggag gatttctgtt ccctccttcc tatgtacctg ttgttatgtc agaattaagt 660
gatcaaatga ttttcatgga gaggataaaa aatatgatat atatgcttta ttttgacttt 720
tggtttcaag catatgatct gaagaagtgg gaccagtttt atagtgaagt tctaggaaga 780
cccactacat tatttgagac aatggggaaa gctgaaatgt ggctcattcg aacctattgg 840
gattttgaat ttcctcgccc attcttacca aatgttgatt ttgttggagg acttcactgt 900
aaaccagcca aacccttgcc taaggaaatg gaagagtttg tgcagagctc tggagaaaat 960
ggtattgtgg tgttttctct ggggtcgatg atcagtaaca tgtcagaaga aagtgccaac 1020
atgattgcat cagcccttgc ccagatccca caaaaggttc tatggagatt tgatggcaag 1080
aagccaaata ctttaggttc caatactcga ctgtataagt ggttacccca gaatgacctt 1140
cttggtcatc ccaaaaccaa agcttttata actcatggtg gaaccaatgg catctatgag 1200
gcgatctacc atgggatccc tatggtgggc attcccttgt ttgcggatca acatgataac 1260
attgctcaca tgaaagccaa gggagcagcc ctcagtgtgg acatcaggac catgtcaagt 1320
agagatttgc tcaatgcatt gaagtcagtc attaatgacc ctatctataa agagaatatc 1380
atgaaattat caagaattca tcatgatcaa ccggtgaagc ccctggatcg agcagtcttc 1440
tggattgagt ttgtcatgcg ccataaagga gccaagcacc ttcgggtcgc agcccacaac 1500
ctcacctgga tccagtacca ctctttggat gtgatagcat tcctgctggc ctgcgtggca 1560
actatgatat ttatgatcac aaaatgttgc ctgttttgtt tccgaaagct tgccaaaaca 1620
ggaaagaaga agaaaaggga ttagttatat caaaagcctg aagtggaatg accaaaagat 1680
gggactcctc ctttattcca gcatggaggg ttttaaatgg aggatttcct ttttcctgcg 1740
acaaaacgtc ttttcacaac ttaccctgtt aagtcaaaat ttattttcca ggaatttaat 1800
atgtacttta gttggaatta ttctatgtca atgattttta agctatgaaa aataataata 1860
taaaacctta tgggcttata ttgaaattta ttattctaat ccaaaagtta ccccacacaa 1920
aagttactga gcttccttat gtttcacaca ttgtatttga acacaaaaca ttaacaactc 1980
cactcatagt atcaacattg ttttgcaaat actcagaata ttttggcttc attttgagca 2040
gaatttttgt ttttaatttt gccaatgaaa tcttcaataa ttaaaaaaaa aaaaaaaaaa 2100
aaaaaaa 2107

<210> 73
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 73
ctgggaatat gattatgctt aatctatgct cagtcgaaag gggctggggc tgctttctcc 60
cctcccttct tgactctctg ttcacagaac tcaggctgcc tccagccagc ctttgcccgc 120
tagactcact ggccctgagc acttgaaggt gcagcaagtc actgagaatg agcactttct 180
tctcggacac agcatggatc tgcctggctg tccccacagt actatgtggg acagtatttt 240
gcaaatacaa gaagagctca gggcagctgt ggagctggat ggtctgcctg gcaggcctct 300
gtgcagtctg cctgctcatc ctgtcccctt tttggggctt gatcctcttc tcggtgtcat 360
gcttcctcat gtatacttac ttatctggcc aagaattgtt acctgtggat cagaaggcag 420
tcctggtgac aggtggtgat tgcgggcttg gccatgcttt gtgcaagtat ctggatgagc 480
tgggcttcac ggtatttgcc ggagttttga atgaaaatgg cccaggagct gaggaattgc 540
gaagaacctg ctctccgcgc ctctcggtgc tccaaatgga catcacgaag ccagtgcaga 600
taaaagatgc ttacagcaag gttgcagcaa tgctgcagga cagaggactg tgggctgtga 660
tcaacaatgc tggggtgctt ggctttccaa ctgatgggga gcttcttctt atgactgact 720
acaaacaatg catggccgtg aacttctttg gaactgtgga ggtcacaaag acgttttgc 780
ctcttcttag aaaatccaaa gggaggctgg tgaatgtcag cagcatggga ggaggggccc 840
caatggaaag gctggcatct tatggctcat caaaggcggc tgtgaccatg ttctcatcag 900
ttatgagact ggagctttcc aagtggggaa ttaaagttgc ttccatccaa cctggaggct 960
tcctaacaaa tatcgcaggc accagtgaca agtgggaaaa gctggagaag gacattctgg 1020
accacctccc cgctgaggta caggaagact acggccagga ctacatctta gcacagcgga 1080
atttcctcct attgatcaac tcgttagcca gcaaggactt ctctccggtg ctgcgggaca 1140
tccagcatgc tatcttggcg aagagccctt ttgcctatta cacgccaggg aaaggcgctt 1200
acttgtggat ctgccttgct cactatttgc ctattggcat atatgattac tttgctaaaa 1260
gacattttgg ccaagacaag cccatgccca gagctctaag aatgcctaac tacaagaaaa 1320
aggccaccta ggcaatggaa gccctcaaag aagtcggaat gtcatagtct tgaaatgaaa 1380
gggaaactgg gaaactgggt ttctcattaa agttgtttcc cactctg 1427

<210> 74
<211> 2396
<212> DNA
<213> Homo sapiens

<400> 74

ggcaccaggt ctcccaggct tcctcagcgt cgacgccggg gagcgccctg gggttgggag 60
cgcccggggc ccgcgaagga ggaggtggct caggtgtcag ggcgcaccgt gggaaccggc 120
cccgggggag gcgtggaaac gcggggcctg ggactcgacc agcctctccc gtgcggatcg 180
caaaatctcg gagctgaaac agcccgttgt tcgcagcctc cctctgaccc gccaccctgc 240
acattgtttt ccattcgccc gggtcgcggg tgggaggaga ggcacgccgg ggttctggag 300
cttggccgcg cgccaggctt gtggccttcg tccccctggg gccactgggg cggccacgcc 360
tctccggcgg gaggagagaa cgcgtgggtc cgggtggctg ctccggccct tccgcctcca 420
gctcggccat ggggtcgcgc agctcccacg ccgcggtcat tcccgacggg gacagtattc 480
ggcgagagac cggcttctcc caagccagcc tgctccgcct gcaccaccgg ttccgggcac 540
tggacaggaa taagaagggc tacctgagcc gcatggatct ccagcagata ggggcgctcg 600
ccgtgaaccc cctgggagac cgaattatag aaagcttctt ccccgatggg agccagcgag 660
tggatttccc aggctttgtc agggtcttgg ctcattttcg ccctgtagaa gatgaggaca 720
cagaaaccca agaccccaag aaacctgaac ctctcaacag cagaaggaac aaacttcact 780
atgcatttca gctctatgac ctggatcgcg atgggaagat ctccaggcat gagatgctgc 840
aggttctccg tctgatggtt ggggtacagg tgacagaaga gcagctggag aacatcgctg 900
accgcacggt gcaggaggct gatgaagatg gggatggggc tgtgtccttc gtggagttca 960
ccaagtcctt agagaagatg gacgttgagc aaaaaatgag catccggatc ctgaagtgac 1020
tccgtttgtg ccttgggctt gctcctgcaa ccagtatctc cttggaattc atccaaagcc 1080
cccatggacg catggacgca gggcgacaat aaactgtatt ttcgtttcta actctattta 1140
gggccaagag aagaaagctg gaaggatgtg tactaaagtc tagctcagca gtccccaacc 1200
tttttggcat cagggacagt ttttccacgg atgggtgaca ggggatggtt ttgggatgat 1260
tcaagtgcat tacatttatt gtgcacttta tttctattat gattacattg taatatataa 1320
tgaaataatt atacaactca ccataatgta gaatcagcag gagccctgag cttgttttcc 1380
tgcaattaga cggtcccata tgggagtgat gggagacagt gacagatcat caggcattag 1440
attctcataa ggagtgcaca atctagatcc tttggtgtgc agttcacagt aggatttggg 1500
ctcctatgat aatctaatgc cactgctgat ctgacaggag gcagagctca ggcggtaatg 1560
caagcaatgg ggagtggctg taaatataga tgaagcttca gctcgcctgc cgctcacctt 1620
gtgctgtgca gcccggttcc taacagacca cagaccccac accaggtcta tctcatttgg 1680
tctcagagct gtgaatcagc cagcaatatt ttagttgcaa atcactgaaa acccaactca 1740
aagtgactta agtcagaaag aaatttttatg aattcaggta attaaaaagt ccagaagtat 1800
ctgcctttag gcacagctgg atccaagggc acaaatgatg tcatcaggct ccagttattc 1860
tccatctccc agctcagctt tttctgtctg taagcctgat tttcaggaag gctctttcct 1920
agtgatggag atgaccacca tcagctccag gcttctatcc tgctaaccca gtaacccagt 1980
gggaagagat ttacttattc caataattcc aagtggagag tgtcattgac ccgtttgggg 2040
tctcatctct acttctaggg gaatgaaaca ctttgagtgg ccaggcctgt gtcatgtgct 2100
aattcctaga gccagggaaa taaggtctga ggattcagga tggggtgaaa ggtggttgct 2160
taaaggaaaa tgaaatacaa ttagcagaat aaggggaaac gagtggtctg ctctgctcgg 2220
gcaaaacaag agatgcccat tactgtgagg gacccttgaa gtctggactc ttaaatgggt 2280
ttttgctgat ttcctgggtg catgctagga tgatggggct tgatgcagta gggaagagac 2340
gatgtaaaaa taataaacaa tatatacctt caaaaaaaaa aaaaaaaaaa aaaaaa 2396

<210> 75
<211> 2863
<212> DNA
<213> Homo sapiens

<400> 75
atctgaaaaa ttaataattc cttaattatc aaatatccat tatttaaatt tataattgtg 60
tcataaatat tgtcataaat agatttgctg ttttaaagct tgttccttca ttttctctgt 120
tttgttttag ataaacattg tcataaatag atttgttgtt ttaaagcttg ttccttcatt 180
ttctctgatt gttttgtttt agattcagag gttacttatg cttgtttgtt acatggatgt 240
tacatgtgta atgggggata ttggacttct agtgtactca tcacccatat actgaacact 300
gtactcaaaa gggattgaaa gaaactagga aacttggcag gaagatcatt cttaagccag 360
gaaaaaaatt tttaatgctc acatgtgaac atgtgatggt cataccagaa ggagcaccca 420
cctccctccc tctgtgacag acacattttc ttagccttca cctttccttc tttcaagttg 480
ctgaaaatcc acagtgtttc tgttcatttg ttactttcat tctcacctat cttctctctt 540
gctccatcta ccagaacaat aattccccat ataatacttc tcacttcact tttcaacgca 600
ggacctcttg ttggtctgat ctgtttgtct gtccgcttta tcaatattat cagatgtaag 660
tttacatgaa tacacacaca tattcactaa actgagggga aaaaatgcct tgtaggtcat 720
aaaaaagcag ggaaattccc aacaattcat atttgatccc tggatccagg ggtggcagca 780
ataagcctgc tttagatatt tactccccat tttatgatcc ggtggtttgg tttttcaaat 840
gatgatatgg ctcctttcgc aatgacttga tgtttaggag gtgtgcttca ataaatacat 900
tttaaaatca acaatcaagt tagagttgta caaatggctc tgaaatgtcc cactacactg 960
ttagaccaag ggcacagatt gtgcttctgt actatttatc ctagtatccc tcggcatata 1020
ttaactgctc taaaaatctc cttggctaca cgctgcatca aatcaaagtt aaatgttata 1080
ccacctttct attctatttt taatattcaa agagggtgct cagattttag aacaaatttc 1140
aatgtttaag tacacacaaa aaaatcatta actcatatat ttcaagagta ggaaatggga 1200

actggtgtta aaactcttat aacaaatgtc actgtcttaa gggacagtgt ttaaaaacgc 1260
atacctggcc gggcgcggtg gctcatgcct gtaatcccag cactttggga ggccgaggcc 1320
ggcggatcac aaggaaaaca aactcaggaa gaaaaaggaa agcagaagtg atcaaggaga 1380
gcgctcgagt tgcaatattt tcctttggct gctgacaggc agttactata aagcattgtg 1440
catggacacc atcttcttgt attatacaag aaaggagtgt acctatcaca cacaggggga 1500
aaaatgctct tttgggtgct aggcctccta atcctctgtg gttttctgtg gactcgtaaa 1560
ggaaaactaa agattgaaga catcactgat aagtacattt ttatcactgg atgtgactcg 1620
ggctttggaa acttggcagc cagaactttt gataaaaagg gatttcatgt aatcgctgcc 1680
tgtctgactg aatcaggatc aacagcttta aaggcagaaa cctcagagag acttcgtact 1740
gtgcttctgg atgtgaccga cccagagaat gtcaagagga ctgcccagtg ggtgaagaac 1800
caagttgggg agaaaggtct ctggggtctg atcaataatg ctggtgttcc cggcgtgctg 1860
gctcccactg actggctgac actagaggac tacagagaac ctattgaagt gaacctgttt 1920
ggactcatca gtgtgacact aaatatgctt cctttggtca agaaagctca agggagagtt 1980
attaatgtct ccagtgttgg aggtcgcctt gcaatcgttg gagggggcta tactccatcc 2040
aaatatgcag tggaaggttt caatgacagc ttaagacggg acatgaaagc ttttggtgtg 2100
cacgtctcat gcattgaacc aggattgttc aaaacaaact tggcagatcc agtaaaggta 2160
attgaaaaaa aactcgccat ttgggagcag ctgtctccag acatcaaaca acaatatgga 2220
gaaggttaca ttgaaaaaag tctagacaaa ctgaaaggca ataaatccta tgtgaacatg 2280
gacctctctc cggtggtaga gtgcatggac cacgctctaa caagtctctt ccctaagact 2340
cattatgccg ctggaaaaga tgccaaaatt ttctggatac ctctgtctca catgccagca 2400
gctttgcaag actttttatt gttgaaacag aaagcagagc tggctaatcc caaggcagtg 2460
tgactcagct aaccacaaat gtctcctcca ggctatgaaa ttggccgatt tcaagaacac 2520
atctcctttt caaccccatt ccttatctgc tccaacctgg actcatttag atcgtgctta 2580
tttggattgc aaaagggagt cccaccatcg ctggtggtat cccagggtcc ctgctcaagt 2640
tttctttgaa aaggagggct ggaatggtac atcacatagg caagtcctgc cctgtattta 2700
ggctttgcct gcttggtgtg atgtaaggga aattgaaaga cttgcccatt caaaatgatc 2760
tttaccgtgg cctgccccat gcttatggtc cccagcattt acagtaactt gtgaatgtta 2820
agtatcatct cttatctaaa tattaaaaga taagtcaaac att 2863

<210> 76
<211> 603
<212> DNA
<213> Homo sapiens

<400> 76
atggggcagg agtttagctg ggaggaggcg gaggcagctg gcgagataga tgtggcggag 60
ctccaggagt ggtacaagaa gtttgtgatg gagtgcccca gcggcacact ctttatgcat 120
gagtttaagc gcttcttcaa ggtcacagac gatgaggagg cctcccagta tgtagagggc 180
atgttccgag ccttcgacaa gaatggggac aacaccatcg acttcctgga gtacgtggca 240
gctctgaatc tcgtgctgag gggcaccctg gagcacaagc tgaagtggac attcaagatc 300
tatgataagg atggcaatgg ctgcatcgac cgcctggagc tactcaacat tgtggaggga 360
atttaccagc tgaagaaagc ctgccggcga gagctacaga ctgagcaaga ccagctgctc 420
acacccgagg aggtcgtgga caggatcttc ctcctggtgg atgagaatgg agatggccag 480
ctgtctctga acgagtttgt tgaaggtgcc cgtcgggaca agtgggtgat gaagatgctg 540
cagatggaca tgaatcccag cagctggctc gctcagcaga gacggaaaag tgccatgttc 600
tga 603

<210> 77
<211> 2407
<212> DNA
<213> Homo sapiens

<400> 77
ggcacgaggc ggaggggct cagtccgcag ccgccgccgc caccgccgcg cctcggcctc 60
ggtgcaggca gcggccgccg ccgccgagac agctgcgcgg gcgagcatcc ccacgcagca 120
ccttggaagt tgttttcaac catatccagc ctttgccgaa tacatcctat ctgccacaca 180
tccagcgtga ggtccctcca gctacaaggt gggcaccatg gcggagaagt ttgactgcca 240
ctactgcagg gatcccttgc aggggaagaa gtatgtgcaa aaggatggcc accactgctg 300
cctgaaatgc tttgacaagt tctgtgccaa cacctgtgtg gaatgccgca agcccatcgg 360
tgcggactcc aaggaggtgc actataagaa ccgcttctgg catgacacct gcttccgctg 420
tgccaagtgc cttcaccct tggccaatga gacctttgtg gccaaggaca acaagatcct 480
gtgcaacaag tgcaccactc gggaggactc ccccaagtgc aaggggtgct tcaaggccat 540
tgtggcagga gatcaaaacg tggagtacaa ggggaccgtc tggcacaaag actgcttcac 600
ctgtagtaac tgcaagcaag tcatcgggac tggaagcttc ttccctaaag gggaggactt 660
ctactgcgtg acttgccatg agaccaagtt tgccaagcat tgcgtgaagt gcaacaaggc 720
catcacatct ggaggaatca cttaccagga tcagccctgg catgccgatt gctttgtgtg 780
tgttacctgc tctaagaagc tggctgggca gcgtttcacc gctgtggagg accagtatta 840

ctgcgtggat tgctacaaga actttgtggc caagaagtgt gctggatgca agaaccccat 900
cactgggttt ggtaaaggct ccagtgtggt ggcctatgaa ggacaatcct ggcacgacta 960
ctgcttccac tgcaaaaaat gctccgtgaa tctggccaac aagcgctttg ttttccacca 1020
ggagcaagtg tattgtcccg actgtgccaa aaagctgtaa actgacaggg gctcctgtcc 1080
tgtaaaatgg catttgaatc tcgttctttg tgtccttact ttctgcccta taccatcaat 1140
aggggaagag tggtccttcc cttctttaaa gttctccttc cgtctttttct cccattttac 1200
agtattactc aaataagggc acacagtgat catattagca tttagcaaaa agcaaccctg 1260
cagcaaagtg aatttctgtc cggctgcaat ttaaaaatga aaacttaggt agattgactc 1320
ttctgcatgt ttctcataga gcagaaaagt gctaatcatt tagccactta gtgatgtaag 1380
caagaagcat aggagataaa acccccactg agatgcctct catgcctcag ctgggaccca 1440
ccgtgtagac acacgacatg caagagttgc agcggctgct ccaactcact gctcaccctc 1500
ttctgtgagc aggaaaagaa ccctactgac atgcatggtt taacttcctc atcagaactc 1560
tgcccttcct tctgttcttt tgtgctttca aataactaac acgaacttcc agaaaattaa 1620
catttgaact tagctgtaat tctaaactga cctttccccg tactaacgtt tggtttcccc 1680
gtgtggcatg ttttctgagc gttcctactt taaagcatgg aacatgcagg tgatttggga 1740
agtgtagaaa gacctgagaa aacgagcctg tttcagagga acatcgtcac aacgaatact 1800
tctggaagct taacaaaact aaccctgctg tccttttttat tgtttttaat taatattttt 1860
gttttaattg atagcaaaat agtttatggg tttggaaact tgcatgaaaa tattttagcc 1920
ccctcagatg ttcctgcagt gctgaaattc atcctacgga agtaaccgca aaactctaga 1980
gggggagttg agcaggcgcc agggctgtca tcaacatgga tatgacattt cacaacagtg 2040
actagttgaa tcccttgtaa cgtagtagtt gtctgctctt tgtccatgtg ttaatgagga 2100
ctgcaaagtc ccttctgttg tgattcctag gacttttcct caagaggaaa tctggatttc 2160
cacctaccgc ttacctgaaa tgcaggatca cctacttact gtattctaca ttattatatg 2220
acatagtata atgagacaat atcaaaagta aacatgtaat gacaatacat actaacattc 2280
ttgtaggagt ggttagagaa gctgatgcct catttctaca ttctgtcatt agctattatc 2340
atctaacgtt tcagtgtatc cttacagaaa taaagcagca tatgaaaaaa aaaaaaaaaa 2400
aaaaaaa 2407

<210> 78
<211> 2175
<212> DNA
<213> Homo sapiens

<400> 78
gagaaattgg agaagataaa actggacact ggggagacca caacttcatg ctgcgtggga 60
tctcccagct acctgcagtg gccaccatgt cttgggtcct gctgcctgta ctttggctca 120
ttgttcaaac tcaagcaata gccataaagc aaacacctga attaacgctc catgaaatag 180
tttgtcctaa aaaacttcac attttacaca aaagagagat caagaacaac cagacagaaa 240
agcatggcaa agaggaaagg tatgaacctg aagttcaata tcagatgatc ttaaatggag 300
aagaaatcat tctctcccta caaaaaacca agcacctcct ggggccagac tacactgaaa 360
cattgtactc acccagagga gaggaaatta ccacgaaacc tgagaacatg gaacactgtt 420
actataaagg aaacatccta aatgaaaaga attctgttgc cagcatcagt acttgtgacg 480
ggttgagagg atacttcaca catcatcacc aaagatacca gataaaacct ctgaaaagca 540
cagacgagaa agaacatgcc gtctttacat ctaaccagga ggaacaagac ccagctaacc 600
acacatgtgg tgtgaagagc actgacggga aacaaggccc aattcgaatc tctagatcac 660
tcaaaagccc agagaaagaa gactttcttc gggcacagaa atacattgat ctctatttgg 720
tgctggataa tgccttttat aagaactata atgagaatct aactctgata agaagctttg 780
tgtttgatgt gatgaaccta ctcaatgtga tatataacac catagatgtt caagtggcct 840
tggtaggtat ggaaatctgg tctgatgggg ataagataaa ggtggtgccc agcgcaagca 900
ccacgtttga caacttcctg agatggcaca gttctaacct ggggaaaaag atccacgacc 960
atgctcagct tctcagcggg attagcttca acaatcgacg tgtgggactg gcagcttcaa 1020
attccttgtg ttccccatct tcggttgctg ttattgaggc taaaaaaaag aataatgtgg 1080
ctcttgtagg agtgatgtca catgagctgg gccatgtcct tggtatgcct gatgttccat 1140
tcaacaccaa gtgtccctct ggcagttgtg tgatgaatca gtatctgagt tcaaaattcc 1200
caaaggattt cagtacatct tgccgtgcac attttgaaag atacctttta tctcagaaac 1260
caaagtgcct gctgcaagca cctattccta caaatataat gacaacacca gtgtgtggga 1320
accacctttct agaagtggga gaagactgtg attgtggctc tcctaaggag tgtaccaatc 1380
tctgctgtga agccctaacg tgtaaactga agcctggaac tgattgcgga ggagatgctc 1440
caaaccatac cacagagtga atccaaaagt ctgcttcact gagatgctac cttgccagga 1500
caagaaccaa gaactctaac tgtcccagga atcttgtgaa ttttcaccca taatggtctt 1560
tcacttgtca ttctactttc tatattgtta tcagtccagg aaacaggtaa acagatgtaa 1620
ttagagacat tggctctttg tttaggccta atctttcttt ttacttttt ttttcttttt 1680
tctttttttt taaagatcat gaatttgtga cttagttctg ccctttggag aacaaaagaa 1740
agcagtcttc catcaaatca ccttaaaatg cacggctaaa ctattcagag ttaacactcc 1800
agaattgtta aattacaagt actatgcttt aatgcttctt tcatcttact agtatggcct 1860
ataaaaaaaa taataccact tgatgggtga aggctttggc aatagaaaga agaatagaat 1920
tcaggtttta tgttattcct ctgtgttcac ttcgccttgc tcttgaaagt gcagtatttt 1980

tctacatcat gtcgagaatg attcaatgta aatatttttc attttatcat gtatatccta 2040
tacacacatc tccttcatca tcatatatga agtttatttt gagaagtcta cattgcttac 2100
attttaattg agccagcaaa gaaggcttaa tgatttattg aaccataatg tcaataaaaa 2160
cacaactttt gaggc 2175

<210> 79
<211> 386
<212> DNA
<213> Homo sapiens

<400> 79
ccaggatcag catggccgtc cgccagtggg taatcgccct ggccttggct gccctccttg 60
ttgtggacag ggaagtgcca gtggcagcag gaaagctccc tttctcaaga atgcccatct 120
gtgaacacat ggtagagtct ccaacctgtt cccagatgtc caacctggtc tgcggcactg 180
atgggctcac atatacgaat gaatgccagc tctgcttggc ccggataaaa accaaacagg 240
acatccagat catgaaagat ggcaaatgct gatcccacag gagcacctca agccatgaag 300
tgtcagctgg agaacagtgg tgggcatgga gaggatatga catgaaataa aagatccagc 360
ccaactgaaa aaaaaaaaaa aaaaaa 386

<210> 80
<211> 1264
<212> DNA
<213> Homo sapiens

<400> 80
gtggtaccca gtcctcaggt gcaaccccct gcgtggtcct ctgtggcagc cttctctcat 60
tcagagctgt tttccacaga ggtagtgaaa agaactggat tttcaagttc actttgcaag 120
agaaaaagaa aactcagtag aagataatgg caagtccaga ctggggatat gatgacaaaa 180
atggtcctga acaatggagc aagctgtatc ccattgccaa tggaaataac caatcccctg 240
ttgatattaa aaccagtgaa accaaacatg acacctctct gaaacctatt agtgtctcct 300
acaacccagc cacagccaaa gaaattatca atgtggggca ttctttccat gtaaattttg 360
aggacaacga taaccgatca gtgctgaaag gtggtccttt ctctgacagc tacaggctct 420
ttcagtttca ttttcactgg ggcagtacaa atgagcatgg ttcagaacat acagtggatg 480
gagtcaaata ttctgccgag cttcacgtag ctcactggaa ttctgcaaag tactccagcc 540
ttgctgaagc tgcctcaaag gctgatggtt tggcagttat tggtgttttg atgaaggttg 600
gtgaggccaa cccaaagctg cagaaagtac ttgatgccct ccaagcaatt aaaaccaagg 660
gcaaacgagc cccattcaca aattttgacc cctctactct ccttccttca tccctggatt 720
tctggaccta ccctggctct ctgactcatc ctcctcttta tgagagtgta acttggatca 780
tctgtaagga gagcatcagt gtcagctcag agcagctggc acaattccgc agccttctat 840
caaatgttga aggtgataac gctgtcccca tgcagcacaa caaccgccca acccaacctc 900
tgaagggcag aacagtgaga gcttcatttt gatgattctg agaagaaact tgtccttcct 960
caagaacaca gccctgcttc tgacataatc cagttaaaat aataattttt aagaaataaa 1020
tttatttcaa tattagcaag acagcatgcc ttcaaatcaa tctgtaaaac taagaaactt 1080
aaattttagt tcttactgct taattcaaat aataattagt aagctagcaa atagtaatct 1140
gtaagcataa gcttatctta aattcaagtt tagtttgagg aattctttaa aattacaact 1200
aagtgatttg tatgtctatt tttttcagtt tatttgaacc aataaaataa ttttatctct 1260
ttct 1264

<210> 81
<211> 2386
<212> DNA
<213> Homo sapiens

<400> 81
agcatacgcc gagccggtct ttgagcgcta acgtctttct gtctccccgc ggtggtgatg 60
acggtgaaaa ctgaggctgc taagggcacc ctcacttact ccaggatgag gggcatggtg 120
gcaattctca tcgctttcat gaagcagagg aggatgggtc tgaacgactt tattcagaag 180
attgccaata actcctatgc atgcaaacac cctgaagttc agtccatctt gaagatctcc 240
caacctcagg agcctgagct tatgaatgcc aacccttctc ctccaccaag tccttctcag 300
caaatcaacc ttggcccgtc gtccaatcct catgctaaac catctgactt tcacttcttg 360
aaagtgatcg gaaagggcag ttttggaaag gttcttctag caagacacaa ggcagaagaa 420
gtgttctatg cagtcaaagt tttacagaag aaagcaatcc tgaaaaagaa agaggagaag 480
catattatgt cggagcggaa tgttctgttg aagaatgtga agcacccttt cctggtgggc 540
cttcacttct ctttccagac tgctgacaaa ttgtactttg tcctagacta cattaatggt 600
ggagagttgt tctaccatct ccagagggaa cgctgcttcc tggaaccacg ggctcgtttc 660
tatgctgctg aaatagccag tgccttgggc tacctgcatt cactgaacat cgtttataga 720
gacttaaaac cagagaatat tttgctagat tcacagggac acattgtcct tactgacttc 780

ggactctgca aggagaacat tgaacacaac agcacaacat ccaccttctg tggcacgccg 840
gagtatctcg cacctgaggt gcttcataag cagccttatg acaggactgt ggactggtgg 900
tgcctgggag ctgtcttgta tgagatgctg tatggcctgc cgccttttta tagccgaaac 960
acagctgaaa tgtacgacaa cattctgaac aagcctctcc agctgaaacc aaatattaca 1020
aattccgcaa gacacctcct ggagggcctc ctgcagaagg acaggacaaa gcggctcggg 1080
gccaaggatg acttcatgga gattaagagt catgtcttct tctccttaat taactgggat 1140
gatctcatta ataagaagat tactccccct tttaacccaa atgtgagtgg gcccaacgac 1200
ctacggcact ttgaccccga gtttaccgaa gagcctgtcc ccaactccat tggcaagtcc 1260
cctgacagcg tcctcgtcac agccagcgtc aaggaagctg ccgaggcttt cctaggcttt 1320
tcctatgcgc ctcccacgga ctctttcctc tgaaccctgt tagggcttgg ttttaaagga 1380
ttttatgtgt gtttccgaat gttttagtta gccttttggt ggagccgcca gctgacagga 1440
catcttacaa gagaatttgc acatctctgg aagcttagca atcttattgc acactgttcg 1500
ctggaagctt tttgaagagc acattctcct cagtgagctc atgaggtttt cattttatt 1560
cttccttcca acgtggtgct atctctgaaa cgagcgttag agtgccgcct tagacggagg 1620
caggagtttc gttagaaagc ggacgctgtt ctaaaaaagg tctcctgcag atctgtctgg 1680
gctgtgatga cgaatattat gaaatgtgcc ttttctgaag agattgtgtt agctccaaag 1740
cttttcctat cgcagtgttt cagttcttta ttttcccttg tggatatgct gtgtgaaccg 1800
tcgtgtgagt gtggtatgcc tgatcacaga tggattttgt tataagcatc aatgtgacac 1860
ttgcaggaca ctacaacgtg ggacattgtt tgtttcttcc atatttggaa gataaattta 1920
tgtgtagact tttttgtaag atacggttaa taactaaaat ttattgaaat ggtcttgcaa 1980
tgactcgtat tcagatgctt aaagaaagca ttgctgctac aaatatttct atttttagaa 2040
agggttttta tggaccaatg ccccagttgt cagtcagagc cgttggtgtt tttcattgtt 2100
taaaatgtca cctgtaaaat gggcattatt tatgtttttt tttttgcatt cctgataatt 2160
gtatgtattg tataaagaac gtctgtacat tgggttataa cactagtata tttaaactta 2220
caggcttatt tgtaatgtaa accaccattt taatgtactg taattaacat ggttataata 2280
cgtacaatcc ttccctcatc ccatcacaca actttttttg tgtgtgataa actgattttg 2340
gtttgcaata aaaccttgaa aaatatttac aaaaaaaaaa aaaaaa 2386

<210> 82
<211> 1432
<212> DNA
<213> Homo sapiens

<400> 82
gctgttcggc ctgcgtcgct ccgggagctg ccgacggacg gagcgccccc gcccccgccc 60
ggccgcccgc ccgccgccgc catgcccttc tccaacagcc acaacgcact gaagctgcgc 120
ttcccggccg aggacgagtt ccccgacctg agcgcccaca acaaccacat ggccaaggtg 180
ctgacccccg agctgtacgc ggagctgcgc gccaagagca cgccgagcgg cttcacgctg 240
gacgacgtca tccagacagg cgtggacaac ccgggccacc cgtacatcat gaccgtgggc 300
tgcgtggcgg gcgacgagga gtcctacgaa gtgttcaagg atctcttcga ccccatcatc 360
gaggaccggc acggcggcta caagcccagc gatgagcaca agaccgacct caaccccgac 420
aacctgcagg gcggcgacga cctggacccc aactacgtgc tgagctcgcg ggtgcgcacg 480
ggccgcagca tccgtggctt ctgcctcccc ccgcactgca gccgcgggga gcgccgcgcc 540
atcgagaagc tcgcggtgga agccctgtcc agcctggacg gcgacctggc gggccgatac 600
tacgcgctca agagcatgac ggaggcggag cagcagcagc tcatcgacga ccacttcctc 660
ttcgacaagc ccgtgtcgcc cctgctgctg gcctcgggca tggcccgcga ctggcccgac 720
gcccgcggta tctggcacaa tgacaataag accttcctgg tgtgggtcaa cgaggaggac 780
cacctgcggg tcatctccat gcagaagggg ggcaacatga aggaggtgtt cacccgcttc 840
tgcaccggcc tcacccagat tgaaactctc ttcaagtcta aggactatga gttcatgtgg 900
aaccctcacc tgggctacat cctcacctgc ccatccaacc tgggcaccgg gctgcgggca 960
ggtgtgcata tcaagctgcc caacctgggc aagcatgaga agttctcgga ggtgcttaag 1020
cggctgcgac ttcagaagcg aggcacaggc ggtgtggaca cggctgcggt gggcggggtc 1080
ttcgacgtct ccaacgctga ccgcctgggc ttctcagagg tggagctggt gcagatggtg 1140
gtggacggag tgaagctgct catcgagatg gagcagcggc tggagcaggg ccaggccatc 1200
gacgacctca tgcctgccca gaaatgaagc ccggcccaca cccgacacca gccctgctgc 1260
ttcctaactt attgcctggg cagtgcccac catgcacccc tgatgttcgc cgtctggcga 1320
gcccttagcc ttgctgtaga gacttccgtc accttggta gagtttattt ttttgatggc 1380
taagatactg ctgatgctga aataaactag ggttttggcc tgcctgcgtc tg 1432

<210> 83
<211> 2832
<212> DNA
<213> Homo sapiens

<400> 83
aggaagctga accatctatc tccagaaatg tcttcagaaa gtaaagagca acataacgtt 60
tcacccagag actcagctga aggaaatgac agttatccat ctgggatcca tctggaactt 120

caaagggaat caagtactga cttcaagcaa tttgagacca atgatcaatg cagaccttat 180
cataggatcc ttattgagcg tcaagagaaa tcagatacaa acttcaagga gtttgttatt 240
aaaaagctgc agaagaattg ccagtgcagt ccagccaaag ccaaaaatat gattttaggt 300
ttccttcctg ttttgcagtg gctcccaaaa tacgacctaa agaaaaacat tttaggggat 360
gtgatgtcag gcttgattgt gggcatatta ttggtgcccc agtccattgc ttattccctg 420
ctggctggcc aagaacctgt ctatggtctg tacacatctt tttttgccag catcatttat 480
tttctcttgg gtacctcccg tcacatctct gtgggcattt ttggagtact gtgccttatg 540
attggtgaga cagttgaccg agaactacag aaagctggct atgacaatgc ccatagtgct 600
ccttccttag gaatggtttc aaatgggagc acattattaa atcatacatc agacaggata 660
tgtgacaaaa gttgctatgc aattatggtt ggcagcactg taacctttat agctggagtt 720
tatcaggtag cgatgggctt ctttcaagtg ggttttgttt ctgtctacct ctcagatgcc 780
ttgctgagtg gatttgtcac tggtgcctcc ttcactattc ttacatctca ggccaagtat 840
cttcttgggc tcaaccttcc tcggactaat ggtgtgggct cactcatcac tacctggata 900
catgtcttca gaaacatcca taagaccaat ctctgtgatc ttatcaccag ccttttgtgc 960
cttttggttc ttttgccaac caaagaactc aatgaacact tcaaatccaa gcttaaggca 1020
ccgattccta ttgaacttgt tgttgttgta gcagccacat tagcctctca ttttggaaaa 1080
ctacatgaaa attataattc tagtattgct ggacatattc ccactgggtt tatgccaccc 1140
aaagtaccag aatggaacct aattcctagt gtggctgtag atgcaatagc tatttccatc 1200
attggttttg ctatcactgt atcactttct gagatgtttg ccaagaaaca tggttacaca 1260
gtcaaagcaa accaggaaat gtatgccatt ggcttttgta atatcatccc ttccttcttc 1320
cactgtttta ctactagtgc agctcttgca aagacattgg ttaaagaatc aacaggctgc 1380
catactcagc tttctggtgt ggtaacagcc ctggttcttt tgttggtcct cctagtaata 1440
gctcctttgt tctattccct tcaaaaaagt gtccttggtg tgatcacaat tgtaaatcta 1500
cggggagccc ttcgtaaatt tagggatctt cccaaaatgt ggagtattag tagaatggat 1560
acagttatct ggtttgttac tatgctgtcc tctgcactgc taagtactga aataggccta 1620
cttgttgggg tttgtttttc tatattttgt gtcatcctcc gcactcagaa gccaaagagt 1680
tcactgcttg gcttggtgga agagtctgag gtctttgaat ctgtgtctgc ttacaagaac 1740
cttcagacta agccaggcat caagattttc cgctttgtag cccctctcta ctacataaac 1800
aaagaatgct ttaaatctgc tttatacaaa caaactgtca acccaatctt aataaaggtg 1860
gcttggaaga aggcagcaaa gagaaagatc aaagaaaaag tagtgactct tggtggaatc 1920
caggatgaaa tgtcagtgca actttcccat gatcccttgg agctgcatac tatagtgatt 1980
gactgcagtg caattcaatt tttagataca gcagggatcc acacactgaa agaagttcgc 2040
agagattatg aagccattgg aatccaggtt ctgctggctc agtgcaatcc cactgtgagg 2100
gattccctaa ccaacggaga atattgcaaa aaggaagaag aaaaccttct cttctatagt 2160
gtgtatgaag cgatggcttt tgcagaagta tctaaaaatc agaaaggagt atgtgttccc 2220
aatggtctga gtcttagtag tgattaattg agaaggtaga tagaagaatg tctagccaat 2280
aggttaaaat ttcaagtgtc caacatttcc cagttccaca gtgggaaatt ttgcacactt 2340
gaaattttaa ccaagtggct agatattatt cctcctttga agctaatggc atttgtatat 2400
acacactgca gcagagcttg tagctggaca gagtcaaaaa gaagaaaata cggtttcagg 2460
ctttcttgca gatatgaagt attcttggaa tgcaataagt atgtattgaa ctgtactgta 2520
aagtagctcc aaaacttaat tactctcctg ttttaggggt tatacatttg gactgtgcat 2580
tctccaagag atgaagcggt gaagttggga tttacattgg aagtgctgta gacttcttta 2640
tgtggctcag tggagagagg gaaagaatgt tgcacctgct ctagtaccat aggtcaagag 2700
gcttctggat cacaaagtca taactagaca ggtttgttct tgtagttttc tatccccagt 2760
ctttgctccc cagatggcag tagtttttag taggaaagtg ccattcctgt ccttaaggca 2820
cagtctcatc ag 2832

<210> 84
<211> 3347
<212> DNA
<213> Homo sapiens

<400> 84
atcccttgga ggcattcatg gctgaagtgg aggatcaggc agctagagac atgaagaggc 60
ttgaagaaaa ggacaaggaa agaaaaaacg taaagggtat tcgagatgac attgaagagg 120
aagatgacca agaagcttat tttcgataca tggcagaaaa cccaactgct ggtgtggttc 180
aggaggaaga ggaagacaat ctagaatatg atagtgacgg aaatccaatt gcacctacca 240
aaaaaatcat tgatcctctt ccccccattg atcattcaga gattgactat ccaccatttg 300
aaaaaaactt ttacaatgag catgaagaga taaccaacct cactccacag cagttaatag 360
atctccggca taagctcaat cttcgggtct ctggtgctgc acctcctaga ccaggaagta 420
gctttgctca ttttgggttt gacgaacaac ttatgcacca gattcggaaa tctgaataca 480
cacagcccac tccaatacag tgccagggtg tgcctgtggc attaagtggt agagacatga 540
ttggtattgc caaaacaggt agtgggaaaa ctgcagcctt catttggccc atgttgattc 600
atataatgga ccagaaggag ttggaaccag gtgatggacc aattgcagtg attgtgtgtc 660
ctaccaggga gctttgccag cagatccatg cagaatgtaa gcggtttgga aaagcatata 720
atcttcgatc agtggccgta tatggaggag ggagtatgtg ggagcaggcc aaggcccttc 780
aggaggggc agagattgtt gtgtgtaccc caggtcgact gatagatcat gtgaaaaaga 840

aagctaccaa tcttcaaaga gtctcttacc ttgtgtttga tgaagcagat cgaatgtttg 900
acatgggatt tgagtaccaa gttcgatcca tagcaagtca tgttcgtcct gacaggcaga 960
ctctcttatt tagtgcaact tttcggaaga agattgaaaa gttggccaga gacatcctga 1020
tcgaccctat tcgagtggtg cagggagata ttggagaggc aaatgaagat gtgacacaga 1080
ttgtggagat tctccattct ggacctagta aatggaactg gcttacccgg cgtctggtag 1140
aatttacctc ttcagggagt gtcctcctct ttgttactaa aaaagccaat gctgaagagc 1200
tagcgaataa ccttaaacag gagggtcata atcttgggct gctccatggg gatatggatc 1260
agagtgagag aaacaaggtc atttcagact ttaagaaaaa ggacatccca gtcctggtgg 1320
ccacagatgt tgcagcccgt ggtctggaca ttccttcaat taagactgtc attaactatg 1380
atgtggcacg agacattgat acccacacgc ataggattgg ccgcacagga agagcgggtg 1440
agaaaggtgt ggcctatacc ctactcactc ccaaggacag caattttgct ggtgacctgg 1500
tccggaactt ggaaggagcc aatcaacacg tttctaagga actcctagat ctggcaatgc 1560
agaatgcctg gtttcggaaa tctcgattca aaggagggaa aggaaaaaag ctgaacattg 1620
gtggaggagg cctaggctac agggagcggc ctggcctggg ctctgagaac atggatcgag 1680
gaaataacaa tgtaatgagc aattatgagg cctacaagcc ttccacagga gctatgggag 1740
atcgactaac ggcaatgaaa gcagctttcc agtcacagta caagagtcac tttgttgcag 1800
ccagtttaag taatcagaag gctggaagtt ctgctgctgg ggcaagtggg tggactagtg 1860
cagggagctt gaattctgtt ccaactaact cagcacaaca gggccataac agtcctgaca 1920
gccccgtcac cagtgccgcc aagggcatcc caggctttgg caatactggc aacatcagtg 1980
gtgcccctgt gacctacccg tctgccggag cccaaggagt caacaacaca gcttcaggga 2040
ataacagccg agaagggact gggggcagca acgggaaaag agagagatat actgagaacc 2100
ggggcagcag cccgtcacag tcacggagag actggcaatc ggcatagcga tagtccacgt 2160
cacggagatg gtggtcgcca tggagatgga taccgccatc cagaaagcag cagccgtcat 2220
actgatggcc atcggcacgg ggagaacaga catggaggaa gcgcaggccg gcatggggag 2280
aaccggggtg caaatgatgg tcggaatggg gaaagcagga aagaagcttt taatcgtgag 2340
agcaagatgg agcccaagat ggaacccaaa gtggacagca gcaagatgga caaggtggac 2400
agcaagacag ataagacagc tgacggcttt gctgtcccag agccgcctaa acgcaagaaa 2460
agtcgatggg acagttagag gggatgtgct aaagcgtgaa atcagttgtc cttaattttt 2520
agaaagattt tggtaactag gtgtctcagg gctgggttgg ggtccaaagt gtaaggaccc 2580
cctgccctta gtggagagct ggagcttgga gacattaccc cttcatcaga aggaatttc 2640
ggatgttttc ttgggaagct gttttggtcc ttggaagcag tgagagctgg gaagcttctt 2700
ttggctctag gtgagttgtc atgtgggtaa gttgaggtta tcttgggata aagggtcttc 2760
tagggcacaa aactcactct aggtttatat tgtatgtagc ttatattttt tactaaggtg 2820
tcaccttata agcatctata aattgacttc tttttcttag ttgtatggcc aggcagtccc 2880
cattttagga gttggcttct gcaaattcaa tccattgagc taactgttgg ggagcaattt 2940
ggtagttgta gacatttgca gggaagggag atgtctgatt ctaaatggga gttgatgctc 3000
aggtccccag ccaggtttgc atccagccct gagacatgta ggaaacacct ttcagaccca 3060
ggctctgaag attcccagaa gccacaagga ttgaagggaa aaggtgatcc tggtaactgt 3120
tccaggattg ctccaggttt gagatggtat tgctaaattt aaaattaaac aagaaaccca 3180
acaacagctt ttaaagtgtc ttctatctca ttgtattttt tttaacttgc cccaatgata 3240
gaaaagtctt ttgctgaaat gattttgatg atttttgttt atcgtttata aaaaggaaaa 3300
gaaatataca aactttgact tttgtgaaaa aaaaaaaaaa aaaaaaa 3347

<210> 85
<211> 15720
<212> DNA
<213> Homo sapiens

<400> 85
caacccacac cgcccctgcc agccaccatg gggctgccac tagcccgcct ggcggctgtg 60
tgcctggccc tgtctttggc agggggctcg gagctccaga cagagggcag aacccgatac 120
cacggccgca acgtctgcag cacctggggc aacttccact acaagacctt cgacggggac 180
gtcttccgct tccccggcct ctgcgactac aacttcgcct ccgactgccg aggctcctac 240
aaggaatttg ctgtgcacct gaagcggggt ccgggccagg ctgaggcccc cgccggggtg 300
gagtccatcc tgctgaccat caaggatgac accatctacc tcacccgcca cctggctgtg 360
cttaacgggg ccgtggtcag caccccgcac tacagccccg ggctgctcat tgagaagagc 420
gatgcctaca ccaaagtcta ctcccgcgcc ggcctcaccc tcatgtggaa ccgggaggat 480
gcactcatgc tggagctgga cactaagttc cggaaccaca cctgtggcct ctgcggggac 540
tacaacggcc tgcagagcta ttcagaattc ctctctgacg gcgtgctctt cagtcccctg 600
gagtttggga acatgcagaa gatcaaccag cccgatgtgg tgtgtgagga tcccgaggag 660
gaggtggccc ccgcatcctg ctccgagcac cgcgccgagt gtgagaggct gctgaccgcc 720
gaggccttcg cggactgtca ggacctggtg ccgctggagc cgtatctgcg cgcctgccag 780
caggaccgct gccggtgccc gggcggtgac acctgcgtct gcagcaccgt ggccgagttc 840
tcccgccagt gctcccacgc cggcggccgg cccgggaact ggaggaccgc cacgctctgc 900
cccaagacct gccccgggaa cctggtgtac ctggagagcg gctcgccctg catggacacc 960
tgctcacacc tggaggtgag cagcctgtgc gaggagcacc gcatggacgg ctgtttctgc 1020
ccagaaggca ccgtatatga cgacatcggg gacagtggct gcgttcctgt gagccagtgc 1080

cactgcaggc tgcacggaca cctgtacaca ccgggccagg agatcaccaa tgactgcgag 1140
cagtgtgtct gtaacgctgg ccgctgggtg tgcaaagacc tgccctgccc cggcacctgt 1200
gccctggaag gcggctccca catcaccacc ttcgatggga agacgtacac cttccacggg 1260
gactgctact atgtcctggc caagggtgac cacaacgatt cctacgctct cctgggcgag 1320
ctggcccccc gtggctccac agacaagcag acctgcctga agacggtggt gctgctggct 1380
gacaagaaga agaatgcggt ggtcttcaag tccgatggca gtgtactgct caaccagctg 1440
caggtgaacc tgccccacgt gaccgcgagc ttctctgtct tccgcccgtc ttcctaccac 1500
atcatggtga gcatggccat tggcgtccgg ctgcaggtgc agctggcccc agtcatgcaa 1560
ctctttgtga cactggacca ggcctcccag gggcaggtgc agggcctctg cgggaacttc 1620
aacggcctgg aaggtgacga cttcaagacg gccagcgggc tggtggaggc cacgggggcc 1680
ggctttgcca acacctggaa ggcacagtca acctgccatg acaagctgga ctggttggac 1740
gatccctgct ccctgaacat cgagagcgcc aactacgccg agcactggtg ctccctcctg 1800
aagaagacag agacccccct tggcaggtgc cactcggctg tggaccctgc tgagtattac 1860
aagaggtgca aatatgacac gtgtaactgt cagaacaatg aggactgcct gtgcgccgcc 1920
ctgtcctcct acgcgcgcgc ctgcaccgcc aagggcgtca tgctgtgggg ctggcgggag 1980
catgtctgca acaaggatgt gggctcctgc cccaactcgc aggtcttcct gtacaacctg 2040
accacctgcc agcagacctg ccgctccctc tccgaggccg acagccactg tctcgagggc 2100
tttgcgcctg tggacggctg cggctgccct gaccacacct tcctggacga gaagggccgc 2160
tgcgtacccc tggccaagtg ctcctgttac caccgcggtc tctacctgga ggcgggggat 2220
gtggtcgtca ggcaggaaga acgatgtgtg tgccgggatg ggcggctgca ctgtaggcag 2280
atccggctga tcggccagag ctgcacggcc ccaaagatcc acatggactg cagcaacctg 2340
actgcactgg ccacctcgaa gccccgagcc ctcagctgcc agacgctggc cgccggctat 2400
taccacacag agtgtgtcag tggctgtgtg tgccccgacg ggctgatgga tgacggccgg 2460
ggtggctgcg tggtggagaa ggaatgccct tgcgtccata acaacgacct gtattcttcc 2520
ggcgccaaga tcaaggtgga ctgcaatacc tgcacctgca agagaggacg ctgggtgtgc 2580
acccaggctg tgtgccatgg cacctgctcc atttacggga gtggccacta catcaccttt 2640
gatgggaagt actacgactt tgacggacac tgctcctacg tggctgttca ggactactgc 2700
ggccagaact cctcactggg ctcattcagc atcatcaccg agaacgtccc ctgtggcact 2760
acgggcgtca cctgctccaa ggccatcaag atcttcatgg ggaggacgga gctgaagttg 2820
gaagacaagc accgtgtggt gatccagcgt gatgagggtc accacgtggc ctacaccacg 2880
cgggaggtgg gccagtacct ggtggtggag tccagcacgg gcatcatcgt catctgggac 2940
aagaggacca ccgtgttcat caagctggct ccctcctaca agggcaccgt gtgtggcctg 3000
tgtgggaact ttgaccaccg ctccaacaac gacttcacca cgcgggacca catggtggtg 3060
agcagcgagc tggacttcgg gaacagctgg aaggaggccc ccacctgccc agatgtgagc 3120
accaacccgg agccctgcag cctgaacccg caccgccgct cctgggccga gaagcagtgc 3180
agcatcctca aaagcagcgt gttcagcatc tgccacagca aggtggaccc caagcccttc 3240
tacgaggcct gtgtgcacga ctcgtgctcc tgtgacacgg gtggggactg tgagtgcttc 3300
tgctctgccg tggcctccta cgcccaggag tgtaccaaag agggggcctg cgtgttctgg 3360
aggacgccgg acctgtgccc catattctgc gactactaca accctccgca tgagtgtgag 3420
tggcactatg agccatgtgg gaaccggagc ttcgagacct gcaggaccat caacggcatc 3480
cactccaaca tctccgtgtc ctacctggag ggctgctacc cccggtgccc caaggacagg 3540
ccgatctatg aggaggatct gaagaagtgt gtcactgcag acaagtgtgg ctgctatgtc 3600
gaggacaccc actacccacc tggagcatcg gttcccaccg aggagacctg caagtcctgc 3660
gtgtgtacta actcctccca agtcgtctgc aggccggagg aaggaaagat tcttaaccag 3720
acccaggatg gcgccttctg ctactgggag atctgtggcc ccaacgggac ggtggagaag 3780
cacttcaaca tctgttccat tacgacacgc ccgtccaccc tgaccacctt caccaccatc 3840
accctcccca ccacccccac ctccttcacc actaccacca ccaccaccac cccgacctcc 3900
agcacagttt tatcaacaac tccgaagctg tgctgcctct ggtctgactg gatcaatgag 3960
gaccacccca gcagtggcag cgacgacggt gaccgagaac catttgatgg ggtctgcggg 4020
gcccctgagg acatcgagtg caggtcggtc aaggatcccc acctcagctt ggagcagcat 4080
ggccagaagg tgcagtgtga tgtctctgtt gggttcattt gcaagaatga agaccagttt 4140
ggaaatggac catttggact gtgttacgac tacaagatac gtgtcaattg ttgctggccc 4200
atggataagt gtatcaccac tcccagccct ccaactacca ctccagccc tccaccaacc 4260
acgacgacca ccccttccacc aaccaccacc cccagccctc caaccaccac cacaaccacc 4320
cctccaccaa ccaccacccc cagccctcca ataaccacca cgaccacccc tctaccaacc 4380
accactccca gccctccaat aagcaccaca accacccctc caccaaccac cactcccagc 4440
cctccaacca ccactcccag ccctccaacc accactccca gccctccaac aaccaccaca 4500
accacccctc caccaaccac cactccagc cctccaatga ctacgcccat cactccacca 4560
gccagcacta ccacccttcc accaaccacc actcccagcc ctccaacaac caccacaacc 4620
acccctccac caaccaccac tcccagtcct ccaacgacta cgcccatcac tccaccaacc 4680
agcactacta cccttccacc aaccaccact cccagccctc caccaaccac cacaaccacc 4740
cctccaccaa ccaccactcc cagccctcca acaaccacca ctcccagtcc tccaacaatc 4800
accacaacca cccctccacc aaccaccact cccagccctc caacaacgac cacaaccacc 4860
cctccaccaa ccaccactcc cagccctcca acgactacac ccatcactcc accaaccagc 4920
actaccaccc ttccaccaac caccactccc agccctccac caaccaccac aaccaccct 4980
ccaccaacca ccactcccag ccctccaaca accaccactc ccagccctcc aataaccacc 5040
acaaccaccc ctccaccaac caccactccc agctctccaa taaccaccac tcccagccct 5100

ccaacaacca ccatgaccac cccttcacca accaccaccc ccagctctcc aataaccacc 5160
acaaccaccc cttcctcaac taccactccc agccctccac caaccaccat gaccaccccт 5220
tcaccaacca ccactcccag ccctccaaca accaccatga ccacccttcc accaaccacc 5280
acttccagcc ctctaacaac tactcctcta cctccatcaa taactcctcc tacattttca 5340
ccattctcaa cgacaacccc tactacccca tgcgtgcctc tctgcaattg gactggctgg 5400
ctggattctg gaaaacccaa ctttcacaaa ccaggtggag acacagaatt gattggagac 5460
gtctgtggac caggctgggc agctaacatc tcttgcagag ccaccatgta tcctgatgtt 5520
cccattggac agcttggaca aacagtggtg tgtgatgtct ctgtggggct gatatgcaaa 5580
aatgaagacc aaaagccagg tggggtcatc cctatggcct tctgcctcaa ctacgagatc 5640
aacgttcagt gctgtgagtg tgtcacccaa cccaccacca tgacaaccac caccacagag 5700
aacccaactc cgccaaccac gacacccatc accaccacca ctacggtgac cccaacccca 5760
acacccaccg gcacacagac cccaaccacg acacccatca ccaccaccac tacggtgacc 5820
ccaaccccaa cacccaccgg cacacagacc ccaaccacga cacccatcac caccaccact 5880
acggtgaccc caaccccaac acccaccggc acacagaccc caaccacgac acccatcacc 5940
accaccacta cggtgacccc aaccccaaca cccaccggca cacagacccc aaccacgaca 6000
cccatcacca ccaccactac ggtgacccca accccaacac ccaccggcac acagacccca 6060
accacgacac ccatcaccac caccactacg gtgaccccaa ccccaacacc caccggcaca 6120
cagaccccaa ccacgacacc catcaccacc accactacgg tgaccccaac cccaacaccc 6180
accggcacac agaccccaac cacgacaccc atcaccacca ccactacggt gaccccaacc 6240
ccaacaccca ccggcacaca gaccccaacc acgacaccca tcaccaccac cactacggtg 6300
accccaaccc caacacccac cggcacacag accccaacca cgacacccat caccaccacc 6360
actacggtga ccccaacccc aacacccacc ggcacacaga ccccaaccac gacacccatc 6420
accaccacca ctacggtgac cccaacccca acacccaccg gcacacagac cccaaccacg 6480
acacccatca ccaccaccac tacggtgacc ccaaccccaa cacccaccgg cacacagacc 6540
ccaaccacga cacccatcac caccaccact acggtgaccc caaccccaac acccaccggc 6600
acacagaccc caaccacgac acccatcacc accaccacta cggtgaccc aaccccaaca 6660
cccaccggca cacagaccc aaccacgaca cccatcacca ccaccactac ggtgacccca 6720
accccaacac ccaccggcac acagacccca accacgacac ccatcaccac caccactacg 6780
gtgaccccaa ccccaacacc caccggcaca cagaccccaa ccacgacacc catcaccacc 6840
accactacgg tgaccccaac cccaacaccc accggcacac agaccccaac cacgacaccc 6900
atcaccacca ccactacggt gaccccaacc ccaacaccca ccggcacaca gaccccaacc 6960
acgacaccca tcaccaccac cactacggtg accccaaccc caacacccac cggcacacag 7020
accccaacca cgacacccat caccaccacc actacggtga ccccaacccc aacacccacc 7080
ggcacacaga ccccaaccac gacacccatc accaccacca ctacggtgac cccaacccca 7140
acacccaccg gcacacagac cccaaccacg acacccatca ccaccaccac tacggtgacc 7200
ccaaccccaa cacccaccgg cacacagacc ccaaccacga cacccatcac caccaccact 7260
acggtgaccc caaccccaac acccaccggc acacagaccc caaccacgac acccatcacc 7320
accaccacta cggtgacccc aaccccaaca cccaccggca cacagacccc aaccacgaca 7380
cccatcacca ccaccactac ggtgacccca accccaacac ccaccggcac acagacccca 7440
accacgacac ccatcaccac caccactacg gtgaccccaa ccccaacacc caccggcaca 7500
cagaccccaa ccacgacacc catcaccacc accactacgg tgaccccaac cccaacaccc 7560
accggcacac agaccccaac cacgacaccc atcaccacca ccactacggt gaccccaacc 7620
ccaacaccca ccggcacaca gaccccaacc acgacaccca tcaccaccac cactacggtg 7680
accccaaccc caacacccac cggcacacag accccaacca cgacacccat caccaccacc 7740
actacggtga ccccaacccc aacacccacc ggcacacaga ccccaaccac gacacccatc 7800
accaccacca ctacggtgac cccaacccca acacccaccg gcacacagac cccaaccacg 7860
acacccatca ccaccaccac tacggtgacc ccaaccccaa cacccaccgg cacacagacc 7920
ccaaccacga cacccatcac caccaccact acggtgaccc caaccccaac acccaccggc 7980
acacagaccc caaccacgac acccatcacc accaccacta cggtgacccc aaccccaaca 8040
cccaccggca cacagaccccc aaccacgaca cccatcacca ccaccactac ggtgacccca 8100
accccaacac ccaccggcac acagacccca accacgacac ccatcaccac caccactacg 8160
gtgaccccaa ccccaacacc caccggcaca cagaccccaa ccacgacacc catcaccacc 8220
accactacgg tgaccccaac cccaacaccc accggcacac agaccccaac cacgacaccc 8280
atcaccacca ccactacggt gaccccaacc ccaacaccca ccggcacaca gaccccaacc 8340
acgacaccca tcaccaccac cactacggtg accccaaccc caacacccac cggcacacag 8400
accccaacca cgacacccat caccaccacc actacggtga ccccaacccc aacacccacc 8460
ggcacacaga ccccaaccac gacacccatc accaccacca ctacggtgac cccaacccca 8520
acacccaccg gcacacagac cccaaccacg acacccatca ccaccaccac tacggtgacc 8580
ccaaccccaa cacccaccgg cacacagacc ccaaccacga cacccatcac caccaccact 8640
acggtgaccc caaccccaac acccaccggc acacagaccc caaccacgac acccatcacc 8700
accaccacta cggtgacccc aaccccaaca cccaccggca cacagacccc aaccacgaca 8760
cccatcacca ccaccactac ggtgacccca accccaacac ccaccggcac acagacccca 8820
accacgacac ccatcaccac caccactacg gtgaccccaa ccccaacacc caccggcaca 8880
cagaccccaa ccacgacacc catcaccacc accactacgg tgaccccaac cccaacaccc 8940
accggcacac agaccccaac cacgacaccc atcaccacca ccactacggt gaccccaacc 9000
ccaacaccca ccggcacaca gaccccaacc acgacaccca tcaccaccac cactacggtg 9060
accccaaccc caacacccac cggcacacag accccaacca cgacacccat caccaccacc 9120

actacggtga ccccaacccc aacacccacc ggcacacaga ccccaaccac gacacccatc 9180
accaccacca ctacggtgac cccaacccca acacccaccg gcacacagac cccaaccacg 9240
acacccatca ccaccaccac tacggtgacc ccaaccccaa cacccaccgg cacacagacc 9300
ccaaccacga cacccatcac caccaccact acggtgaccc caaccccaac acccaccggc 9360
acacagaccc caaccacgac acccatcacc accaccacta cggtgacccc aaccccaaca 9420
cccaccggca cacagacccc aaccacgaca cccatcacca ccaccactac ggtgacccca 9480
accccaacac ccaccggcac acagacccca accacgacac ccatcaccac caccactacg 9540
gtgaccccaa ccccaacacc caccggcaca cagaccccaa ccacgacacc catcaccacc 9600
accactacgg tgaccccaac cccaacaccc accggcacac agaccccaac cacgacaccc 9660
atcaccacca ccactacggt gaccccaacc ccaacaccca ccggcacaca gaccccaacc 9720
acgacaccca tcaccaccac cactacggtg accccaaccc caacacccac cggcacacag 9780
accccaacca cgacacccat caccaccacc actacggtga ccccaacccc aacacccacc 9840
ggcacacaga ccccaaccac gacacccatc accaccacca ctacggtgac cccaacccca 9900
acacccaccg gcacacagac cccaaccacg acacccatca ccaccaccac tacggtgacc 9960
ccaaccccaa cacccaccgg cacacagacc ccaaccacga cacccatcac caccaccact 10020
acggtgaccc caaccccaac acccaccggc acacagaccc caaccacgac acccatcacc 10080
accaccacta cggtgacccc aaccccaaca cccaccggca cacagacccc aaccacgaca 10140
cccatcacca ccaccactac ggtgacccca accccaacac ccaccggcac acagacccca 10200
accacgacac ccatcaccac caccactacg gtgaccccaa ccccaacacc caccggcaca 10260
cagaccccaa ccacgacacc catcaccacc accactacgg tgaccccaac cccaacaccc 10320
accggcacac agaccccaac cacgacaccc atcaccacca ccactacggt gaccccaacc 10380
ccaacaccca ccggcacaca gaccccaacc acgacaccca tcaccaccac cactacggtg 10440
accccaaccc caacacccac cggcacacag accccaacca cgacacccat caccaccacc 10500
actacggtga ccccaacccc aacacccacc ggcacacaga ccccaaccac gacacccatc 10560
accaccacca ctacggtgac cccaacccca acacccaccg gcacacagac cccaaccacg 10620
acacccatca ccaccaccac tacggtgacc ccaaccccaa cacccaccgg cacacagacc 10680
ccaaccacga cacccatcac caccaccact acggtgaccc caaccccaac acccaccggc 10740
acacagaccc caaccacgac acccatcacc accaccacta cggtgacccc aaccccaaca 10800
cccaccggca cacagacccc aaccacgaca cccatcacca ccaccactac ggtgacccca 10860
accccaacac ccaccggcac acagacccca accacgacac ccatcaccac caccactacg 10920
gtgaccccaa ccccaacacc caccggcaca cagaccccaa ccacgacacc catcaccacc 10980
accactacgg tgaccccaac cccaacaccc accggcacac agaccccaac cacgacaccc 11040
atcaccacca ccactacggt gaccccaacc ccaacaccca ccggcacaca gaccccaacc 11100
acgacaccca tcaccaccac cactacggtg accccaaccc caacacccac cggcacacag 11160
accccaacca cgacacccat caccaccacc actacggtga ccccaacccc aacacccacc 11220
ggcacacaga ccccaaccac gacacccatc accaccacca ctacggtgac cccaacccca 11280
acacccaccg gcacacagac cccaaccacg acacccatca ccaccaccac tacggtgacc 11340
ccaaccccaa cacccaccgg cacacagacc ccaaccacga cacccatcac caccaccact 11400
acggtgaccc caaccccaac acccaccggc acacagaccc caaccacgac acccatcacc 11460
accaccacta cggtgacccc aaccccaaca cccaccggca cacagacccc aaccacgaca 11520
cccatcacca ccaccactac ggtgacccca accccaacac ccaccggcac acagacccca 11580
accacgacac ccatcaccac caccactacg gtgaccccaa ccccaacacc caccggcaca 11640
cagaccccaa ccacgacacc catcaccacc accactacgg tgaccccaac cccaacaccc 11700
accggcacac agaccccaac cacgacaccc atcaccacca ccactacggt gaccccaacc 11760
ccaacaccca ccggcacaca gaccccaacc acgacaccca tcaccaccac cactacggtg 11820
accccaaccc caacacccac cggcacacag accccaacca cgacacccat caccaccacc 11880
actacggtga ccccaacccc aacacccacc ggcacacaga ccccaaccac gacacccatc 11940
accaccacca ctacggtgac cccaacccca acacccaccg gcacacagac cccaaccacg 12000
acacccatca ccaccaccac tacggtgacc ccaaccccaa cacccaccgg cacacagacc 12060
ccaaccacga cacccatcac caccaccact acggtgaccc caaccccaac acccaccggc 12120
acacagaccc caaccacgac acccatcacc accaccacta cggtgacccc aaccccaaca 12180
cccaccggca cacagacccc aaccacgaca cccatcacca ccaccactac ggtgacccca 12240
accccaacac ccaccggcac acagacccca accacgacac ccatcaccac caccactacg 12300
gtgaccccaa ccccaacacc caccggcaca cagaccccaa ccacgacacc catcaccacc 12360
accactacgg tgaccccaac cccaacaccc accggcacac agaccccaac cacgacaccc 12420
atcaccacca ccactacggt gaccccaacc ccaacaccca ccggcacaca gaccccaacc 12480
acgacaccca tcaccaccac cactacggtg accccaaccc caacacccac cggcacacag 12540
accccaacca cgacacccat caccaccacc actacggtga ccccaacccc aacacccacc 12600
ggcacacaga ccgggccccc cacccacaca agcacagcac cgattgctga gttgaccaca 12660
tccaatcctc cgcctgagtc ctcaaccccc cagacctctc ggtccacctc ttcccctctc 12720
acggagtcaa ccacccttct gagtacccta ccacctgcca ttgagatgac cagcacggcc 12780
ccaccctcca cacccacggc acccacgacc acgagcggag gccacacact gtctccaccg 12840
cccagcacca ccacgtcccc tccaggcacc cccactcgcg gtaccacgac cgggtcatct 12900
tcagccccca cccccagcac tgtgcagacg accaccacca gtgcctggac cccaacgccg 12960
accccactct ccacacccag catcatcagg accacaggcc tgaggcccta cccttcctct 13020
gtgcttatct gctgtgtcct gaacgacacc tactacgcac caggtgagga ggtgtacaac 13080
ggcacatacg gagacacctg ttatttcgtc aactgctcac tgagctgtac gttggagttc 13140

tataactggt cctgcccatc cacgccctcc ccaacaccca cgccctccaa gtcgacgccc 13200
acgccttcca agccatcgtc cacgccctcc aagccgacgc ccggcaccaa gccccccgag 13260
tgcccagact ttgatcctcc cagacaggag aacgagactt ggtggctgtg cgactgcttc 13320
atggccacgt gcaagtacaa caacacggtg gagatcgtga aggtggagtg tgagccgccg 13380
cccatgccca cctgctccaa cggcctccaa cccgtgcgcg tcgaggaccc cgacggctgc 13440
tgctggcact gggagtgcga ctgctactgc acgggctggg gcgacccgca ctatgtcacc 13500
ttcgacggac tctactacag ctaccagggc aactgcacct acgtgctggt ggaggagatc 13560
agcccctccg tggacaactt cggagtttac atcgacaact accactgcga tcccaacgac 13620
aaggtgtcct gtccccgcac cctcatcgtg cgccacgaga cccaggaggt gctgatcaag 13680
accgtgcata tgatgcccat gcaggtgcag gtgcaggtga acaggcaggc ggtggcactg 13740
ccctacaaga agtacgggct ggaggtgtac cagtctggca tcaactacgt ggtggacatc 13800
cccgagctgg gtgtcctcgt ctcctacaat ggcctgtcct tctccgtcag gctgccctac 13860
caccggtttg gcaacaacac caagggccag tgtggcacct gcaccaacac cacctccgac 13920
gactgcattc tgcccagcgg ggagatcgtc tccaactgtg aggctgcggc tgaccagtgg 13980
ctggtgaacg acccctccaa gccacactgc ccccacagca gctccacgac caagcgcccg 14040
gccgtcactg tgcccggggg cggtaaaacg accccacaca aggactgcac cccatctccc 14100
ctctgccagc tcatcaagga cagcctgttt gcccagtgcc acgcactggt gcccccgcag 14160
cactactacg atgcctgcgt gttcgacagc tgcttcatgc cgggctcgag cctggagtgc 14220
gccagtctgc aggcctacgc agccctctgt gcccagcaga acatctgcct cgactggcgg 14280
aaccacacgc atggggcctg cttggtggag tgcccatctc acagggagta ccaggcctgt 14340
ggccctgcag aagagcccac gtgcaaatcc agctcctccc agcagaacaa cacagtcctg 14400
gtggaaggct gcttctgtcc tgagggcacc atgaactacg ctcctggctt tgatgtctgc 14460
gtgaagacct gcggctgtgt gggacctgac aatgtgccca gagagtttgg ggagcacttc 14520
gagttcgact gcaagaactg tgtctgcctg gagggtggaa gtggcatcat ctgccaaccc 14580
aagaggtgca gccagaagcc cgttacccac tgcgtggaag acggcaccta cctcgccacg 14640
gaggtcaacc ctgccgacac ctgctgcaac attaccgtct gcaagtgcaa caccagcctg 14700
tgcaaagaga agccctccgt gtgcccgctg ggattcgaag tgaagagcaa gatggtgcct 14760
ggaaggtgct gtcccttcta ctggtgtgag tccaaggggg tgtgtgttca cgggaatgct 14820
gagtaccagc ccggttctcc agtttattcc tccaagtgcc aggactgcgt gtgcacggac 14880
aaggtggaca acaacaccct gctcaacgtc atcgcctgca cccacgtgcc ctgcaacacc 14940
tcctgcagcc ctggcttcga actcatggag gcccccgggg agtgctgtaa gaagtgtgaa 15000
cagacgcact gtatcatcaa acggcccgac aaccagcacg tcatcctgaa gcccggggac 15060
ttcaagagcg acccgaagaa caactgcaca ttcttcagct gcgtgaagat ccacaaccag 15120
ctcatctcgt ccgtctccaa catcacctgc cccaactttg atgccagcat ttgcatcccg 15180
ggctccatca cattcatgcc caatggatgc tgcaagacct gcacccctcg caatgagacc 15240
agggtgccct gctccaccgt ccccgtcacc acggaggttt cgtacgccgg ctgcaccaag 15300
accgtcctca tgaatcattg ctccgggtcc tgcgggacat ttgtcatgta ctcggccaag 15360
gcccaggccc tggaccacag ctgctcctgc tgcaaagagg agaaaaccag ccagcgtgag 15420
gtggtcctga gctgccccaa tggcggctcg ctgacacaca cctacaccca catcgagagc 15480
tgccagtgcc aggacaccgt ctgcgggctc cccaccggca cctcccgccg ggcccggcgc 15540
tcccctaggc atctggggag cgggtgagcg gggtgggcac agcccccttc actgccctcg 15600
acagctttac ctccccccgga ccctctgagc ctcctaagct cggcttcctc tcttcagata 15660
tttattgtct gagtctttgt tcagtccttg ctttccaata ataaactcag ggggacatgc 15720

<210> 86
<211> 2058
<212> DNA
<213> Homo sapiens

<400> 86
cggtttctgc tgggtttctg aactgctggg tttctgcttg ctcctctgga gatgcagcgt 60
ctgttgactc cagtgaagcg cattctgcaa ctgacaagag cggtgcagga aacctccctc 120
acacctgctc gcctgctccc agtagcccac caaaggtttt ctacagcctc tgctgtcccc 180
ctggccaaaa cagatacttg gccaaaggac gtgggcatcc tggccctgga ggtctacttc 240
ccagcccaat atgtggacca aactgacctg gagaagtata acaatgtgga agcaggaaag 300
tatacagtgg gcttgggcca gacccgtatg ggcttctgct cagtccaaga ggacatcaac 360
tccctgtgcc tgacggtggt gcaacggctg atggagcgca tacagctccc atgggactct 420
gtgggcaggc tggaagtagg cactgagacc atcattgaca agtccaaagc tgtcaaaaca 480
gtgctcatgg aactcttcca ggattcaggc aatactgata ttgagggcat agataccacc 540
aatgcctgct acggtggtac tgcctccctc ttcaatgctg ccaactggat ggagtccagt 600
tcctgggatg gtcgttatgc catggtggtc tgtggagaca ttgccgtcta tcccagtggt 660
aatgctcgtc ccacaggtgg ggccggagct gtggctatgc tgattggccc aaaggcccct 720
ctggccctgg agcgagggct gaggggaacc catatggaga atgtgtatga cttctacaaa 780
ccaaatttgg cctcggagta cccaatagtg gatgggaagc tttccatcca gtgctacttg 840
cgggccttgg atcgatgtta cacatcatac cgtaaaaaaa tccagaatca gtggaagcaa 900
gctggcagcg atcgaccctt cacccttgac gatttacagt atatgatctt tcatacaccc 960

ttttgcaaga tggtccagaa gtctctggct cgcctgatgt tcaatgactt cctgtcagcc 1020
agcagtgaca cacaaaccag cttatataag gggctggagg ctttcggggg gctaaagctg 1080
gaagacacct acaccaacaa ggacctggat aaagcacttc taaaggcctc tcaggacatg 1140
ttcgacaaga aaaccaaggc ttcccтttac ctctccactc acaatgggaa catgtacacc 1200
tcatccctgt acgggtgcct ggcctcgctt ctgtcccacc actctgccca agaactggct 1260
ggctccagga ttggtgcctt ctcttatggc tctggtttag cagcaagttt cttttcattt 1320
cgagtatccc aggatgctgc tccaggctct cccctggaca agttggtgtc cagcacatca 1380
gacctgccaa aacgcctagc ctcccgaaag tgtgtgtctc ctgaggagtt cacagaaata 1440
atgaaccaaa gagagcaatt ctaccataag gtgaatttct ccccacctgg tgacacaaac 1500
agccttttcc caggtacttg gtacctggag cgagtggacg agcagcatcg ccgaaagtat 1560
gcccggcgtc ccgtctaaag gtgttctgca gatccatgga aagcttcctg ggaaacgtat 1620
gctagcagag cttctccccg tgaatcatat ttttaagatc ccactcttag ctggtaaatg 1680
aatttgaatc gacatagtag ccccataagc atcagccctg tagagtgagg agccatctct 1740
agcgggccct tcattcctct ccatgctgca atcactgtcc tgggcttatg gtgcctatgg 1800
actaggggtc ctttgtgaaa gagcaagatg gagcaatgga gagaagacct cttcctgaat 1860
cactggactc cagaaatgtg catgcagatc agctgttgcc ttcaagatcc agataaactt 1920
tcctgtcatg tgttagaact ttattattat taatattgtt aaacttctgt gctgttcctg 1980
tgaatctcca aattttgtac cttgttctaa gctaatatat agcaattaaa aagagagaaa 2040
gagaaaaaaa aaaaaaaa 2058

<210> 87
<211> 3311
<212> DNA
<213> Homo sapiens

<400> 87
tgctaatgct tttggtacaa atggatgtgg aatataattg aatattttct tgtttaaggg 60
gagcatgaag aggtgttgag gttatgtcaa gcatctggca cagctgaagg cagatggaaa 120
tatttacaag tacgcaattt gagactaaga tattgttatc attctcctat tgaagacaag 180
agcaatagta aaacacatca ggtcaggggg ttaaagacct gtgataaacc acttccgata 240
agttggaaac gtgtgtctat attttcatat ctgtatatat ataatggtaa agaaagacac 300
cttcgtaacc cgcattttcc aaagagagga atcacaggga gatgtacagc aatggggcca 360
tttaagagtt ctgtgttcat cttgattctt caccttctag aaggggccct gagtaattca 420
ctcattcagc tgaacaacaa tggctatgaa ggcattgtcg ttgcaatcga ccccaatgtg 480
ccagaagatg aaacactcat tcaacaaata aaggacatgg tgacccaggc atctctgtat 540
ctgtttgaag ctacaggaaa gcgattttat ttcaaaaatg ttgccatttt gattcctgaa 600
acatggaaga caaaggctga ctatgtgaga ccaaaacttg agacctacaa aaatgctgat 660
gttctggttg ctgagtctac tcctccaggt aatgatgaac cctacactga gcagatgggc 720
aactgtggag agaagggtga aaggatccac ctcactcctg atttcattgc aggaaaaaag 780
ttagctgaat atggaccaca aggtaaggca tttgtccatg agtgggctca tctacgatgg 840
ggagtatttg acgagtacaa taatgatgag aaattctact tatccaatgg aagaatacaa 900
gcagtaagat gttcagcagg tattactggt acaaatgtag taaagaagtg tcagggaggc 960
agctgttaca ccaaaagatg cacattcaat aaagttacag gactctatga aaaaggatgt 1020
gagtttgttc tccaatcccg ccagacggag aaggcttcta taatgtttgc acaacatgtt 1080
gattctatag ttgaattctg tacagaacaa aaccacaaca aagaagctcc aaacaagcaa 1140
aatcaaaaat gcaatctccg aagcacatgg gaagtgatcc gtgattctga ggactttaag 1200
aaaaccactc ctatgacaac acagccacca aatcccacct tctcattgct gcagattgga 1260
caaagaattg tgtgtttagt ccttgacaaa tctggaagca tggcgactgg taaccgcctc 1320
aatcgactga atcaagcagg ccagctttтc ctgctgcaga cagttgagct ggggtcctgg 1380
gttgggatgg tgacatttga cagtgctgcc catgtacaaa gtgaactcat acagataaac 1440
agtggcagtg acagggacac actcgccaaa agattacctg cagcagcttc aggagggacg 1500
tccatctgca gcgggcttcg atcggcattt actgtgatta ggaagaaata tccaactgat 1560
ggatctgaaa ttgtgctgct gacggatggg gaagacaaca ctataagtgg gtgctttaac 1620
gaggtcaaac aaagtggtgc catcatccac acagtcgctt tggggccctc tgcagctcaa 1680
gaactagagg agctgtccaa aatgacagga ggtttacaga catatgcttc agatcaagtt 1740
cagaacaatg gcctcattga tgcttttggg gccctttcat caggaaatgg agctgtctct 1800
cagcgctcca tccagcttga gagtaaggga ttaaccctcc agaacagcca gtggatgaat 1860
ggcacagtga tcgtggacag caccgtggga aaggacactt tgtttcttat cacctggaca 1920
acgcagcctc cccaaatcct tctctgggat cccagtggac agaagcaagg tggctttgta 1980
gtggacaaaa acaccaaaat ggcctacctc caaatcccag gcattgctaa ggttggcact 2040
tggaaataca gtctgcaagc aagctcacaa accttgaccc tgactgtcac gtcccgtgcg 2100
tccaatgcta ccctgcctcc aattacagtg acttccaaaa cgaacaagga caccagcaaa 2160
ttccccagcc ctctggtagt ttatgcaaat attcgccaag gagcctcccc aattctcagg 2220
gccagtgtca cagccctgat tgaatcagtg aatggaaaaa cagttacctt ggaactactg 2280
gataatggag caggtgctga tgctactaag gatgacggtg tctactcaag gtatttcaca 2340
acttatgaca cgaatggtag atacagtgta aaagtgcggg ctctgggagg agttaacgca 2400
gccagacgga gagtgatacc ccagcagagt ggagcactgt acatacctgg ctggattgag 2460

aatgatgaaa tacaatggaa tccaccaaga cctgaaatta ataaggatga tgttcaacac 2520
aagcaagtgt gtttcagcag aacatcctcg ggaggctcat ttgtggcttc tgatgtccca 2580
aatgctccca tacctgatct cttcccacct ggccaaatca ccgacctgaa ggcggaaatt 2640
cacgggggca gtctcattaa tctgacttgg acagctcctg gggatgatta tgaccatgga 2700
acagctcaca agtatatcat tcgaataagt acaagtattc ttgatctcag agacaagttc 2760
aatgaatctc ttcaagtgaa tactactgct ctcatcccaa aggaagccaa ctctgaggaa 2820
gtctttttgt ttaaaccaga aaacattact tttgaaaatg gcacagatct tttcattgct 2880
attcaggctg ttgataaggt cgatctgaaa tcagaaatat ccaacattgc acgagtatct 2940
ttgtttattc ctccacagac tccgccagag acacctagtc ctgatgaaac gtctgctcct 3000
tgtcctaata ttcatatcaa cagcaccatt cctggcattc acattttaaa aattatgtgg 3060
aagtggatag gagaactgca gctgtcaata gcctagggct gaatttttgt cagataaata 3120
aaataaatca ttcatccttt ttttgattat aaaatttttct aaaatgtatt ttagacttcc 3180
tgtaggggggc gatatactaa atgtatatag tacatttata ctaaatgtat tcctgtaggg 3240
ggcgatatac taaatgtatt ttagacttcc tgtagggggc gataaaataa aatgctaaac 3300
aactgggtaa a 3311

<210> 88
<211> 468
<212> DNA
<213> Homo sapiens

<400> 88
gccccctccc ctgactatca aagcagcggc cggctgttgg ggtccaccac gccttccacc 60
tgccccactg cttcttcgct tctctcttgg aaagtccagt ctctcctcgg cttgcaatgg 120
accccaactg ctcctgcgcc gctggtgtct cctgcacctg cgctggttcc tgcaagtgca 180
aagagtgcaa atgcacctcc tgcaagaaga gctgctgctc ctgctgcccc gtgggctgta 240
gcaagtgtgc ccagggctgt gtttgcaaag gggcgtcaga gaagtgcagc tgctgcgact 300
gatgccagga caacctttct cccagatgta aacagagaga catgtacaaa cctggatttt 360
tttttatacc accttgaccc atttgctaca ttccttttcc tgtgaaatat gtgagtgata 420
attaaacact ttagacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 468

<210> 89
<211> 1551
<212> DNA
<213> Homo sapiens

<400> 89
ggcgcccaag ccgccgccgc cagatcggtg ccgattcctg ccctgccccg accgccagcg 60
cgaccatgtc ccatcactgg gggtacggca aacacaacgg acctgagcac tggcataagg 120
acttccccat tgccaaggga gagcgccagt cccctgttga catcgacact catacagcca 180
agtatgaccc ttccctgaag cccctgtctg tttcctatga tcaagcaact tccctgagga 240
tcctcaacaa tggtcatgct ttcaacgtgg agtttgatga ctctcaggac aaagcagtgc 300
tcaagggagg acccctggat ggcacttaca gattgattca gtttcacttt cactggggtt 360
cacttgatgg acaaggttca gagcatactg tggataaaaa gaaatatgct gcagaacttc 420
acttggttca ctggaacacc aaatatgggg attttgggaa agctgtgcag caacctgatg 480
gactggccgt tctaggtatt tttttgaagg ttggcagcgc taaaccgggc cttcagaaag 540
ttgttgatgt gctggattcc attaaaaaca agggcaagag tgctgacttc actaacttcg 600
atcctcgtgg cctccttcct gaatccctgg attactggac ctacccaggc tcactgacca 660
cccctcctct tctggaatgt gtgacctgga ttgtgctcaa ggaacccatc agcgtcagca 720
gcgagcaggt gttgaaattc cgtaaactta acttcaatgg ggagggtgaa cccgaagaac 780
tgatggtgga caactggcgc ccagctcagc cactgaagaa caggcaaatc aaagcttcct 840
tcaaataaga tggtcccata gtctgtatcc aaataatgaa tcttcgggtg tttcccttta 900
gctaagcaca gatctacctt ggtgatttgg accctggttg ctttgtgtct agttttctag 960
acccttcatc tcttacttga tagacttact aataaaatgt gaagactaga ccaattgtca 1020
tgcttgacac aactgctgtg gctggttggt gctttgttta tggtagtagt ttttctgtaa 1080
cacagaatat aggataagaa ataagaataa agtaccttga ctttgttcac agcatgtagg 1140
gtgatgagca ctcacaattg ttgactaaaa tgctgctttt aaaacatagg aaagtagaat 1200
ggttgagtgc aaatccatag cacaagataa attgagctag ttaaggcaaa tcaggtaaaa 1260
tagtcatgat tctatgtaat gtaaaccaga aaaaataaat gttcatgatt tcaagatgtt 1320
atattaaaga aaaactttaa aaattattat atatttatag caaagttatc ttaaatatga 1380
attctgttgt aatttaatga cttttgaatt acagagatat aaatgaagta ttatctgtaa 1440
aaattgttat aattagagtt gtgatacaga gtatatttcc attcagacaa tatatcataa 1500
cttaataaat attgtatttt agatatattc tctaataaaa ttcagaattc t 1551

<210> 90
<211> 367
<212> DNA

<213> Homo sapiens

<400> 90
ctccagtctc acctcggctt gcaatggacc ccaactgctc ctgcgaggct ggtggctcct 60
gcgcctgcgc cggctcctgc aagtgcaaaa agtgcaaatg cacctcctgc aagaagagct 120
gctgctcctg ttgccccctg ggctgtgcca agtgtgccca gggctgcatc tgcaaagggg 180
cgtcagagaa gtgcagctgc tgtgcctgat gtcgggacag ccctgctgtc agatgaaaac 240
agaatgacac gtaaaatccg aggtttttt tttctacaac tccgactcat ttgctacatt 300
ccttttttc tgtgaaatat gtgaataata attaaacact tagacttgaa aaaaaaaaaa 360
aaaaaaa 367

<210> 91
<211> 396
<212> DNA
<213> Homo sapiens

<400> 91
actccgcctt ccacgtgcac ccactgcctc ttcccttctc gcttgggaac tctagtctcg 60
cctcgggttg caatggaccc caactgctcc tgtgccgctg gtgtctcctg cacctgcgcc 120
agctcctgca agtgcaaaga gtgcaaatgc acctcctgca agaagagctg ctgctcctgc 180
tgccctgtgg gctgtgccaa gtgtgcccaa ggctgcatct gcaaaggggc atcggagaag 240
tgcagctgct gcgcctgatg tcgggacagc cctgctccca agtacaaata gagtgacccg 300
taaaatctag gatttttgt tttttgctac aatcttgacc cctttgctac attccctttt 360
ttctgtgaaa tatgtgaata ataattaaac acttag 396

<210> 92
<211> 632
<212> DNA
<213> Homo sapiens

<400> 92
cccagaatgt tgacagtcgc tctcctagcc cttctctgtg cctcagcctc tggcaatgcc 60
attcaggcca ggtcttcctc ctatagtgga gagtatggaa gtggtggtgg aaagcgattc 120
tctcattctg gcaaccagtt ggacggcccc atcaccgccc tccgggtccg agtcaacaca 180
tactacatcg taggtcttca ggtgcgctat ggcaaggtgt ggagcgacta tgtgggtggt 240
cgcaacggag acctggagga gatctttctg caccctgggg aatcagtgat ccaggtttct 300
gggaagtaca agtggtacct gaagaagctg gtatttgtga cagacaaggg ccgctatctg 360
tcttttggga aagacagtgg cacaagtttc aatgccgtcc ccttgcaccc caacaccgtg 420
ctccgcttca tcagtggccg gtctggttct ctcatcgatg ccattggcct gcactgggat 480
gtttacccca ctagctgcag cagatgctga gcctcctctc cttggcaggg gcactgtgat 540
gaggagtaag aactccctta tcactaaccc ccatccaaat ggctcaataa aaaaatatgg 600
ttaaggctaa aaaaaaaaaa aaaaaaaaaa aa 632

<210> 93
<211> 257
<212> DNA
<213> Homo sapiens

<400> 93
accacgcttt tcatctgtcc cgctgcgtgt tttcctcttg atcgggaact cctgcttctc 60
cttgcctcga aatggacccc aactgctcct gctcgcctgt tggctcctgt gcctgtgccg 120
gctcctgcaa atgcaaagag tgcaaatgca cctcctgcaa gaagagctgc tgctcctgct 180
gccctgtcgg ctgtgccaag tgtgcccagg gctgcatctg caaagggacg tcagacaagt 240
gcagctgctg tgcctga 257

<210> 94
<211> 422
<212> PRT
<213> Homo sapiens

<400> 94
Met Asn Ser Gly His Ser Phe Ser Gln Thr Pro Ser Ala Ser Phe His
1 5 10 15
Gly Ala Gly Gly Gly Trp Gly Arg Pro Arg Ser Phe Pro Arg Ala Pro
20 25 30
Thr Val His Gly Gly Ala Gly Gly Ala Arg Ile Ser Leu Ser Phe Thr
35 40 45

```
Thr Arg Ser Cys Pro Pro Pro Gly Gly Ser Trp Gly Ser Gly Arg Ser
    50                  55                  60
Ser Pro Leu Leu Gly Gly Asn Gly Lys Ala Thr Met Gln Asn Leu Asn
65                  70                  75                  80
Asp Arg Leu Ala Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala
                85                  90                  95
Asn Met Lys Leu Glu Ser Arg Ile Leu Lys Trp His Gln Gln Arg Asp
            100                 105                 110
Pro Gly Ser Lys Lys Asp Tyr Ser Gln Tyr Glu Glu Asn Ile Thr His
        115                 120                 125
Leu Gln Glu Gln Ile Val Asp Gly Lys Met Thr Asn Ala Gln Ile Ile
    130                 135                 140
Leu Leu Ile Asp Asn Ala Arg Met Ala Val Asp Asp Phe Asn Leu Lys
145                 150                 155                 160
Tyr Glu Asn Glu His Ser Phe Lys Lys Asp Leu Glu Ile Glu Val Glu
                165                 170                 175
Gly Leu Arg Arg Thr Leu Asp Asn Leu Thr Ile Val Thr Thr Asp Leu
            180                 185                 190
Glu Gln Glu Val Glu Gly Met Arg Lys Glu Leu Ile Leu Met Lys Lys
        195                 200                 205
His His Glu Gln Glu Met Glu Lys His His Val Pro Ser Asp Phe Asn
    210                 215                 220
Val Asn Val Lys Val Asp Thr Gly Pro Arg Glu Asp Leu Ile Lys Val
225                 230                 235                 240
Leu Glu Asp Met Arg Gln Glu Tyr Glu Leu Ile Ile Lys Lys Lys His
                245                 250                 255
Arg Asp Leu Asp Thr Trp Tyr Lys Glu Gln Ser Ala Ala Met Ser Gln
            260                 265                 270
Glu Ala Ala Ser Pro Ala Thr Val Gln Ser Arg Gln Gly Asp Ile His
        275                 280                 285
Glu Leu Lys Arg Thr Phe Gln Ala Leu Glu Ile Asp Leu Gln Thr Gln
    290                 295                 300
Tyr Ser Thr Lys Ser Ala Leu Glu Asn Met Leu Ser Glu Thr Gln Ser
305                 310                 315                 320
Arg Tyr Ser Cys Lys Leu Gln Asp Met Gln Glu Ile Ile Ser His Tyr
                325                 330                 335
Glu Glu Glu Leu Thr Gln Leu Arg His Glu Leu Glu Arg Gln Asn Asn
            340                 345                 350
Glu Tyr Gln Val Leu Leu Gly Ile Lys Thr His Leu Glu Lys Glu Ile
        355                 360                 365
Thr Thr Tyr Arg Arg Leu Leu Glu Gly Glu Ser Glu Gly Thr Arg Glu
    370                 375                 380
Glu Ser Lys Ser Ser Met Lys Val Ser Ala Thr Pro Lys Ile Lys Ala
385                 390                 395                 400
Ile Thr Gln Glu Thr Ile Asn Gly Arg Leu Val Leu Cys Gln Val Asn
                405                 410                 415
Glu Ile Gln Lys His Ala
            420


<210> 95
<211> 166
<212> PRT
<213> Homo sapiens

<400> 95
Met Ala Gln Thr Ser Ser Tyr Phe Met Leu Ile Ser Cys Leu Met Phe
 1               5                  10                  15
Leu Ser Gln Ser Gln Gly Gln Glu Ala Gln Thr Glu Leu Pro Gln Ala
            20                  25                  30
Arg Ile Ser Cys Pro Glu Gly Thr Asn Ala Tyr Arg Ser Tyr Cys Tyr
        35                  40                  45
Tyr Phe Asn Glu Asp Arg Glu Thr Trp Val Asp Ala Asp Leu Tyr Cys
    50                  55                  60
Gln Asn Met Asn Ser Gly Asn Leu Val Ser Val Leu Thr Gln Ala Glu
65                  70                  75                  80
Gly Ala Phe Val Ala Ser Leu Ile Lys Glu Ser Gly Thr Asp Asp Phe
```

85 90 95
Asn Val Trp Ile Gly Leu His Asp Pro Lys Lys Asn Arg Arg Trp His
100 105 110
Trp Ser Ser Gly Ser Leu Val Ser Tyr Lys Ser Trp Gly Ile Gly Ala
115 120 125
Pro Ser Ser Val Asn Pro Gly Tyr Cys Val Ser Leu Thr Ser Ser Thr
130 135 140
Gly Phe Gln Lys Trp Lys Asp Val Pro Cys Glu Asp Lys Phe Ser Phe
145 150 155 160
Val Cys Lys Phe Lys Asn
165

<210> 96
<211> 166
<212> PRT
<213> Homo sapiens

<400> 96
Met Ala Gln Thr Asn Ser Phe Phe Met Leu Ile Ser Ser Leu Met Phe
1 5 10 15
Leu Ser Leu Ser Gln Gly Gln Glu Ser Gln Thr Glu Leu Pro Asn Pro
20 25 30
Arg Ile Ser Cys Pro Glu Gly Thr Asn Ala Tyr Arg Ser Tyr Cys Tyr
35 40 45
Tyr Phe Asn Glu Asp Pro Glu Thr Trp Val Asp Ala Asp Leu Tyr Cys
50 55 60
Gln Asn Met Asn Ser Gly Asn Leu Val Ser Val Leu Thr Gln Ala Glu
65 70 75 80
Gly Ala Phe Val Ala Ser Leu Ile Lys Glu Ser Ser Thr Asp Asp Ser
85 90 95
Asn Val Trp Ile Gly Leu His Asp Pro Lys Lys Asn Arg Arg Trp His
100 105 110
Trp Ser Ser Gly Ser Leu Val Ser Tyr Lys Ser Trp Asp Thr Gly Ser
115 120 125
Pro Ser Ser Ala Asn Ala Gly Tyr Cys Ala Ser Leu Thr Ser Cys Ser
130 135 140
Gly Phe Lys Lys Trp Lys Asp Glu Ser Cys Glu Lys Lys Phe Ser Phe
145 150 155 160
Val Cys Lys Phe Lys Asn
165

<210> 97
<211> 411
<212> PRT
<213> Homo sapiens

<400> 97
Met Trp Ser Gly Trp Trp Leu Trp Pro Leu Val Ala Val Cys Thr Ala
1 5 10 15
Asp Phe Phe Arg Asp Glu Ala Glu Arg Ile Met Arg Asp Ser Pro Val
20 25 30
Ile Asp Gly His Asn Asp Leu Pro Trp Gln Leu Leu Asp Met Phe Asn
35 40 45
Asn Arg Leu Gln Asp Glu Arg Ala Asn Leu Thr Thr Leu Ala Gly Thr
50 55 60
His Thr Asn Ile Pro Lys Leu Arg Ala Gly Phe Val Gly Gly Gln Phe
65 70 75 80
Trp Ser Val Tyr Thr Pro Cys Asp Thr Gln Asn Lys Asp Ala Val Arg
85 90 95
Arg Thr Leu Glu Gln Met Asp Val Val His Arg Met Cys Arg Met Tyr
100 105 110
Pro Glu Thr Phe Leu Tyr Val Thr Ser Ser Ala Gly Ile Arg Gln Ala
115 120 125
Phe Arg Glu Gly Lys Val Ala Ser Leu Ile Gly Val Glu Gly Gly His
130 135 140

Ser Ile Asp Ser Ser Leu Gly Val Leu Arg Ala Leu Tyr Gln Leu Gly
145 150 155 160
Met Arg Tyr Leu Thr Leu Thr His Ser Cys Asn Thr Pro Trp Ala Asp
165 170 175
Asn Trp Leu Val Asp Thr Gly Asp Ser Glu Pro Gln Ser Gln Gly Leu
180 185 190
Ser Pro Phe Gly Gln Arg Val Val Lys Glu Leu Asn Arg Leu Gly Val
195 200 205
Leu Ile Asp Leu Ala His Val Ser Val Ala Thr Met Lys Ala Thr Leu
210 215 220
Gln Leu Ser Arg Ala Pro Val Ile Phe Ser His Ser Ser Ala Tyr Ser
225 230 235 240
Val Cys Ala Ser Arg Arg Asn Val Pro Asp Asp Val Leu Arg Leu Val
245 250 255
Lys Gln Thr Asp Ser Leu Val Met Val Asn Phe Tyr Asn Asn Tyr Ile
260 265 270
Ser Cys Thr Asn Lys Ala Asn Leu Ser Gln Val Ala Asp His Leu Asp
275 280 285
His Ile Lys Glu Val Ala Gly Ala Arg Ala Val Gly Phe Gly Gly Asp
290 295 300
Phe Asp Gly Val Pro Arg Val Pro Glu Gly Leu Glu Asp Val Ser Lys
305 310 315 320
Tyr Pro Asp Leu Ile Ala Glu Leu Leu Arg Arg Asn Trp Thr Glu Ala
325 330 335
Glu Val Lys Gly Ala Leu Ala Asp Asn Leu Leu Arg Val Phe Glu Ala
340 345 350
Val Glu Gln Ala Ser Asn Leu Thr Gln Ala Pro Glu Glu Glu Pro Ile
355 360 365
Pro Leu Asp Gln Leu Gly Gly Ser Cys Arg Thr His Tyr Gly Tyr Ser
370 375 380
Ser Gly Ala Ser Ser Leu His Arg His Trp Gly Leu Leu Leu Ala Ser
385 390 395 400
Leu Ala Pro Leu Val Leu Cys Leu Ser Leu Leu
405 410

<210> 98
<211> 99
<212> PRT
<213> Homo sapiens

<400> 98
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15
Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
85 90 95
Glu Asn Ser

<210> 99
<211> 469
<212> PRT
<213> Homo sapiens

<400> 99
Met His Ser Phe Pro Pro Leu Leu Leu Leu Leu Phe Trp Gly Val Val
1 5 10 15
Ser His Ser Phe Pro Ala Thr Leu Glu Thr Gln Glu Gln Asp Val Asp

```
            20                  25                  30
Leu Val Gln Lys Tyr Leu Glu Lys Tyr Tyr Asn Leu Lys Asn Asp Gly
        35                  40                  45
Arg Gln Val Glu Lys Arg Arg Asn Ser Gly Pro Val Val Glu Lys Leu
    50                  55                  60
Lys Gln Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp
65                  70                  75                  80
Ala Glu Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp
                85                  90                  95
Val Ala Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr
            100                 105                 110
His Leu Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala
        115                 120                 125
Asp Val Asp His Ala Ile Glu Lys Ala Phe Gln Leu Trp Ser Asn Val
    130                 135                 140
Thr Pro Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met
145                 150                 155                 160
Ile Ser Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly
                165                 170                 175
Pro Gly Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly
            180                 185                 190
Gly Asp Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Arg
        195                 200                 205
Glu Tyr Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu
    210                 215                 220
Gly Leu Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr
225                 230                 235                 240
Thr Phe Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile
                245                 250                 255
Gln Ala Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro
            260                 265                 270
Gln Thr Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr
        275                 280                 285
Thr Ile Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg
    290                 295                 300
Thr Asn Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Ile Ser Val Phe
305                 310                 315                 320
Trp Pro Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp
                325                 330                 335
Arg Asp Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln
            340                 345                 350
Gly Gln Asn Val Leu His Gly Tyr Pro Lys Asp Ile Tyr Ser Ser Phe
        355                 360                 365
Gly Phe Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu
    370                 375                 380
Asn Thr Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr
385                 390                 395                 400
Asp Glu Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala
                405                 410                 415
His Asp Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys
            420                 425                 430
Asp Gly Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp
        435                 440                 445
Pro Lys Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe
    450                 455                 460
Asn Cys Arg Lys Asn
465
```

<210> 100
<211> 267
<212> PRT
<213> Homo sapiens

<400> 100

```
Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu
 1               5                  10                  15
```

Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp
20 25 30
Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
35 40 45
Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
50 55 60
Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
65 70 75 80
Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
85 90 95
Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
100 105 110
Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
115 120 125
Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
130 135 140
Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
145 150 155 160
Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
165 170 175
Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
180 185 190
Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
195 200 205
Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
210 215 220
Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp
225 230 235 240
Pro Gln Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys
245 250 255
Leu Tyr Gly Lys Arg Ser Asn Ser Arg Lys Lys
260 265

<210> 101
<211> 300
<212> PRT
<213> Homo sapiens

<400> 101
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1 5 10 15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20 25 30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35 40 45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
50 55 60
Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
65 70 75 80
Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
85 90 95
Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
100 105 110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
115 120 125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
130 135 140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
145 150 155 160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
165 170 175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
180 185 190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
195 200 205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His

210 215 220
Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
225 230 235 240
Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
245 250 255
Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
260 265 270
Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
275 280 285
Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
290 295 300

<210> 102
<211> 98
<212> PRT
<213> Homo sapiens

<400> 102
Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
1 5 10 15
Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
20 25 30
Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
35 40 45
Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
50 55 60
Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
65 70 75 80
Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Met Ser Lys Arg
85 90 95
Ser Pro

<210> 103
<211> 871
<212> PRT
<213> Homo sapiens

<400> 103
Met Lys Tyr Ser Cys Cys Ala Leu Val Leu Ala Val Leu Gly Thr Glu
1 5 10 15
Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
20 25 30
Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
35 40 45
Pro Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
50 55 60
Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
65 70 75 80
Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
85 90 95
Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
100 105 110
Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
115 120 125
Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
130 135 140
Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145 150 155 160
Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
165 170 175
Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
180 185 190
Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
195 200 205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
210 215 220
His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225 230 235 240
Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
245 250 255
Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
260 265 270
Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
275 280 285
Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
290 295 300
Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305 310 315 320
Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
325 330 335
Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
340 345 350
Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
355 360 365
Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
370 375 380
Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385 390 395 400
Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
405 410 415
Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
420 425 430
Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
435 440 445
Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
450 455 460
Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465 470 475 480
Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
485 490 495
Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
500 505 510
Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
515 520 525
Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
530 535 540
Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545 550 555 560
Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
565 570 575
His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
580 585 590
Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
595 600 605
Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610 615 620
Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625 630 635 640
Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
645 650 655
Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
660 665 670
Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
675 680 685
Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
690 695 700
Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705 710 715 720
Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
725 730 735
Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn

740 745 750
His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
755 760 765
Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
770 775 780
Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785 790 795 800
Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
805 810 815
Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
820 825 830
Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
835 840 845
Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
850 855 860
Leu Trp Asp Gly Trp Glu Gly
865 870

<210> 104
<211> 1496
<212> PRT
<213> Homo sapiens

<400> 104
Met Met Ala Asn Trp Ala Glu Ala Arg Pro Leu Leu Ile Leu Ile Val
1 5 10 15
Leu Leu Gly Gln Phe Val Ser Ile Lys Ala Gln Glu Glu Asp Glu Asp
20 25 30
Glu Gly Tyr Gly Glu Glu Ile Ala Cys Thr Gln Asn Gly Gln Met Tyr
35 40 45
Leu Asn Arg Asp Ile Trp Lys Pro Ala Pro Cys Gln Ile Cys Val Cys
50 55 60
Asp Asn Gly Ala Ile Leu Cys Asp Lys Ile Glu Cys Gln Asp Val Leu
65 70 75 80
Asp Cys Ala Asp Pro Val Thr Pro Pro Gly Glu Cys Cys Pro Val Cys
85 90 95
Ser Gln Thr Pro Gly Gly Gly Asn Thr Asn Phe Gly Arg Gly Arg Lys
100 105 110
Gly Gln Lys Gly Glu Pro Gly Leu Val Pro Val Val Thr Gly Ile Arg
115 120 125
Gly Arg Pro Gly Pro Ala Gly Pro Pro Gly Ser Gln Gly Pro Arg Gly
130 135 140
Glu Arg Gly Pro Lys Gly Arg Pro Gly Pro Arg Gly Pro Gln Gly Ile
145 150 155 160
Asp Gly Glu Pro Gly Val Pro Gly Gln Pro Gly Ala Pro Gly Pro Pro
165 170 175
Gly His Pro Ser His Pro Gly Pro Asp Gly Leu Ser Arg Pro Phe Ser
180 185 190
Ala Gln Met Ala Gly Leu Asp Glu Lys Ser Gly Leu Gly Ser Gln Val
195 200 205
Gly Leu Met Pro Gly Ser Val Gly Pro Val Gly Pro Arg Gly Pro Gln
210 215 220
Gly Leu Gln Gly Gln Gln Gly Gly Ala Gly Pro Thr Gly Pro Pro Gly
225 230 235 240
Glu Pro Gly Asp Pro Gly Pro Met Gly Pro Ile Gly Ser Arg Gly Pro
245 250 255
Glu Gly Pro Pro Gly Lys Pro Gly Glu Asp Gly Glu Pro Gly Arg Asn
260 265 270
Gly Asn Pro Gly Glu Val Gly Phe Ala Gly Ser Pro Gly Ala Arg Gly
275 280 285
Phe Pro Gly Ala Pro Gly Leu Pro Gly Leu Lys Gly His Arg Gly His
290 295 300
Lys Gly Leu Glu Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Ser Lys
305 310 315 320
Gly Glu Ala Gly Pro Thr Gly Pro Met Gly Ala Met Gly Pro Leu Gly
325 330 335

Pro Arg Gly Met Pro Gly Glu Arg Gly Arg Leu Gly Pro Gln Gly Ala
340 345 350
Pro Gly Gln Arg Gly Ala His Gly Met Pro Gly Lys Pro Gly Pro Met
355 360 365
Gly Pro Leu Gly Ile Pro Gly Ser Ser Gly Phe Pro Gly Asn Pro Gly
370 375 380
Met Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly Pro Glu Gly Pro
385 390 395 400
Gln Gly Gln Arg Gly Glu Thr Gly Pro Pro Gly Pro Val Gly Ser Pro
405 410 415
Gly Leu Pro Gly Ala Ile Gly Thr Asp Gly Thr Pro Gly Pro Lys Gly
420 425 430
Pro Thr Gly Ser Pro Gly Thr Ser Gly Pro Pro Gly Ser Ala Gly Pro
435 440 445
Pro Gly Ser Pro Gly Pro Gln Gly Ser Thr Gly Pro Gln Gly Asn Ser
450 455 460
Gly Leu Pro Gly Asp Pro Gly Phe Lys Gly Glu Ala Gly Pro Lys Gly
465 470 475 480
Glu Pro Gly Pro His Gly Ile Gln Gly Pro Ile Gly Pro Pro Gly Glu
485 490 495
Glu Gly Lys Arg Gly Pro Arg Gly Asp Pro Gly Thr Leu Gly Pro Pro
500 505 510
Gly Pro Val Gly Glu Arg Gly Ala Pro Gly Asn Arg Gly Phe Pro Gly
515 520 525
Ser Asp Gly Leu Pro Gly Pro Lys Gly Ala Gln Gly Glu Arg Gly Pro
530 535 540
Val Gly Ser Ser Gly Pro Lys Gly Ser Gln Gly Asp Pro Gly Arg Pro
545 550 555 560
Gly Glu Pro Gly Leu Pro Gly Ala Arg Gly Leu Thr Gly Asn Pro Gly
565 570 575
Val Gln Gly Pro Glu Gly Lys Leu Gly Pro Leu Gly Ala Pro Gly Glu
580 585 590
Asp Gly Arg Pro Gly Pro Pro Gly Ser Ile Gly Ile Lys Gly Gln Pro
595 600 605
Gly Thr Met Gly Leu Pro Gly Pro Lys Gly Ser Asn Gly Asp Pro Gly
610 615 620
Lys Pro Gly Glu Ala Gly Asn Pro Gly Val Pro Gly Gln Arg Gly Ala
625 630 635 640
Pro Gly Lys Asp Gly Lys Val Gly Pro Tyr Gly Pro Pro Gly Pro Pro
645 650 655
Gly Leu Arg Gly Glu Arg Gly Glu Gln Gly Pro Pro Gly Pro Thr Gly
660 665 670
Phe Gln Gly His Pro Gly Pro Pro Gly Pro Pro Gly Glu Gly Gly Lys
675 680 685
Pro Gly Asp Gln Gly Val Pro Gly Gly Pro Gly Ala Val Gly Pro Leu
690 695 700
Gly Pro Arg Gly Glu Arg Gly Asn Pro Gly Glu Arg Gly Glu Pro Gly
705 710 715 720
Ile Thr Gly Leu Pro Gly Glu Lys Gly Met Ala Gly Gly His Gly Pro
725 730 735
Asp Gly Pro Lys Gly Ser Pro Gly Pro Ser Gly Thr Pro Gly Asp Thr
740 745 750
Gly Pro Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ile Ala Gly
755 760 765
Thr Pro Gly Pro Lys Gly Asp Arg Gly Gly Ile Gly Glu Lys Gly Ala
770 775 780
Glu Gly Thr Ala Gly Asn Asp Gly Ala Gly Gly Leu Pro Gly Pro Leu
785 790 795 800
Gly Pro Pro Gly Pro Ala Gly Leu Leu Gly Glu Lys Gly Glu Pro Gly
805 810 815
Pro Arg Gly Leu Val Gly Pro Pro Gly Ser Arg Gly Asn Pro Gly Ser
820 825 830
Arg Gly Glu Asn Gly Pro Thr Gly Ala Val Gly Phe Ala Gly Pro Gln
835 840 845
Gly Ser Asp Gly Gln Pro Gly Val Lys Gly Glu Pro Gly Glu Pro Gly
850 855 860
Gln Lys Gly Asp Ala Gly Ser Pro Gly Pro Gln Gly Leu Ala Gly Ser

865 870 875 880
Pro Gly Pro His Gly Pro Asn Gly Val Pro Gly Leu Lys Gly Gly Arg
885 890 895
Gly Thr Gln Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ser Ala Gly
900 905 910
Arg Val Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Pro Ala Gly Pro
915 920 925
Leu Gly Glu Pro Gly Lys Glu Gly Pro Pro Gly Pro Arg Gly Asp Pro
930 935 940
Gly Ser His Gly Arg Val Gly Val Arg Gly Pro Ala Gly Pro Pro Gly
945 950 955 960
Gly Pro Gly Asp Lys Gly Asp Pro Gly Glu Asp Gly Gln Pro Gly Pro
965 970 975
Asp Gly Pro Pro Gly Pro Ala Gly Thr Thr Gly Gln Arg Gly Ile Val
980 985 990
Gly Met Pro Gly Gln Arg Gly Glu Arg Gly Met Pro Gly Leu Pro Gly
995 1000 1005
Pro Ala Gly Thr Pro Gly Lys Val Gly Pro Thr Gly Ala Thr Gly Asp
1010 1015 1020
Lys Gly Pro Pro Gly Pro Val Gly Pro Pro Gly Ser Asn Gly Pro Val
1025 1030 1035 1040
Gly Glu Pro Gly Pro Glu Gly Pro Ala Gly Asn Asp Gly Thr Pro Gly
1045 1050 1055
Arg Asp Gly Ala Val Gly Glu Arg Gly Asp Arg Gly Asp Pro Gly Pro
1060 1065 1070
Ala Gly Leu Pro Gly Ser Gln Gly Ala Pro Gly Thr Pro Gly Pro Val
1075 1080 1085
Gly Ala Pro Gly Asp Ala Gly Gln Arg Gly Asp Pro Gly Ser Arg Gly
1090 1095 1100
Pro Ile Gly His Leu Gly Arg Ala Gly Lys Arg Gly Leu Pro Gly Pro
1105 1110 1115 1120
Gln Gly Pro Arg Gly Asp Lys Gly Asp His Gly Asp Arg Gly Asp Arg
1125 1130 1135
Gly Gln Lys Gly His Arg Gly Phe Thr Gly Leu Gln Gly Leu Pro Gly
1140 1145 1150
Pro Pro Gly Pro Asn Gly Glu Gln Gly Ser Ala Gly Ile Pro Gly Pro
1155 1160 1165
Phe Gly Pro Arg Gly Pro Pro Gly Pro Val Gly Pro Ser Gly Lys Glu
1170 1175 1180
Gly Asn Pro Gly Pro Leu Gly Pro Leu Gly Pro Pro Gly Val Arg Gly
1185 1190 1195 1200
Ser Val Gly Glu Ala Gly Pro Glu Gly Pro Pro Gly Glu Pro Gly Pro
1205 1210 1215
Pro Gly Pro Pro Gly Pro Pro Gly His Leu Thr Ala Ala Leu Gly Asp
1220 1225 1230
Ile Met Gly His Tyr Asp Glu Ser Met Pro Asp Pro Leu Pro Glu Phe
1235 1240 1245
Thr Glu Asp Gln Ala Ala Pro Asp Asp Lys Asn Lys Thr Asp Pro Gly
1250 1255 1260
Val His Ala Thr Leu Lys Ser Leu Ser Ser Gln Ile Glu Thr Met Arg
1265 1270 1275 1280
Ser Pro Asp Gly Ser Lys Lys His Pro Ala Arg Thr Cys Asp Asp Leu
1285 1290 1295
Lys Leu Cys His Ser Ala Lys Gln Ser Gly Glu Tyr Trp Ile Asp Pro
1300 1305 1310
Asn Gln Gly Ser Val Glu Asp Ala Ile Lys Val Tyr Cys Asn Met Glu
1315 1320 1325
Thr Gly Glu Thr Cys Ile Ser Ala Asn Pro Ser Ser Val Pro Arg Lys
1330 1335 1340
Thr Trp Trp Ala Ser Lys Ser Pro Asp Asn Lys Pro Val Trp Tyr Gly
1345 1350 1355 1360
Leu Asp Met Asn Arg Gly Ser Gln Phe Ala Tyr Gly Asp His Gln Ser
1365 1370 1375
Pro Asn Thr Ala Ile Thr Gln Met Thr Phe Leu Arg Leu Leu Ser Lys
1380 1385 1390
Glu Ala Ser Gln Asn Ile Thr Tyr Ile Cys Lys Asn Ser Val Gly Tyr
1395 1400 1405

Met Asp Asp Gln Ala Lys Asn Leu Lys Lys Ala Val Val Leu Lys Gly
1410 1415 1420
Ala Asn Asp Leu Asp Ile Lys Ala Glu Gly Asn Ile Arg Phe Arg Tyr
1425 1430 1435 1440
Ile Val Leu Gln Asp Thr Cys Ser Lys Arg Asn Gly Asn Val Gly Lys
1445 1450 1455
Thr Val Phe Glu Tyr Arg Thr Gln Asn Val Ala Arg Leu Pro Ile Ile
1460 1465 1470
Asp Leu Ala Pro Val Asp Val Gly Gly Thr Asp Gln Glu Phe Gly Val
1475 1480 1485
Glu Ile Gly Pro Val Cys Phe Val
1490 1495

<210> 105
<211> 107
<212> PRT
<213> Homo sapiens

<400> 105
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1 5 10 15
Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
20 25 30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
35 40 45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
85 90 95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

<210> 106
<211> 89
<212> PRT
<213> Homo sapiens

<400> 106
Met Lys Gly Leu Ala Ala Ala Leu Leu Val Leu Val Cys Thr Met Ala
1 5 10 15
Leu Cys Ser Cys Ala Gln Val Gly Thr Asn Lys Glu Leu Cys Cys Leu
20 25 30
Val Tyr Thr Ser Trp Gln Ile Pro Gln Lys Phe Ile Val Asp Tyr Ser
35 40 45
Glu Thr Ser Pro Gln Cys Pro Lys Pro Gly Val Ile Leu Leu Thr Lys
50 55 60
Arg Gly Arg Gln Ile Cys Ala Asp Pro Asn Lys Lys Trp Val Gln Lys
65 70 75 80
Tyr Ile Ser Asp Leu Lys Leu Asn Ala
85

<210> 107
<211> 796
<212> PRT
<213> Homo sapiens

<400> 107
Met Lys Glu Asn Tyr Cys Leu Gln Ala Ala Leu Val Cys Leu Gly Met
1 5 10 15
Leu Cys His Ser His Ala Phe Ala Pro Glu Arg Arg Gly His Leu Arg
20 25 30
Pro Ser Phe His Gly His His Glu Lys Gly Lys Glu Gly Gln Val Leu

```
          35                  40                  45
Gln Arg Ser Lys Arg Gly Trp Val Trp Asn Gln Phe Phe Val Ile Glu
    50                  55                  60
Glu Tyr Thr Gly Pro Asp Pro Val Leu Val Gly Arg Leu His Ser Asp
65                  70                  75                  80
Ile Asp Ser Gly Asp Gly Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly
                85                  90                  95
Ala Gly Thr Ile Phe Val Ile Asp Asp Lys Ser Gly Asn Ile His Ala
            100                 105                 110
Thr Lys Thr Leu Asp Arg Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala
        115                 120                 125
Gln Ala Val Asp Arg Asp Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu
    130                 135                 140
Phe Ile Val Lys Val Gln Asp Ile Asn Asp Asn Pro Pro Glu Phe Leu
145                 150                 155                 160
His Glu Thr Tyr His Ala Asn Val Pro Glu Arg Ser Asn Val Gly Thr
                165                 170                 175
Ser Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Thr Tyr Gly
            180                 185                 190
Asn Ser Ala Lys Leu Val Tyr Ser Ile Leu Glu Gly Gln Pro Tyr Phe
        195                 200                 205
Ser Val Glu Ala Gln Thr Gly Ile Ile Arg Thr Ala Leu Pro Asn Met
    210                 215                 220
Asp Arg Glu Ala Lys Glu Glu Tyr His Val Val Ile Gln Ala Lys Asp
225                 230                 235                 240
Met Gly Gly His Met Gly Gly Leu Ser Gly Thr Thr Lys Val Thr Ile
                245                 250                 255
Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Lys Phe Pro Gln Ser Val
            260                 265                 270
Tyr Gln Met Ser Val Ser Glu Ala Ala Val Pro Gly Glu Glu Val Gly
        275                 280                 285
Arg Val Lys Ala Lys Asp Pro Asp Ile Gly Glu Asn Gly Leu Val Thr
    290                 295                 300
Tyr Asn Ile Val Asp Gly Asp Gly Met Glu Ser Phe Glu Ile Thr Thr
305                 310                 315                 320
Asp Tyr Glu Thr Gln Glu Gly Val Ile Lys Leu Lys Lys Pro Val Asp
                325                 330                 335
Phe Glu Thr Lys Arg Ala Tyr Ser Leu Lys Val Glu Ala Ala Asn Val
            340                 345                 350
His Ile Asp Pro Lys Phe Ile Ser Asn Gly Pro Phe Lys Asp Thr Val
        355                 360                 365
Thr Val Lys Ile Ser Val Glu Asp Ala Asp Glu Pro Pro Met Phe Leu
    370                 375                 380
Ala Pro Ser Tyr Ile His Glu Val Gln Glu Asn Ala Ala Ala Gly Thr
385                 390                 395                 400
Val Val Gly Arg Val His Ala Lys Asp Pro Asp Ala Ala Asn Ser Pro
                405                 410                 415
Ile Arg Tyr Ser Ile Asp Arg His Thr Asp Leu Asp Arg Phe Phe Thr
            420                 425                 430
Ile Asn Pro Glu Asp Gly Phe Ile Lys Thr Thr Lys Pro Leu Asp Arg
        435                 440                 445
Glu Glu Thr Ala Trp Leu Asn Ile Thr Val Phe Ala Ala Glu Ile His
    450                 455                 460
Asn Arg His Gln Glu Ala Lys Val Pro Val Ala Ile Arg Val Leu Asp
465                 470                 475                 480
Val Asn Asp Asn Ala Pro Lys Phe Ala Ala Pro Tyr Glu Gly Phe Ile
                485                 490                 495
Cys Glu Ser Asp Gln Thr Lys Pro Leu Ser Asn Gln Pro Ile Val Thr
            500                 505                 510
Ile Ser Ala Asp Asp Lys Asp Asp Thr Ala Asn Gly Pro Arg Phe Ile
        515                 520                 525
Phe Ser Leu Pro Pro Glu Ile Ile His Asn Pro Asn Phe Thr Val Arg
    530                 535                 540
Asp Asn Arg Asp Asn Thr Ala Gly Val Tyr Ala Arg Arg Gly Gly Phe
545                 550                 555                 560
Ser Arg Gln Lys Gln Asp Leu Tyr Leu Leu Pro Ile Val Ile Ser Asp
                565                 570                 575
```

```
Gly Gly Ile Pro Pro Met Ser Ser Thr Asn Thr Leu Thr Ile Lys Val
            580                 585                 590
Cys Gly Cys Asp Val Asn Gly Ala Leu Leu Ser Cys Asn Ala Glu Ala
        595                 600                 605
Tyr Ile Leu Asn Ala Gly Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu
    610                 615                 620
Ala Cys Ile Val Ile Leu Leu Val Ile Val Val Leu Phe Val Thr Leu
625                 630                 635                 640
Arg Arg Gln Lys Lys Glu Pro Leu Ile Val Phe Glu Glu Glu Asp Val
                645                 650                 655
Arg Glu Asn Ile Ile Thr Tyr Asp Asp Glu Gly Gly Gly Glu Glu Asp
            660                 665                 670
Thr Glu Ala Phe Asp Ile Ala Thr Leu Gln Asn Pro Asp Gly Ile Asn
        675                 680                 685
Gly Phe Ile Pro Arg Lys Asp Ile Lys Pro Glu Tyr Gln Tyr Met Pro
    690                 695                 700
Arg Pro Gly Leu Arg Pro Ala Pro Asn Ser Val Asp Val Asp Asp Phe
705                 710                 715                 720
Ile Asn Thr Arg Ile Gln Glu Ala Asp Asn Asp Pro Thr Ala Pro Pro
                725                 730                 735
Tyr Asp Ser Ile Gln Ile Tyr Gly Tyr Glu Gly Arg Gly Ser Val Ala
            740                 745                 750
Gly Ser Leu Ser Ser Leu Glu Ser Ala Thr Thr Asp Ser Asp Leu Asp
        755                 760                 765
Tyr Asp Tyr Leu Gln Asn Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp
    770                 775                 780
Leu Tyr Gly Ser Lys Asp Thr Phe Asp Asp Asp Ser
785                 790                 795


<210> 108
<211> 180
<212> PRT
<213> Homo sapiens

<400> 108
Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
 1                   5                  10                  15
Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
            20                  25                  30
Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
        35                  40                  45
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
    50                  55                  60
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
65                  70                  75                  80
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
                85                  90                  95
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
            100                 105                 110
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
        115                 120                 125
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
    130                 135                 140
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
145                 150                 155                 160
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
                165                 170                 175
Ala Leu Leu Gln
            180


<210> 109
<211> 358
<212> PRT
<213> Homo sapiens
```

<400> 109
Met Arg Ala Thr Pro Leu Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys
1 5 10 15
Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln
20 25 30
Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu
35 40 45
Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr
50 55 60
Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly
65 70 75 80
Arg Ala Tyr Gln Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys
85 90 95
Lys Val Tyr Pro Val Gln Glu Ala Pro Ala Val Leu Glu Pro Tyr Ala
100 105 110
Arg Leu Pro Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala
115 120 125
Gly Thr Gln Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met
130 135 140
His Ser Leu Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala
145 150 155 160
Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His
165 170 175
Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp
180 185 190
Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val
195 200 205
Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala
210 215 220
Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys
225 230 235 240
Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu Ala
245 250 255
Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe Gly Lys
260 265 270
Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala
275 280 285
Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu
290 295 300
Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln Asp Pro Met
305 310 315 320
Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val
325 330 335
Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg
340 345 350
Glu Val Val Leu Tyr Gly
355

<210> 110
<211> 1172
<212> PRT
<213> Homo sapiens

<400> 110
Met Val Trp Arg Leu Val Leu Leu Ala Leu Trp Val Trp Pro Ser Thr
1 5 10 15
Gln Ala Gly His Gln Asp Lys Asp Thr Thr Phe Asp Leu Phe Ser Ile
20 25 30
Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro
35 40 45
Asp Pro Gly Val Pro Ala Tyr Arg Phe Val Arg Phe Asp Tyr Ile Pro
50 55 60
Pro Val Asn Ala Asp Asp Leu Ser Lys Ile Thr Lys Ile Met Arg Gln
65 70 75 80
Lys Glu Gly Phe Phe Leu Thr Ala Gln Leu Lys Gln Asp Gly Lys Ser
85 90 95

Arg Gly Thr Leu Leu Ala Leu Glu Gly Pro Gly Leu Ser Gln Arg Gln
100 105 110
Phe Glu Ile Val Ser Asn Gly Pro Ala Asp Thr Leu Asp Leu Thr Tyr
115 120 125
Trp Ile Asp Gly Thr Arg His Val Val Ser Leu Glu Asp Val Gly Leu
130 135 140
Ala Asp Ser Gln Trp Lys Asn Val Thr Val Gln Val Ala Gly Glu Thr
145 150 155 160
Tyr Ser Leu His Val Gly Cys Asp Leu Ile Gly Pro Val Ala Leu Asp
165 170 175
Glu Pro Phe Tyr Glu His Leu Gln Ala Glu Lys Ser Arg Met Tyr Val
180 185 190
Ala Lys Gly Ser Ala Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn
195 200 205
Val His Leu Val Phe Glu Asn Ser Val Glu Asp Ile Leu Ser Lys Lys
210 215 220
Gly Cys Gln Gln Gly Gln Gly Ala Glu Ile Asn Ala Ile Ser Glu Asn
225 230 235 240
Thr Glu Thr Leu Arg Leu Gly Pro His Val Thr Thr Glu Tyr Val Gly
245 250 255
Pro Ser Ser Glu Arg Arg Pro Glu Val Cys Glu Arg Ser Cys Glu Glu
260 265 270
Leu Gly Asn Met Val Gln Glu Leu Ser Gly Leu His Val Leu Val Asn
275 280 285
Gln Leu Ser Glu Asn Leu Lys Arg Val Ser Asn Asp Asn Gln Phe Leu
290 295 300
Trp Glu Leu Ile Gly Gly Pro Pro Lys Thr Arg Asn Met Ser Ala Cys
305 310 315 320
Trp Gln Asp Gly Arg Phe Phe Ala Glu Asn Glu Thr Trp Val Val Asp
325 330 335
Ser Cys Thr Thr Cys Thr Cys Lys Lys Phe Lys Thr Ile Cys His Gln
340 345 350
Ile Thr Cys Pro Pro Ala Thr Cys Ala Ser Pro Ser Phe Val Glu Gly
355 360 365
Glu Cys Cys Pro Ser Cys Leu His Ser Val Asp Gly Glu Glu Gly Trp
370 375 380
Ser Pro Trp Ala Glu Trp Thr Gln Cys Ser Val Thr Cys Gly Ser Gly
385 390 395 400
Thr Gln Gln Arg Gly Arg Ser Cys Asp Val Thr Ser Asn Thr Cys Leu
405 410 415
Gly Pro Ser Ile Gln Thr Arg Ala Cys Ser Leu Ser Lys Cys Asp Thr
420 425 430
Arg Ile Arg Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser
435 440 445
Cys Ser Val Thr Cys Gly Val Gly Asn Ile Thr Arg Ile Arg Leu Cys
450 455 460
Asn Ser Pro Val Pro Gln Met Gly Gly Lys Asn Cys Lys Gly Ser Gly
465 470 475 480
Arg Glu Thr Lys Ala Cys Gln Gly Ala Pro Cys Pro Ile Asp Gly Arg
485 490 495
Trp Ser Pro Trp Ser Pro Trp Ser Ala Cys Thr Val Thr Cys Ala Gly
500 505 510
Gly Ile Arg Glu Arg Thr Arg Val Cys Asn Ser Pro Glu Pro Gln Tyr
515 520 525
Gly Gly Lys Ala Cys Val Gly Asp Val Gln Glu Arg Gln Met Cys Asn
530 535 540
Lys Arg Ser Cys Pro Val Asp Gly Cys Leu Ser Asn Pro Cys Phe Pro
545 550 555 560
Gly Ala Gln Cys Ser Ser Phe Pro Asp Gly Ser Trp Ser Cys Gly Phe
565 570 575
Cys Pro Val Gly Phe Leu Gly Asn Gly Thr His Cys Glu Asp Leu Asp
580 585 590
Glu Cys Ala Leu Val Pro Asp Ile Cys Phe Ser Thr Ser Lys Val Pro
595 600 605
Arg Cys Val Asn Thr Gln Pro Gly Phe His Cys Leu Pro Cys Pro Pro
610 615 620
Arg Tyr Arg Gly Asn Gln Pro Val Gly Val Gly Leu Glu Ala Ala Lys

625 630 635 640
Thr Glu Lys Gln Val Cys Glu Pro Glu Asn Pro Cys Lys Asp Lys Thr
645 650 655
His Asn Cys His Lys His Ala Glu Cys Ile Tyr Leu Gly His Phe Ser
660 665 670
Asp Pro Met Tyr Lys Cys Glu Cys Gln Thr Gly Tyr Ala Gly Asp Gly
675 680 685
Leu Ile Cys Gly Glu Asp Ser Asp Leu Asp Gly Trp Pro Asn Leu Asn
690 695 700
Leu Val Cys Ala Thr Asn Ala Thr Tyr His Cys Ile Lys Asp Asn Cys
705 710 715 720
Pro His Leu Pro Asn Ser Gly Gln Glu Asp Phe Asp Lys Asp Gly Ile
725 730 735
Gly Asp Ala Cys Asp Asp Asp Asp Asp Asn Asp Gly Val Thr Asp Glu
740 745 750
Lys Asp Asn Cys Gln Leu Leu Phe Asn Pro Arg Gln Ala Asp Tyr Asp
755 760 765
Lys Asp Glu Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Val His Asn
770 775 780
Pro Ala Gln Ile Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ser
785 790 795 800
Val Asp Ile Asp Gly Asp Asp Val Phe Asn Glu Arg Asp Asn Cys Pro
805 810 815
Tyr Val Tyr Asn Thr Asp Gln Arg Asp Thr Asp Gly Asp Gly Val Gly
820 825 830
Asp His Cys Asp Asn Cys Pro Leu Val His Asn Pro Asp Gln Thr Asp
835 840 845
Val Asp Asn Asp Leu Val Gly Asp Gln Cys Asp Asn Asn Glu Asp Ile
850 855 860
Asp Asp Asp Gly His Gln Asn Asn Gln Asp Asn Cys Pro Tyr Ile Ser
865 870 875 880
Asn Ala Asn Gln Ala Asp His Asp Arg Asp Gly Gln Gly Asp Ala Cys
885 890 895
Asp Pro Asp Asp Asp Asn Asp Gly Val Pro Asp Asp Arg Asp Asn Cys
900 905 910
Arg Leu Val Phe Asn Pro Asp Gln Glu Asp Leu Asp Gly Asp Gly Arg
915 920 925
Gly Asp Ile Cys Lys Asp Asp Phe Asp Asn Asp Asn Ile Pro Asp Ile
930 935 940
Asp Asp Val Cys Pro Glu Asn Asn Ala Ile Ser Glu Thr Asp Phe Arg
945 950 955 960
Asn Phe Gln Met Val Pro Leu Asp Pro Lys Gly Thr Thr Gln Ile Asp
965 970 975
Pro Asn Trp Val Ile Arg His Gln Gly Lys Glu Leu Val Gln Thr Ala
980 985 990
Asn Ser Asp Pro Gly Ile Ala Val Gly Phe Asp Glu Phe Gly Ser Val
995 1000 1005
Asp Phe Ser Gly Thr Phe Tyr Val Asn Thr Asp Arg Asp Asp Asp Tyr
1010 1015 1020
Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val
1025 1030 1035 1040
Met Trp Lys Gln Val Thr Gln Thr Tyr Trp Glu Asp Gln Pro Thr Arg
1045 1050 1055
Ala Tyr Gly Tyr Ser Gly Val Ser Leu Lys Val Val Asn Ser Thr Thr
1060 1065 1070
Gly Thr Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr
1075 1080 1085
Pro Gly Gln Val Arg Thr Leu Trp His Asp Pro Arg Asn Ile Gly Trp
1090 1095 1100
Lys Asp Tyr Thr Ala Tyr Arg Trp His Leu Thr His Arg Pro Lys Thr
1105 1110 1115 1120
Gly Tyr Ile Arg Val Leu Val His Glu Gly Lys Gln Val Met Ala Asp
1125 1130 1135
Ser Gly Pro Ile Tyr Asp Gln Thr Tyr Ala Gly Gly Arg Leu Gly Leu
1140 1145 1150
Phe Val Phe Ser Gln Glu Met Val Tyr Phe Ser Asp Leu Lys Tyr Glu
1155 1160 1165

Cys Arg Asp Ile
1170

<210> 111
<211> 138
<212> PRT
<213> Homo sapiens

<400> 111
Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
1 5 10 15
Thr Cys Ser Gly Val Glu Ala Gly Glu Asn Ala Gly Lys Asp Ala Gly
20 25 30
Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly Phe Trp Lys
35 40 45
Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu
50 55 60
Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala
65 70 75 80
Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro
85 90 95
Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser
100 105 110
Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His
115 120 125
Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
130 135

<210> 112
<211> 184
<212> PRT
<213> Homo sapiens

<400> 112
Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu Leu Gly
1 5 10 15
Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln Gly Ala
20 25 30
Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln
35 40 45
Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg
50 55 60
Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala
65 70 75 80
Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr
85 90 95
Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr
100 105 110
Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro
115 120 125
Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys
130 135 140
Lys Pro Lys Lys Phe Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu
145 150 155 160
Leu Gln Pro Pro Thr Lys Lys Lys Arg Val Thr Arg Val Lys Gln Cys
165 170 175
Arg Cys Ile Ser Ile Asp Leu Asp
180

<210> 113
<211> 707
<212> PRT
<213> Homo sapiens

<400> 113

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1 5 10 15
Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
20 25 30
Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
35 40 45
Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
50 55 60
Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65 70 75 80
Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
85 90 95
Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100 105 110
Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115 120 125
Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
130 135 140
Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145 150 155 160
Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165 170 175
Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180 185 190
Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195 200 205
Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210 215 220
Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225 230 235 240
Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245 250 255
Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260 265 270
Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
275 280 285
Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
290 295 300
Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305 310 315 320
Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
325 330 335
Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
340 345 350
Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
355 360 365
Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
370 375 380
Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385 390 395 400
His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
405 410 415
Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
420 425 430
Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
435 440 445
Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
450 455 460
Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465 470 475 480
Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
485 490 495
Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
500 505 510
Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
515 520 525

```
Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
    530                 535                 540
Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545                 550                 555                 560
Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
                565                 570                 575
Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
            580                 585                 590
Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
        595                 600                 605
Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
    610                 615                 620
Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625                 630                 635                 640
Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
                645                 650                 655
Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
            660                 665                 670
Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
        675                 680                 685
Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
    690                 695                 700
Pro Glu Asp
705
```

<210> 114
<211> 194
<212> PRT
<213> Homo sapiens

<400> 114

```
Met Ala Ile Arg Glu Leu Lys Val Cys Leu Leu Gly Asp Thr Gly Val
 1               5                  10                  15
Gly Lys Ser Ser Ile Val Cys Arg Phe Val Gln Asp His Phe Asp His
            20                  25                  30
Asn Ile Ser Pro Thr Ile Gly Ala Ser Phe Met Thr Lys Thr Val Pro
        35                  40                  45
Cys Gly Asn Glu Leu His Lys Phe Leu Ile Trp Asp Thr Ala Gly Gln
    50                  55                  60
Glu Arg Phe His Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ser Ala Ala
65                  70                  75                  80
Ala Val Ile Val Tyr Asp Ile Thr Lys Gln Asp Ser Phe Tyr Thr Leu
                85                  90                  95
Lys Lys Trp Val Lys Glu Leu Lys Glu His Gly Pro Glu Asn Ile Val
            100                 105                 110
Met Ala Ile Ala Gly Asn Lys Cys Asp Leu Ser Asp Ile Arg Glu Val
        115                 120                 125
Pro Leu Lys Asp Ala Lys Glu Tyr Ala Glu Ser Ile Gly Ala Ile Val
    130                 135                 140
Val Glu Thr Ser Ala Lys Asn Ala Ile Asn Ile Glu Glu Leu Phe Gln
145                 150                 155                 160
Gly Ile Ser Arg Gln Ile Pro Pro Leu Asp Pro His Glu Asn Gly Asn
                165                 170                 175
Asn Gly Thr Ile Lys Val Glu Lys Pro Thr Met Gln Ala Ser Arg Arg
            180                 185                 190
Cys Cys
```

<210> 115
<211> 114
<212> PRT
<213> Homo sapiens

<400> 115

```
Met Ser Ala Leu Ser Leu Leu Ile Leu Gly Leu Leu Thr Ala Val Pro
```

```
 1               5                  10                  15
Pro Ala Ser Cys Gln Gln Gly Leu Gly Asn Leu Gln Pro Trp Met Gln
            20                  25                  30
Gly Leu Ile Ala Val Ala Val Phe Leu Val Leu Val Ala Ile Ala Phe
        35                  40                  45
Ala Val Asn His Phe Trp Cys Gln Glu Glu Pro Glu Pro Ala His Met
    50                  55                  60
Ile Leu Thr Val Gly Asn Lys Ala Asp Gly Val Leu Val Gly Thr Asp
65                  70                  75                  80
Gly Arg Tyr Ser Ser Met Ala Ala Ser Phe Arg Ser Ser Glu His Glu
                85                  90                  95
Asn Ala Tyr Glu Asn Val Pro Glu Glu Glu Gly Lys Val Arg Ser Thr
            100                 105                 110
Pro Met
```

<210> 116
<211> 117
<212> PRT
<213> Homo sapiens

<400> 116

```
Met Ala Leu Glu Thr Val Pro Lys Asp Leu Arg His Leu Arg Ala Cys
 1               5                  10                  15
Leu Leu Cys Ser Leu Val Lys Thr Ile Asp Gln Phe Glu Tyr Asp Gly
            20                  25                  30
Cys Asp Asn Cys Asp Ala Tyr Leu Gln Met Lys Gly Asn Arg Glu Met
        35                  40                  45
Val Tyr Asp Cys Thr Ser Ser Ser Phe Asp Gly Ile Ile Ala Met Met
    50                  55                  60
Ser Pro Glu Asp Ser Trp Val Ser Lys Trp Gln Arg Val Ser Asn Phe
65                  70                  75                  80
Lys Pro Gly Val Tyr Ala Val Ser Val Thr Gly Arg Leu Pro Gln Gly
                85                  90                  95
Ile Val Arg Glu Leu Lys Ser Arg Gly Val Ala Tyr Lys Ser Arg Asp
            100                 105                 110
Thr Ala Ile Lys Thr
        115
```

<210> 117
<211> 178
<212> PRT
<213> Homo sapiens

<400> 117

```
Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
 1               5                  10                  15
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
            20                  25                  30
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
        35                  40                  45
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro
    50                  55                  60
Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly
65                  70                  75                  80
Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys
                85                  90                  95
Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser
            100                 105                 110
Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly
        115                 120                 125
Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys
    130                 135                 140
Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile
145                 150                 155                 160
```

Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Arg Leu Cys Arg Asn Arg
165 170 175
Cys Arg

<210> 118
<211> 3396
<212> PRT
<213> Homo sapiens

<400> 118
Met Phe Ile Asn Ile Lys Ser Ile Leu Trp Met Cys Ser Thr Leu Ile
1 5 10 15
Val Thr His Ala Leu His Lys Val Lys Val Gly Lys Ser Pro Pro Val
20 25 30
Arg Gly Ser Leu Ser Gly Lys Val Ser Leu Pro Cys His Phe Ser Thr
35 40 45
Met Pro Thr Leu Pro Pro Ser Tyr Asn Thr Ser Glu Phe Leu Arg Ile
50 55 60
Lys Trp Ser Lys Ile Glu Val Asp Lys Asn Gly Lys Asp Leu Lys Glu
65 70 75 80
Thr Thr Val Leu Val Ala Gln Asn Gly Asn Ile Lys Ile Gly Gln Asp
85 90 95
Tyr Lys Gly Arg Val Ser Val Pro Thr His Pro Glu Ala Val Gly Asp
100 105 110
Ala Ser Leu Thr Val Val Lys Leu Leu Ala Ser Asp Ala Gly Leu Tyr
115 120 125
Arg Cys Asp Val Met Tyr Gly Ile Glu Asp Thr Gln Asp Thr Val Ser
130 135 140
Leu Thr Val Asp Gly Val Val Phe His Tyr Arg Ala Ala Thr Ser Arg
145 150 155 160
Tyr Thr Leu Asn Phe Glu Ala Ala Gln Lys Ala Cys Leu Asp Val Gly
165 170 175
Ala Val Ile Ala Thr Pro Glu Gln Leu Phe Ala Ala Tyr Glu Asp Gly
180 185 190
Phe Glu Gln Cys Asp Ala Gly Trp Leu Ala Asp Gln Thr Val Arg Tyr
195 200 205
Pro Ile Arg Ala Pro Arg Val Gly Cys Tyr Gly Asp Lys Met Gly Lys
210 215 220
Ala Gly Val Arg Thr Tyr Gly Phe Arg Ser Pro Gln Glu Thr Tyr Asp
225 230 235 240
Val Tyr Cys Tyr Val Asp His Leu Asp Gly Asp Val Phe His Leu Thr
245 250 255
Val Pro Ser Lys Phe Thr Phe Glu Glu Ala Ala Lys Glu Cys Glu Asn
260 265 270
Gln Asp Ala Arg Leu Ala Thr Val Gly Glu Leu Gln Ala Ala Trp Arg
275 280 285
Asn Gly Phe Asp Gln Cys Asp Tyr Gly Trp Leu Ser Asp Ala Ser Val
290 295 300
Arg His Pro Val Thr Val Ala Arg Ala Gln Cys Gly Gly Gly Leu Leu
305 310 315 320
Gly Val Arg Thr Leu Tyr Arg Phe Glu Asn Gln Thr Gly Phe Pro Pro
325 330 335
Pro Asp Ser Arg Phe Asp Ala Tyr Cys Phe Lys Pro Lys Glu Ala Thr
340 345 350
Thr Ile Asp Leu Ser Ile Leu Ala Glu Thr Ala Ser Pro Ser Leu Ser
355 360 365
Lys Glu Pro Gln Met Val Ser Asp Arg Thr Thr Pro Ile Ile Pro Leu
370 375 380
Val Asp Glu Leu Pro Val Ile Pro Thr Glu Phe Pro Pro Val Gly Asn
385 390 395 400
Ile Val Ser Phe Glu Gln Lys Ala Thr Val Gln Pro Gln Ala Ile Thr
405 410 415
Asp Ser Leu Ala Thr Lys Leu Pro Thr Pro Thr Gly Ser Thr Lys Lys
420 425 430
Pro Trp Asp Met Asp Asp Tyr Ser Pro Ser Ala Ser Gly Pro Leu Gly

435 440 445
Lys Leu Asp Ile Ser Glu Ile Lys Glu Glu Val Leu Gln Ser Thr Thr
450 455 460
Gly Val Ser His Tyr Ala Thr Asp Ser Trp Asp Gly Val Val Glu Asp
465 470 475 480
Lys Gln Thr Gln Glu Ser Val Thr Gln Ile Glu Gln Ile Glu Val Gly
485 490 495
Pro Leu Val Thr Ser Met Glu Ile Leu Lys His Ile Pro Ser Lys Glu
500 505 510
Phe Pro Val Thr Glu Thr Pro Leu Val Thr Ala Arg Met Ile Leu Glu
515 520 525
Ser Lys Thr Glu Lys Lys Met Val Ser Thr Val Ser Glu Leu Val Thr
530 535 540
Thr Gly His Tyr Gly Phe Thr Leu Gly Glu Glu Asp Asp Glu Asp Arg
545 550 555 560
Thr Leu Thr Val Gly Ser Asp Glu Ser Thr Leu Ile Phe Asp Gln Ile
565 570 575
Pro Glu Val Ile Thr Val Ser Lys Thr Ser Glu Asp Thr Ile His Thr
580 585 590
His Leu Glu Asp Leu Glu Ser Val Ser Ala Ser Thr Thr Val Ser Pro
595 600 605
Leu Ile Met Pro Asp Asn Asn Gly Ser Ser Met Asp Asp Trp Glu Glu
610 615 620
Arg Gln Thr Ser Gly Arg Ile Thr Glu Glu Phe Leu Gly Lys Tyr Leu
625 630 635 640
Ser Thr Thr Pro Phe Pro Ser Gln His Arg Thr Glu Ile Glu Leu Phe
645 650 655
Pro Tyr Ser Gly Asp Lys Ile Leu Val Glu Gly Ile Ser Thr Val Ile
660 665 670
Tyr Pro Ser Leu Gln Thr Glu Met Thr His Arg Arg Glu Arg Thr Glu
675 680 685
Thr Leu Ile Pro Glu Met Arg Thr Asp Thr Tyr Thr Asp Glu Ile Gln
690 695 700
Glu Glu Ile Thr Lys Ser Pro Phe Met Gly Lys Thr Glu Glu Glu Val
705 710 715 720
Phe Ser Gly Met Lys Leu Ser Thr Ser Leu Ser Glu Pro Ile His Val
725 730 735
Thr Glu Ser Ser Val Glu Met Thr Lys Ser Phe Asp Phe Pro Thr Leu
740 745 750
Ile Thr Lys Leu Ser Ala Glu Pro Thr Glu Val Arg Asp Met Glu Glu
755 760 765
Asp Phe Thr Ala Thr Pro Gly Thr Thr Lys Tyr Asp Glu Asn Ile Thr
770 775 780
Thr Val Leu Leu Ala His Gly Thr Leu Ser Val Glu Ala Ala Thr Val
785 790 795 800
Ser Lys Trp Ser Trp Asp Glu Asp Asn Thr Thr Ser Lys Pro Leu Glu
805 810 815
Ser Thr Glu Pro Ser Ala Ser Ser Lys Leu Pro Pro Ala Leu Leu Thr
820 825 830
Thr Val Gly Met Asn Gly Lys Asp Lys Asp Ile Pro Ser Phe Thr Glu
835 840 845
Asp Gly Ala Asp Glu Phe Thr Leu Ile Pro Asp Ser Thr Gln Lys Gln
850 855 860
Leu Glu Glu Val Thr Asp Glu Asp Ile Ala Ala His Gly Lys Phe Thr
865 870 875 880
Ile Arg Phe Gln Pro Thr Thr Ser Thr Gly Ile Ala Glu Lys Ser Thr
885 890 895
Leu Arg Asp Ser Thr Thr Glu Glu Lys Val Pro Pro Ile Thr Ser Thr
900 905 910
Glu Gly Gln Val Tyr Ala Thr Met Glu Gly Ser Ala Leu Gly Glu Val
915 920 925
Glu Asp Val Asp Leu Ser Lys Pro Val Ser Thr Val Pro Gln Phe Ala
930 935 940
His Thr Ser Glu Val Glu Gly Leu Ala Phe Val Ser Tyr Ser Ser Thr
945 950 955 960
Gln Glu Pro Thr Thr Tyr Val Asp Ser Ser His Thr Ile Pro Leu Ser
965 970 975

Val Ile Pro Lys Thr Asp Trp Gly Val Leu Val Pro Ser Val Pro Ser
980 985 990
Glu Asp Glu Val Leu Gly Glu Pro Ser Gln Asp Ile Leu Val Ile Asp
995 1000 1005
Gln Thr Arg Leu Glu Ala Thr Ile Ser Pro Glu Thr Met Arg Thr Thr
1010 1015 1020
Lys Ile Thr Glu Gly Thr Thr Gln Glu Glu Phe Pro Trp Lys Glu Gln
1025 1030 1035 1040
Thr Ala Glu Lys Pro Val Pro Ala Leu Ser Ser Thr Ala Trp Thr Pro
1045 1050 1055
Lys Glu Ala Val Thr Pro Leu Asp Glu Gln Glu Gly Asp Gly Ser Ala
1060 1065 1070
Tyr Thr Val Ser Glu Asp Glu Leu Leu Thr Gly Ser Glu Arg Val Pro
1075 1080 1085
Val Leu Glu Thr Thr Pro Val Gly Lys Ile Asp His Ser Val Ser Tyr
1090 1095 1100
Pro Pro Gly Ala Val Thr Glu His Lys Val Lys Thr Asp Glu Val Val
1105 1110 1115 1120
Thr Leu Thr Pro Arg Ile Gly Pro Lys Val Ser Leu Ser Pro Gly Pro
1125 1130 1135
Glu Gln Lys Tyr Glu Thr Glu Gly Ser Ser Thr Thr Gly Phe Thr Ser
1140 1145 1150
Ser Leu Ser Pro Phe Ser Thr His Ile Thr Gln Leu Met Glu Glu Thr
1155 1160 1165
Thr Thr Glu Lys Thr Ser Leu Glu Asp Ile Asp Leu Gly Ser Gly Leu
1170 1175 1180
Phe Glu Lys Pro Lys Ala Thr Glu Leu Ile Glu Phe Ser Thr Ile Lys
1185 1190 1195 1200
Val Thr Val Pro Ser Asp Ile Thr Thr Ala Phe Ser Ser Val Asp Arg
1205 1210 1215
Leu His Thr Thr Ser Ala Phe Lys Pro Ser Ser Ala Ile Thr Lys Lys
1220 1225 1230
Pro Pro Leu Ile Asp Arg Glu Pro Gly Glu Glu Thr Thr Ser Asp Met
1235 1240 1245
Val Ile Ile Gly Glu Ser Thr Ser His Val Pro Pro Thr Thr Leu Glu
1250 1255 1260
Asp Ile Val Ala Lys Glu Thr Glu Thr Asp Ile Asp Arg Glu Tyr Phe
1265 1270 1275 1280
Thr Thr Ser Ser Pro Pro Ala Thr Gln Pro Thr Arg Pro Pro Thr Val
1285 1290 1295
Glu Asp Lys Glu Ala Phe Gly Pro Gln Ala Leu Ser Thr Pro Gln Pro
1300 1305 1310
Pro Ala Ser Thr Lys Phe His Pro Asp Ile Asn Val Tyr Ile Ile Glu
1315 1320 1325
Val Arg Glu Asn Lys Thr Gly Arg Met Ser Asp Leu Ser Val Ile Gly
1330 1335 1340
His Pro Ile Asp Ser Glu Ser Lys Glu Asp Glu Pro Cys Ser Glu Glu
1345 1350 1355 1360
Thr Asp Pro Val His Asp Leu Met Ala Glu Ile Leu Pro Glu Phe Pro
1365 1370 1375
Asp Ile Ile Glu Ile Asp Leu Tyr His Ser Glu Glu Asn Glu Glu Glu
1380 1385 1390
Glu Glu Glu Cys Ala Asn Ala Thr Asp Val Thr Thr Thr Pro Ser Val
1395 1400 1405
Gln Tyr Ile Asn Gly Lys His Leu Val Thr Thr Val Pro Lys Asp Pro
1410 1415 1420
Glu Ala Ala Glu Ala Arg Arg Gly Gln Phe Glu Ser Val Ala Pro Ser
1425 1430 1435 1440
Gln Asn Phe Ser Asp Ser Ser Glu Ser Asp Thr His Pro Phe Val Ile
1445 1450 1455
Ala Lys Thr Glu Leu Ser Thr Ala Val Gln Pro Asn Glu Ser Thr Glu
1460 1465 1470
Thr Thr Glu Ser Leu Glu Val Thr Trp Lys Pro Glu Thr Tyr Pro Glu
1475 1480 1485
Thr Ser Glu His Phe Ser Gly Gly Glu Pro Asp Val Phe Pro Thr Val
1490 1495 1500
Pro Phe His Glu Glu Phe Glu Ser Gly Thr Ala Lys Lys Gly Ala Glu

1505 1510 1515 1520
Ser Val Thr Glu Arg Asp Thr Glu Val Gly His Gln Ala His Glu His
1525 1530 1535
Thr Glu Pro Val Ser Leu Phe Pro Glu Glu Ser Ser Gly Glu Ile Ala
1540 1545 1550
Ile Asp Gln Glu Ser Gln Lys Ile Ala Phe Ala Arg Ala Thr Glu Val
1555 1560 1565
Thr Phe Gly Glu Glu Val Glu Lys Ser Thr Ser Val Thr Tyr Thr Pro
1570 1575 1580
Thr Ile Val Pro Ser Ser Ala Ser Ala Tyr Val Ser Glu Glu Glu Ala
1585 1590 1595 1600
Val Thr Leu Ile Gly Asn Pro Trp Pro Asp Asp Leu Leu Ser Thr Lys
1605 1610 1615
Glu Ser Trp Val Glu Ala Thr Pro Arg Gln Val Val Glu Leu Ser Gly
1620 1625 1630
Ser Ser Ser Ile Pro Ile Thr Glu Gly Ser Gly Glu Ala Glu Glu Asp
1635 1640 1645
Glu Asp Thr Met Phe Thr Met Val Thr Asp Leu Ser Gln Arg Asn Thr
1650 1655 1660
Thr Asp Thr Leu Ile Thr Leu Asp Thr Ser Arg Ile Ile Thr Glu Ser
1665 1670 1675 1680
Phe Phe Glu Val Pro Ala Thr Thr Ile Tyr Pro Val Ser Glu Gln Pro
1685 1690 1695
Ser Ala Lys Val Val Pro Thr Lys Phe Val Ser Glu Thr Asp Thr Ser
1700 1705 1710
Glu Trp Ile Ser Ser Thr Thr Val Glu Glu Lys Lys Arg Lys Glu Glu
1715 1720 1725
Glu Gly Thr Thr Gly Thr Ala Ser Thr Phe Glu Val Tyr Ser Ser Thr
1730 1735 1740
Gln Arg Ser Asp Gln Leu Ile Leu Pro Phe Glu Leu Glu Ser Pro Asn
1745 1750 1755 1760
Val Ala Thr Ser Ser Asp Ser Gly Thr Arg Lys Ser Phe Met Ser Leu
1765 1770 1775
Thr Thr Pro Thr Gln Ser Glu Arg Glu Met Thr Asp Ser Thr Pro Val
1780 1785 1790
Phe Thr Glu Thr Asn Thr Leu Glu Asn Leu Gly Ala Gln Thr Thr Glu
1795 1800 1805
His Ser Ser Ile His Gln Pro Gly Val Gln Glu Gly Leu Thr Thr Leu
1810 1815 1820
Pro Arg Ser Pro Ala Ser Val Phe Met Glu Gln Gly Ser Gly Glu Ala
1825 1830 1835 1840
Ala Ala Asp Pro Glu Thr Thr Thr Val Ser Ser Phe Ser Leu Asn Val
1845 1850 1855
Glu Tyr Ala Ile Gln Ala Glu Lys Glu Val Ala Gly Thr Leu Ser Pro
1860 1865 1870
His Val Glu Thr Thr Phe Ser Thr Glu Pro Thr Gly Leu Val Leu Ser
1875 1880 1885
Thr Val Met Asp Arg Val Val Ala Glu Asn Ile Thr Gln Thr Ser Arg
1890 1895 1900
Glu Ile Val Ile Ser Glu Arg Leu Gly Glu Pro Asn Tyr Gly Ala Glu
1905 1910 1915 1920
Ile Arg Gly Phe Ser Thr Gly Phe Pro Leu Glu Glu Asp Phe Ser Gly
1925 1930 1935
Asp Phe Arg Glu Tyr Ser Thr Val Ser His Pro Ile Ala Lys Glu Glu
1940 1945 1950
Thr Val Met Met Glu Gly Ser Gly Asp Ala Ala Phe Arg Asp Thr Gln
1955 1960 1965
Thr Ser Pro Ser Thr Val Pro Thr Ser Val His Ile Ser His Ile Ser
1970 1975 1980
Asp Ser Glu Gly Pro Ser Ser Thr Met Val Ser Thr Ser Ala Phe Pro
1985 1990 1995 2000
Trp Glu Glu Phe Thr Ser Ser Ala Glu Gly Ser Gly Glu Gln Leu Val
2005 2010 2015
Thr Val Ser Ser Ser Val Val Pro Val Leu Pro Ser Ala Val Gln Lys
2020 2025 2030
Phe Ser Gly Thr Ala Ser Ser Ile Ile Asp Glu Gly Leu Gly Glu Val
2035 2040 2045

Gly Thr Val Asn Glu Ile Asp Arg Arg Ser Thr Ile Leu Pro Thr Ala
2050 2055 2060
Glu Val Glu Gly Thr Lys Ala Pro Val Glu Lys Glu Glu Val Lys Val
2065 2070 2075 2080
Ser Gly Thr Val Ser Thr Asn Phe Pro Gln Thr Ile Glu Pro Ala Lys
2085 2090 2095
Leu Trp Ser Arg Gln Glu Val Asn Pro Val Arg Gln Glu Ile Glu Ser
2100 2105 2110
Glu Thr Thr Ser Glu Glu Gln Ile Gln Glu Glu Lys Ser Phe Glu Ser
2115 2120 2125
Pro Gln Asn Ser Pro Ala Thr Glu Gln Thr Ile Phe Asp Ser Gln Thr
2130 2135 2140
Phe Thr Glu Thr Glu Leu Lys Thr Thr Asp Tyr Ser Val Leu Thr Thr
2145 2150 2155 2160
Lys Lys Thr Tyr Ser Asp Asp Lys Glu Met Lys Glu Glu Asp Thr Ser
2165 2170 2175
Leu Val Asn Met Ser Thr Pro Asp Pro Asp Ala Asn Gly Leu Glu Ser
2180 2185 2190
Tyr Thr Thr Leu Pro Glu Ala Thr Glu Lys Ser His Phe Phe Leu Ala
2195 2200 2205
Thr Ala Leu Val Thr Glu Ser Ile Pro Ala Glu His Val Val Thr Asp
2210 2215 2220
Ser Pro Ile Lys Lys Glu Glu Ser Thr Lys His Phe Pro Lys Gly Met
2225 2230 2235 2240
Arg Pro Thr Ile Gln Glu Ser Asp Thr Glu Leu Leu Phe Ser Gly Leu
2245 2250 2255
Gly Ser Gly Glu Glu Val Leu Pro Thr Leu Pro Thr Glu Ser Val Asn
2260 2265 2270
Phe Thr Glu Val Glu Gln Ile Asn Asn Thr Leu Tyr Pro His Thr Ser
2275 2280 2285
Gln Val Glu Ser Thr Ser Ser Asp Lys Ile Glu Asp Phe Asn Arg Met
2290 2295 2300
Glu Asn Val Ala Lys Glu Val Gly Pro Leu Val Ser Gln Thr Asp Ile
2305 2310 2315 2320
Phe Glu Gly Ser Gly Ser Val Thr Ser Thr Thr Leu Ile Glu Ile Leu
2325 2330 2335
Ser Asp Thr Gly Ala Glu Gly Pro Thr Val Ala Pro Leu Pro Phe Ser
2340 2345 2350
Thr Asp Ile Gly His Pro Gln Asn Gln Thr Val Arg Trp Ala Glu Glu
2355 2360 2365
Ile Gln Thr Ser Arg Pro Gln Thr Ile Thr Glu Gln Asp Ser Asn Lys
2370 2375 2380
Asn Ser Ser Thr Ala Glu Ile Asn Glu Thr Thr Thr Ser Ser Thr Asp
2385 2390 2395 2400
Phe Leu Ala Arg Ala Tyr Gly Phe Glu Met Ala Lys Glu Phe Val Thr
2405 2410 2415
Ser Ala Pro Lys Pro Ser Asp Leu Tyr Tyr Glu Pro Ser Gly Glu Gly
2420 2425 2430
Ser Gly Glu Val Asp Ile Val Asp Ser Phe His Thr Ser Ala Thr Thr
2435 2440 2445
Gln Ala Thr Arg Gln Glu Ser Ser Thr Thr Phe Val Ser Asp Gly Ser
2450 2455 2460
Leu Glu Lys His Pro Glu Val Pro Ser Ala Lys Ala Val Thr Ala Asp
2465 2470 2475 2480
Gly Phe Pro Thr Val Ser Val Met Leu Pro Leu His Ser Glu Gln Asn
2485 2490 2495
Lys Ser Ser Pro Asp Pro Thr Ser Thr Leu Ser Asn Thr Val Ser Tyr
2500 2505 2510
Glu Arg Ser Thr Asp Gly Ser Phe Gln Asp Arg Phe Arg Glu Phe Glu
2515 2520 2525
Asp Ser Thr Leu Lys Pro Asn Arg Lys Lys Pro Thr Glu Asn Ile Ile
2530 2535 2540
Ile Asp Leu Asp Lys Glu Asp Lys Asp Leu Ile Leu Thr Ile Thr Glu
2545 2550 2555 2560
Ser Thr Ile Leu Glu Ile Leu Pro Glu Leu Thr Ser Asp Lys Asn Thr
2565 2570 2575
Ile Ile Asp Ile Asp His Thr Lys Pro Val Tyr Glu Asp Ile Leu Gly

2580 2585 2590
Met Gln Thr Asp Ile Asp Thr Glu Val Pro Ser Glu Pro His Asp Ser
2595 2600 2605
Asn Asp Glu Ser Asn Asp Asp Ser Thr Gln Val Gln Glu Ile Tyr Glu
2610 2615 2620
Ala Ala Val Asn Leu Ser Leu Thr Glu Glu Thr Phe Glu Gly Ser Ala
2625 2630 2635 2640
Asp Val Leu Ala Ser Tyr Thr Gln Ala Thr His Asp Glu Ser Met Thr
2645 2650 2655
Tyr Glu Asp Arg Ser Gln Leu Asp His Met Gly Phe His Phe Thr Thr
2660 2665 2670
Gly Ile Pro Ala Pro Ser Thr Glu Thr Glu Leu Asp Val Leu Leu Pro
2675 2680 2685
Thr Ala Thr Ser Leu Pro Ile Pro Arg Lys Ser Ala Thr Val Ile Pro
2690 2695 2700
Glu Ile Glu Gly Ile Lys Ala Glu Ala Lys Ala Leu Asp Asp Met Phe
2705 2710 2715 2720
Glu Ser Ser Thr Leu Ser Asp Gly Gln Ala Ile Ala Asp Gln Ser Glu
2725 2730 2735
Ile Ile Pro Thr Leu Gly Gln Phe Glu Arg Thr Gln Glu Glu Tyr Glu
2740 2745 2750
Asp Lys Lys His Ala Gly Pro Ser Phe Gln Pro Glu Phe Ser Ser Gly
2755 2760 2765
Ala Glu Glu Ala Leu Val Asp His Thr Pro Tyr Leu Ser Ile Ala Thr
2770 2775 2780
Thr His Leu Met Asp Gln Ser Val Thr Glu Val Pro Asp Val Met Glu
2785 2790 2795 2800
Gly Ser Asn Pro Pro Tyr Tyr Thr Asp Thr Thr Leu Ala Val Ser Thr
2805 2810 2815
Phe Ala Lys Leu Ser Ser Gln Thr Pro Ser Ser Pro Leu Thr Ile Tyr
2820 2825 2830
Ser Gly Ser Glu Ala Ser Gly His Thr Glu Ile Pro Gln Pro Ser Ala
2835 2840 2845
Leu Pro Gly Ile Asp Val Gly Ser Ser Val Met Ser Pro Gln Asp Ser
2850 2855 2860
Phe Lys Glu Ile His Val Asn Ile Glu Ala Thr Phe Lys Pro Ser Ser
2865 2870 2875 2880
Glu Glu Tyr Leu His Ile Thr Glu Pro Pro Ser Leu Ser Pro Asp Thr
2885 2890 2895
Lys Leu Glu Pro Ser Glu Asp Asp Gly Lys Pro Glu Leu Leu Glu Glu
2900 2905 2910
Met Glu Ala Ser Pro Thr Glu Leu Ile Ala Val Glu Gly Thr Glu Ile
2915 2920 2925
Leu Gln Asp Phe Gln Asn Lys Thr Asp Gly Gln Val Ser Gly Glu Ala
2930 2935 2940
Ile Lys Met Phe Pro Thr Ile Lys Thr Pro Glu Ala Gly Thr Val Ile
2945 2950 2955 2960
Thr Thr Ala Asp Glu Ile Glu Leu Glu Gly Ala Thr Gln Trp Pro His
2965 2970 2975
Ser Thr Ser Ala Ser Ala Thr Tyr Gly Val Glu Ala Gly Val Val Pro
2980 2985 2990
Trp Leu Ser Pro Gln Thr Ser Glu Arg Pro Thr Leu Ser Ser Ser Pro
2995 3000 3005
Glu Ile Asn Pro Glu Thr Gln Ala Ala Leu Ile Arg Gly Gln Asp Ser
3010 3015 3020
Thr Ile Ala Ala Ser Glu Gln Gln Val Ala Ala Arg Ile Leu Asp Ser
3025 3030 3035 3040
Asn Asp Gln Ala Thr Val Asn Pro Val Glu Phe Asn Thr Glu Val Ala
3045 3050 3055
Thr Pro Pro Phe Ser Leu Leu Glu Thr Ser Asn Glu Thr Asp Phe Leu
3060 3065 3070
Ile Gly Ile Asn Glu Glu Ser Val Glu Gly Thr Ala Ile Tyr Leu Pro
3075 3080 3085
Gly Pro Asp Arg Cys Lys Met Asn Pro Cys Leu Asn Gly Gly Thr Cys
3090 3095 3100
Tyr Pro Thr Glu Thr Ser Tyr Val Cys Thr Cys Val Pro Gly Tyr Ser
3105 3110 3115 3120

Gly Asp Gln Cys Glu Leu Asp Phe Asp Glu Cys His Ser Asn Pro Cys
3125 3130 3135
Arg Asn Gly Ala Thr Cys Val Asp Gly Phe Asn Thr Phe Arg Cys Leu
3140 3145 3150
Cys Leu Pro Ser Tyr Val Gly Ala Leu Cys Glu Gln Asp Thr Glu Thr
3155 3160 3165
Cys Asp Tyr Gly Trp His Lys Phe Gln Gly Gln Cys Tyr Lys Tyr Phe
3170 3175 3180
Ala His Arg Arg Thr Trp Asp Ala Ala Glu Arg Glu Cys Arg Leu Gln
3185 3190 3195 3200
Gly Ala His Leu Thr Ser Ile Leu Ser His Glu Glu Gln Met Phe Val
3205 3210 3215
Asn Arg Val Gly His Asp Tyr Gln Trp Ile Gly Leu Asn Asp Lys Met
3220 3225 3230
Phe Glu His Asp Phe Arg Trp Thr Asp Gly Ser Thr Leu Gln Tyr Glu
3235 3240 3245
Asn Trp Arg Pro Asn Gln Pro Asp Ser Phe Phe Ser Ala Gly Glu Asp
3250 3255 3260
Cys Val Val Ile Ile Trp His Glu Asn Gly Gln Trp Asn Asp Val Pro
3265 3270 3275 3280
Cys Asn Tyr His Leu Thr Tyr Thr Cys Lys Lys Gly Thr Val Ala Cys
3285 3290 3295
Gly Gln Pro Pro Val Val Glu Asn Ala Lys Thr Phe Gly Lys Met Lys
3300 3305 3310
Pro Arg Tyr Glu Ile Asn Ser Leu Ile Arg Tyr His Cys Lys Asp Gly
3315 3320 3325
Phe Ile Gln Arg His Leu Pro Thr Ile Arg Cys Leu Gly Asn Gly Arg
3330 3335 3340
Trp Ala Ile Pro Lys Ile Thr Cys Met Asn Pro Ser Ala Tyr Gln Arg
3345 3350 3355 3360
Thr Tyr Ser Met Lys Tyr Phe Lys Asn Ser Ser Ser Ala Lys Asp Asn
3365 3370 3375
Ser Ile Asn Thr Ser Lys His Asp His Arg Trp Ser Arg Arg Trp Gln
3380 3385 3390
Glu Ser Arg Arg
3395

<210> 119
<211> 317
<212> PRT
<213> Homo sapiens

<400> 119
Met Thr Ser Arg Thr Arg Val Thr Trp Pro Ser Pro Pro Arg Pro Leu
1 5 10 15
Pro Val Pro Ala Ala Ala Ala Val Ala Phe Gly Ala Lys Gly Thr Asp
20 25 30
Pro Ala Glu Ala Arg Ser Ser Arg Gly Ile Glu Glu Ala Gly Pro Arg
35 40 45
Ala His Gly Arg Ala Gly Arg Glu Pro Glu Arg Arg Arg Ser Arg Gln
50 55 60
Gln Arg Arg Gly Gly Leu Gln Ala Arg Arg Ser Thr Leu Leu Lys Thr
65 70 75 80
Cys Ala Arg Ala Arg Ala Thr Ala Pro Gly Ala Met Lys Met Val Ala
85 90 95
Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys Leu Cys Cys His Val
100 105 110
Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala
115 120 125
Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr
130 135 140
Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe Glu Phe Met Asp Asp
145 150 155 160
Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu Leu Met Ile Leu Ile
165 170 175
Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln Arg Ala Ala Trp Ile

180 185 190
Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn Met Leu
195 200 205
Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile
210 215 220
Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met Ser Val
225 230 235 240
Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile
245 250 255
Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg
260 265 270
Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu Val Tyr Val Thr Ser
275 280 285
Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn
290 295 300
Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val Ser Ala
305 310 315

<210> 120
<211> 474
<212> PRT
<213> Homo sapiens

<400> 120
Met Val Gln Gln Thr Asn Asn Ala Glu Asn Thr Glu Ala Leu Leu Ala
1 5 10 15
Gly Glu Ser Ser Asp Ser Gly Ala Gly Leu Glu Leu Gly Ile Ala Ser
20 25 30
Ser Pro Thr Pro Gly Ser Thr Ala Ser Thr Gly Gly Lys Ala Asp Asp
35 40 45
Pro Ser Trp Cys Lys Thr Pro Ser Gly His Ile Lys Arg Pro Met Asn
50 55 60
Ala Phe Met Val Trp Ser Gln Ile Glu Arg Arg Lys Ile Met Glu Gln
65 70 75 80
Ser Pro Asp Met His Asn Ala Glu Ile Ser Lys Arg Leu Gly Lys Arg
85 90 95
Trp Lys Leu Leu Lys Asp Ser Asp Lys Ile Pro Phe Ile Arg Glu Ala
100 105 110
Glu Arg Leu Arg Leu Lys His Met Ala Asp Tyr Pro Asp Tyr Lys Tyr
115 120 125
Arg Pro Arg Lys Lys Val Lys Ser Gly Asn Ala Asn Ser Ser Ser Ser
130 135 140
Ala Ala Ala Ser Ser Lys Pro Gly Glu Lys Gly Asp Lys Val Gly Gly
145 150 155 160
Ser Gly Gly Gly Gly His Gly Gly Gly Gly Gly Gly Gly Ser Ser Asn
165 170 175
Ala Gly Gly Gly Gly Gly Gly Ala Ser Gly Gly Gly Ala Asn Ser Lys
180 185 190
Pro Ala Gln Lys Lys Ser Cys Gly Ser Lys Val Ala Gly Gly Ala Gly
195 200 205
Gly Gly Val Ser Lys Pro His Ala Lys Leu Ile Leu Ala Gly Gly Gly
210 215 220
Gly Gly Gly Lys Ala Ala Ala Ala Ala Ala Ala Ser Phe Ala Ala Glu
225 230 235 240
Gln Ala Gly Ala Ala Ala Leu Leu Pro Leu Gly Ala Ala Ala Asp His
245 250 255
His Ser Leu Tyr Lys Ala Arg Thr Pro Ser Ala Ser Ala Ser Ala Ser
260 265 270
Ser Ala Ala Ser Ala Ser Ala Ala Leu Ala Ala Pro Gly Lys His Leu
275 280 285
Ala Glu Lys Lys Val Lys Arg Val Tyr Leu Phe Gly Gly Leu Gly Thr
290 295 300
Ser Ser Ser Pro Val Gly Gly Val Gly Ala Gly Ala Asp Pro Ser Asp
305 310 315 320
Pro Leu Gly Leu Tyr Glu Glu Glu Gly Ala Gly Cys Ser Pro Asp Ala
325 330 335

Pro Ser Leu Ser Gly Arg Ser Ser Ala Ala Ser Ser Pro Ala Ala Gly
340 345 350
Arg Ser Pro Ala Asp His Arg Gly Tyr Ala Ser Leu Arg Ala Ala Ser
355 360 365
Pro Ala Pro Ser Ser Ala Pro Ser His Ala Ser Ser Ser Ala Ser Ser
370 375 380
His Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser Asp Asp Glu
385 390 395 400
Phe Glu Asp Asp Leu Leu Asp Leu Asn Pro Ser Ser Asn Phe Glu Ser
405 410 415
Met Ser Leu Gly Ser Phe Ser Ser Ser Ser Ala Leu Asp Arg Asp Leu
420 425 430
Asp Phe Asn Phe Glu Pro Gly Ser Gly Ser His Phe Glu Phe Pro Asp
435 440 445
Tyr Cys Thr Pro Glu Val Ser Glu Met Ile Ser Gly Asp Trp Leu Glu
450 455 460
Ser Ser Ile Ser Asn Leu Val Phe Thr Tyr
465 470

<210> 121
<211> 357
<212> PRT
<213> Homo sapiens

<400> 121
Met Ala Ala Ala Ala Lys Pro Asn Asn Leu Ser Leu Val Val His Gly
1 5 10 15
Pro Gly Asp Leu Arg Leu Glu Asn Tyr Pro Ile Pro Glu Pro Gly Pro
20 25 30
Asn Glu Val Leu Leu Arg Met His Ser Val Gly Ile Cys Gly Ser Asp
35 40 45
Val His Tyr Trp Glu Tyr Gly Arg Ile Gly Asn Phe Ile Val Lys Lys
50 55 60
Pro Met Val Leu Gly His Glu Ala Ser Gly Thr Val Glu Lys Val Gly
65 70 75 80
Ser Ser Val Lys His Leu Lys Pro Gly Asp Arg Val Ala Ile Glu Pro
85 90 95
Gly Ala Pro Arg Glu Asn Asp Glu Phe Cys Lys Met Gly Arg Tyr Asn
100 105 110
Leu Ser Pro Ser Ile Phe Phe Cys Ala Thr Pro Pro Asp Asp Gly Asn
115 120 125
Leu Cys Arg Phe Tyr Lys His Asn Ala Ala Phe Cys Tyr Lys Leu Pro
130 135 140
Asp Asn Val Thr Phe Glu Glu Gly Ala Leu Ile Glu Pro Leu Ser Val
145 150 155 160
Gly Ile His Ala Cys Arg Arg Gly Gly Val Thr Leu Gly His Lys Val
165 170 175
Leu Val Cys Gly Ala Gly Pro Ile Gly Met Val Thr Leu Leu Val Ala
180 185 190
Lys Ala Met Gly Ala Ala Gln Val Val Val Thr Asp Leu Ser Ala Thr
195 200 205
Arg Leu Ser Lys Ala Lys Glu Ile Gly Ala Asp Leu Val Leu Gln Ile
210 215 220
Ser Lys Glu Ser Pro Gln Glu Ile Ala Arg Lys Val Glu Gly Gln Leu
225 230 235 240
Gly Cys Lys Pro Glu Val Thr Ile Glu Cys Thr Gly Ala Glu Ala Ser
245 250 255
Ile Gln Ala Gly Ile Tyr Ala Thr Arg Ser Gly Gly Thr Leu Val Leu
260 265 270
Val Gly Leu Gly Ser Glu Met Thr Thr Val Pro Leu Leu His Ala Ala
275 280 285
Ile Arg Glu Val Asp Ile Lys Gly Val Phe Arg Tyr Cys Asn Thr Trp
290 295 300
Pro Val Ala Ile Ser Met Leu Ala Ser Lys Ser Val Asn Val Lys Pro
305 310 315 320
Leu Val Thr His Arg Phe Pro Leu Glu Lys Ala Leu Glu Ala Phe Glu

325 330 335
Thr Phe Lys Lys Gly Leu Gly Leu Lys Ile Met Leu Lys Cys Asp Pro
340 345 350
Ser Asp Gln Asn Pro
355

<210> 122
<211> 470
<212> PRT
<213> Homo sapiens

<400> 122
Met Lys Phe Leu Leu Ile Leu Leu Leu Gln Ala Thr Ala Ser Gly Ala
1 5 10 15
Leu Pro Leu Asn Ser Ser Thr Ser Leu Glu Lys Asn Asn Val Leu Phe
20 25 30
Gly Glu Arg Tyr Leu Glu Lys Phe Tyr Gly Leu Glu Ile Asn Lys Leu
35 40 45
Pro Val Thr Lys Met Lys Tyr Ser Gly Asn Leu Met Lys Glu Lys Ile
50 55 60
Gln Glu Met Gln His Phe Leu Gly Leu Lys Val Thr Gly Gln Leu Asp
65 70 75 80
Thr Ser Thr Leu Glu Met Met His Ala Pro Arg Cys Gly Val Pro Asp
85 90 95
Leu His His Phe Arg Glu Met Pro Gly Gly Pro Val Trp Arg Lys His
100 105 110
Tyr Ile Thr Tyr Arg Ile Asn Asn Tyr Thr Pro Asp Met Asn Arg Glu
115 120 125
Asp Val Asp Tyr Ala Ile Arg Lys Ala Phe Gln Val Trp Ser Asn Val
130 135 140
Thr Pro Leu Lys Phe Ser Lys Ile Asn Thr Gly Met Ala Asp Ile Leu
145 150 155 160
Val Val Phe Ala Arg Gly Ala His Gly Asp Phe His Ala Phe Asp Gly
165 170 175
Lys Gly Gly Ile Leu Ala His Ala Phe Gly Pro Gly Ser Gly Ile Gly
180 185 190
Gly Asp Ala His Phe Asp Glu Asp Glu Phe Trp Thr Thr His Ser Gly
195 200 205
Gly Thr Asn Leu Phe Leu Thr Ala Val His Glu Ile Gly His Ser Leu
210 215 220
Gly Leu Gly His Ser Ser Asp Pro Lys Ala Val Met Phe Pro Thr Tyr
225 230 235 240
Lys Tyr Val Asp Ile Asn Thr Phe Arg Leu Ser Ala Asp Asp Ile Arg
245 250 255
Gly Ile Gln Ser Leu Tyr Gly Asp Pro Lys Glu Asn Gln Arg Leu Pro
260 265 270
Asn Pro Asp Asn Ser Glu Pro Ala Leu Cys Asp Pro Asn Leu Ser Phe
275 280 285
Asp Ala Val Thr Thr Val Gly Asn Lys Ile Phe Phe Phe Lys Asp Arg
290 295 300
Phe Phe Trp Leu Lys Val Ser Glu Arg Pro Lys Thr Ser Val Asn Leu
305 310 315 320
Ile Ser Ser Leu Trp Pro Thr Leu Pro Ser Gly Ile Glu Ala Ala Tyr
325 330 335
Glu Ile Glu Ala Arg Asn Gln Val Phe Leu Phe Lys Asp Asp Lys Tyr
340 345 350
Trp Leu Ile Ser Asn Leu Arg Pro Glu Pro Asn Tyr Pro Lys Ser Ile
355 360 365
His Ser Phe Gly Phe Pro Asn Phe Val Lys Lys Ile Asp Ala Ala Val
370 375 380
Phe Asn Pro Arg Phe Tyr Arg Thr Tyr Phe Phe Val Asp Asn Gln Tyr
385 390 395 400
Trp Arg Tyr Asp Glu Arg Arg Gln Met Met Asp Pro Gly Tyr Pro Lys
405 410 415
Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile Asp Ala Val
420 425 430

Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly Ser Asn Gln
435 440 445
Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr Leu Lys Ser
450 455 460
Asn Ser Trp Phe Gly Cys
465 470

<210> 123
<211> 165
<212> PRT
<213> Homo sapiens

<400> 123
Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
1 5 10 15
Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
20 25 30
Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
35 40 45
Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
50 55 60
Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65 70 75 80
Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
85 90 95
Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
100 105 110
Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
115 120 125
Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
130 135 140
Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145 150 155 160
Tyr Cys Ile Gly Gly
165

<210> 124
<211> 2828
<212> PRT
<213> Homo sapiens

<400> 124
Met Pro Lys Arg Ala His Trp Gly Ala Leu Ser Val Val Leu Ile Leu
1 5 10 15
Leu Trp Gly His Pro Arg Val Ala Leu Ala Cys Pro His Pro Cys Ala
20 25 30
Cys Tyr Val Pro Ser Glu Val His Cys Thr Phe Arg Ser Leu Ala Ser
35 40 45
Val Pro Ala Gly Ile Ala Arg His Val Glu Arg Ile Asn Leu Gly Phe
50 55 60
Asn Ser Ile Gln Ala Leu Ser Glu Thr Ser Phe Ala Gly Leu Thr Lys
65 70 75 80
Leu Glu Leu Leu Met Ile His Gly Asn Glu Ile Pro Ser Ile Pro Asp
85 90 95
Gly Ala Leu Arg Asp Leu Ser Ser Leu Gln Val Phe Lys Phe Ser Tyr
100 105 110
Asn Lys Leu Arg Val Ile Thr Gly Gln Thr Leu Gln Gly Leu Ser Asn
115 120 125
Leu Met Arg Leu His Ile Asp His Asn Lys Ile Glu Phe Ile His Pro
130 135 140
Gln Ala Phe Asn Gly Leu Thr Ser Leu Arg Leu Leu His Leu Glu Gly
145 150 155 160
Asn Leu Leu His Gln Leu His Pro Ser Thr Phe Ser Thr Phe Thr Phe
165 170 175
Leu Asp Tyr Phe Arg Leu Ser Thr Ile Arg His Leu Tyr Leu Ala Glu

180 185 190
Asn Met Val Arg Thr Leu Pro Ala Ser Met Leu Arg Asn Met Pro Leu
195 200 205
Leu Glu Asn Leu Tyr Leu Gln Gly Asn Pro Trp Thr Cys Asp Cys Glu
210 215 220
Met Arg Trp Phe Leu Glu Trp Asp Ala Lys Ser Arg Gly Ile Leu Lys
225 230 235 240
Cys Lys Lys Asp Lys Ala Tyr Glu Gly Gly Gln Leu Cys Ala Met Cys
245 250 255
Phe Ser Pro Lys Lys Leu Tyr Lys His Glu Ile His Lys Leu Lys Asp
260 265 270
Met Thr Cys Leu Lys Pro Ser Ile Glu Ser Pro Leu Arg Gln Asn Arg
275 280 285
Ser Arg Ser Ile Glu Glu Glu Gln Glu Gln Glu Glu Asp Gly Gly Ser
290 295 300
Gln Leu Ile Leu Glu Lys Phe Gln Leu Pro Gln Trp Ser Ile Ser Leu
305 310 315 320
Asn Met Thr Asp Glu His Gly Asn Met Val Asn Leu Val Cys Asp Ile
325 330 335
Lys Lys Pro Met Asp Val Tyr Lys Ile His Leu Asn Gln Thr Asp Pro
340 345 350
Pro Asp Ile Asp Ile Asn Ala Thr Val Ala Leu Asp Phe Glu Cys Pro
355 360 365
Met Thr Arg Glu Asn Tyr Glu Lys Leu Trp Lys Leu Ile Ala Tyr Tyr
370 375 380
Ser Glu Val Pro Val Lys Leu His Arg Glu Leu Met Leu Ser Lys Asp
385 390 395 400
Pro Arg Val Ser Tyr Gln Tyr Arg Gln Asp Ala Asp Glu Glu Ala Leu
405 410 415
Tyr Tyr Thr Gly Val Arg Ala Gln Ile Leu Ala Glu Pro Glu Trp Val
420 425 430
Met Gln Pro Ser Ile Asp Ile Gln Leu Asn Arg Arg Gln Ser Thr Ala
435 440 445
Lys Lys Val Leu Leu Ser Tyr Tyr Thr Gln Tyr Ser Gln Thr Ile Ser
450 455 460
Thr Lys Asp Thr Arg Gln Ala Arg Gly Arg Ser Trp Val Met Ile Glu
465 470 475 480
Pro Ser Gly Ala Val Gln Arg Asp Gln Thr Val Leu Glu Gly Gly Pro
485 490 495
Cys Gln Leu Ser Cys Asn Val Lys Ala Ser Glu Ser Pro Ser Ile Phe
500 505 510
Trp Val Leu Pro Asp Gly Ser Ile Leu Lys Ala Pro Met Asp Asp Pro
515 520 525
Asp Ser Lys Phe Ser Ile Leu Ser Ser Gly Trp Leu Arg Ile Lys Ser
530 535 540
Met Glu Pro Ser Asp Ser Gly Leu Tyr Gln Cys Ile Ala Gln Val Arg
545 550 555 560
Asp Glu Met Asp Arg Met Val Tyr Arg Val Leu Val Gln Ser Pro Ser
565 570 575
Thr Gln Pro Ala Glu Lys Asp Thr Val Thr Ile Gly Lys Asn Pro Gly
580 585 590
Glu Ser Val Thr Leu Pro Cys Asn Ala Leu Ala Ile Pro Glu Ala His
595 600 605
Leu Ser Trp Ile Leu Pro Asn Arg Arg Ile Ile Asn Asp Leu Ala Asn
610 615 620
Thr Ser His Val Tyr Met Leu Pro Asn Gly Thr Leu Ser Ile Pro Lys
625 630 635 640
Val Gln Val Ser Asp Ser Gly Tyr Tyr Arg Cys Val Ala Val Asn Gln
645 650 655
Gln Gly Ala Asp His Phe Thr Val Gly Ile Thr Val Thr Lys Lys Gly
660 665 670
Ser Gly Leu Pro Ser Lys Arg Gly Arg Arg Pro Gly Ala Lys Ala Leu
675 680 685
Ser Arg Val Arg Glu Asp Ile Val Glu Asp Glu Gly Gly Ser Gly Met
690 695 700
Gly Asp Glu Glu Asn Thr Ser Arg Arg Leu Leu His Pro Lys Asp Gln
705 710 715 720

Glu Val Phe Leu Lys Thr Lys Asp Asp Ala Ile Asn Gly Asp Lys Lys
725 730 735
Ala Lys Lys Gly Arg Arg Lys Leu Lys Leu Trp Lys His Ser Glu Lys
740 745 750
Glu Pro Glu Thr Asn Val Ala Glu Gly Arg Arg Val Phe Glu Ser Arg
755 760 765
Arg Arg Ile Asn Met Ala Asn Lys Gln Ile Asn Pro Glu Arg Trp Ala
770 775 780
Asp Ile Leu Ala Lys Val Arg Gly Lys Asn Leu Pro Lys Gly Thr Glu
785 790 795 800
Val Pro Pro Leu Ile Lys Thr Thr Ser Pro Pro Ser Leu Ser Leu Glu
805 810 815
Val Thr Pro Pro Phe Pro Ala Val Ser Pro Pro Ser Ala Ser Pro Val
820 825 830
Gln Thr Val Thr Ser Ala Glu Glu Ser Ser Ala Asp Val Pro Leu Leu
835 840 845
Gly Glu Glu Glu His Val Leu Gly Thr Ile Ser Ser Ala Ser Met Gly
850 855 860
Leu Glu His Asn His Asn Gly Val Ile Leu Val Glu Pro Glu Val Thr
865 870 875 880
Ser Thr Pro Leu Glu Glu Val Val Asp Asp Leu Ser Glu Lys Thr Glu
885 890 895
Glu Ile Thr Ser Thr Glu Gly Asp Leu Lys Gly Thr Ala Ala Pro Thr
900 905 910
Leu Ile Ser Glu Pro Tyr Glu Pro Ser Pro Thr Leu His Thr Leu Asp
915 920 925
Thr Val Tyr Glu Lys Pro Thr His Glu Glu Thr Ala Thr Glu Gly Trp
930 935 940
Ser Ala Ala Asp Val Gly Ser Ser Pro Glu Pro Thr Ser Ser Glu Tyr
945 950 955 960
Glu Pro Pro Leu Asp Ala Val Ser Leu Ala Glu Ser Glu Pro Met Gln
965 970 975
Tyr Phe Asp Pro Asp Leu Glu Thr Lys Ser Gln Pro Asp Glu Asp Lys
980 985 990
Met Lys Glu Asp Thr Phe Ala His Leu Thr Pro Thr Pro Thr Ile Trp
995 1000 1005
Val Asn Asp Ser Ser Thr Ser Gln Leu Phe Glu Asp Ser Thr Ile Gly
1010 1015 1020
Glu Pro Gly Val Pro Gly Gln Ser His Leu Gln Gly Leu Thr Asp Asn
1025 1030 1035 1040
Ile His Leu Val Lys Ser Ser Leu Ser Thr Gln Asp Thr Leu Leu Ile
1045 1050 1055
Lys Lys Gly Met Lys Glu Met Ser Gln Thr Leu Gln Gly Gly Asn Met
1060 1065 1070
Leu Glu Gly Asp Pro Thr His Ser Arg Ser Ser Glu Ser Glu Gly Gln
1075 1080 1085
Glu Ser Lys Ser Ile Thr Leu Pro Asp Ser Thr Leu Gly Ile Met Ser
1090 1095 1100
Ser Met Ser Pro Val Lys Lys Pro Ala Glu Thr Thr Val Gly Thr Leu
1105 1110 1115 1120
Leu Asp Lys Asp Thr Thr Thr Val Thr Thr Thr Pro Arg Gln Lys Val
1125 1130 1135
Ala Pro Ser Ser Thr Met Ser Thr His Pro Ser Arg Arg Arg Pro Asn
1140 1145 1150
Gly Arg Arg Arg Leu Arg Pro Asn Lys Phe Arg His Arg His Lys Gln
1155 1160 1165
Thr Pro Pro Thr Thr Phe Ala Pro Ser Glu Thr Phe Ser Thr Gln Pro
1170 1175 1180
Thr Gln Ala Pro Asp Ile Lys Ile Ser Ser Gln Val Glu Ser Ser Leu
1185 1190 1195 1200
Val Pro Thr Ala Trp Val Asp Asn Thr Val Asn Thr Pro Lys Gln Leu
1205 1210 1215
Glu Met Glu Lys Asn Ala Glu Pro Thr Ser Lys Gly Thr Pro Arg Arg
1220 1225 1230
Lys His Gly Lys Arg Pro Asn Lys His Arg Tyr Thr Pro Ser Thr Val
1235 1240 1245
Ser Ser Arg Ala Ser Gly Ser Lys Pro Ser Pro Ser Pro Glu Asn Lys

1250 1255 1260
His Arg Asn Ile Val Thr Pro Ser Ser Glu Thr Ile Leu Leu Pro Arg
1265 1270 1275 1280
Thr Val Ser Leu Lys Thr Glu Gly Pro Tyr Asp Ser Leu Asp Tyr Met
1285 1290 1295
Thr Thr Thr Arg Lys Ile Tyr Ser Ser Tyr Pro Lys Val Gln Glu Thr
1300 1305 1310
Leu Pro Val Thr Tyr Lys Pro Thr Ser Asp Gly Lys Glu Ile Lys Asp
1315 1320 1325
Asp Val Ala Thr Asn Val Asp Lys His Lys Ser Asp Ile Leu Val Thr
1330 1335 1340
Gly Glu Ser Ile Thr Asn Ala Ile Pro Thr Ser Arg Ser Leu Val Ser
1345 1350 1355 1360
Thr Met Gly Glu Phe Lys Glu Glu Ser Ser Pro Val Gly Phe Pro Gly
1365 1370 1375
Thr Pro Thr Trp Asn Pro Ser Arg Thr Ala Gln Pro Gly Arg Leu Gln
1380 1385 1390
Thr Asp Ile Pro Val Thr Thr Ser Gly Glu Asn Leu Thr Asp Pro Pro
1395 1400 1405
Leu Leu Lys Glu Leu Glu Asp Val Asp Phe Thr Ser Glu Phe Leu Ser
1410 1415 1420
Ser Leu Thr Val Ser Thr Pro Phe His Gln Glu Glu Ala Gly Ser Ser
1425 1430 1435 1440
Thr Thr Leu Ser Ser Ile Lys Val Glu Val Ala Ser Ser Gln Ala Glu
1445 1450 1455
Thr Thr Thr Leu Asp Gln Asp His Leu Glu Thr Thr Val Ala Ile Leu
1460 1465 1470
Leu Ser Glu Thr Arg Pro Gln Asn His Thr Pro Thr Ala Ala Arg Met
1475 1480 1485
Lys Glu Pro Ala Ser Ser Ser Pro Ser Thr Ile Leu Met Ser Leu Gly
1490 1495 1500
Gln Thr Thr Thr Thr Lys Pro Ala Leu Pro Ser Pro Arg Ile Ser Gln
1505 1510 1515 1520
Ala Ser Arg Asp Ser Lys Glu Asn Val Phe Leu Asn Tyr Val Gly Asn
1525 1530 1535
Pro Glu Thr Glu Ala Thr Pro Val Asn Asn Glu Gly Thr Gln His Met
1540 1545 1550
Ser Gly Pro Asn Glu Leu Ser Thr Pro Ser Ser Asp Arg Asp Ala Phe
1555 1560 1565
Asn Leu Ser Thr Lys Leu Glu Leu Glu Lys Gln Val Phe Gly Ser Arg
1570 1575 1580
Ser Leu Pro Arg Gly Pro Asp Ser Gln Arg Gln Asp Gly Arg Val His
1585 1590 1595 1600
Ala Ser His Gln Leu Thr Arg Val Pro Ala Lys Pro Ile Leu Pro Thr
1605 1610 1615
Ala Thr Val Arg Leu Pro Glu Met Ser Thr Gln Ser Ala Ser Arg Tyr
1620 1625 1630
Phe Val Thr Ser Gln Ser Pro Arg His Trp Thr Asn Lys Pro Glu Ile
1635 1640 1645
Thr Thr Tyr Pro Ser Gly Ala Leu Pro Glu Asn Lys Gln Phe Thr Thr
1650 1655 1660
Pro Arg Leu Ser Ser Thr Thr Ile Pro Leu Pro Leu His Met Ser Lys
1665 1670 1675 1680
Pro Ser Ile Pro Ser Lys Phe Thr Asp Arg Arg Thr Asp Gln Phe Asn
1685 1690 1695
Gly Tyr Ser Lys Val Phe Gly Asn Asn Asn Ile Pro Glu Ala Arg Asn
1700 1705 1710
Pro Val Gly Lys Pro Pro Ser Pro Arg Ile Pro His Tyr Ser Asn Gly
1715 1720 1725
Arg Leu Pro Phe Phe Thr Asn Lys Thr Leu Ser Phe Pro Gln Leu Gly
1730 1735 1740
Val Thr Arg Arg Pro Gln Ile Pro Thr Ser Pro Ala Pro Val Met Arg
1745 1750 1755 1760
Glu Arg Lys Val Ile Pro Gly Ser Tyr Asn Arg Ile His Ser His Ser
1765 1770 1775
Thr Phe His Leu Asp Phe Gly Pro Pro Ala Pro Pro Leu Leu His Thr
1780 1785 1790

Pro Gln Thr Thr Gly Ser Pro Ser Thr Asn Leu Gln Asn Ile Pro Met
1795 1800 1805
Val Ser Ser Thr Gln Ser Ser Ile Ser Phe Ile Thr Ser Ser Val Gln
1810 1815 1820
Ser Ser Gly Ser Phe His Gln Ser Ser Ser Lys Phe Phe Ala Gly Gly
1825 1830 1835 1840
Pro Pro Ala Ser Lys Phe Trp Ser Leu Gly Glu Lys Pro Gln Ile Leu
1845 1850 1855
Thr Lys Ser Pro Gln Thr Val Ser Val Thr Ala Glu Thr Asp Thr Val
1860 1865 1870
Phe Pro Cys Glu Ala Thr Gly Lys Pro Lys Pro Phe Val Thr Trp Thr
1875 1880 1885
Lys Val Ser Thr Gly Ala Leu Met Thr Pro Asn Thr Arg Ile Gln Arg
1890 1895 1900
Phe Glu Val Leu Lys Asn Gly Thr Leu Val Ile Arg Lys Val Gln Val
1905 1910 1915 1920
Gln Asp Arg Gly Gln Tyr Met Cys Thr Ala Ser Asn Leu His Gly Leu
1925 1930 1935
Asp Arg Met Val Val Leu Leu Ser Val Thr Val Gln Gln Pro Gln Ile
1940 1945 1950
Leu Ala Ser His Tyr Gln Asp Val Thr Val Tyr Leu Gly Asp Thr Ile
1955 1960 1965
Ala Met Glu Cys Leu Ala Lys Gly Thr Pro Ala Pro Gln Ile Ser Trp
1970 1975 1980
Ile Phe Pro Asp Arg Arg Val Trp Gln Thr Val Ser Pro Val Glu Ser
1985 1990 1995 2000
Arg Ile Thr Leu His Glu Asn Arg Thr Leu Ser Ile Lys Glu Ala Ser
2005 2010 2015
Phe Ser Asp Arg Gly Val Tyr Lys Cys Val Ala Ser Asn Ala Ala Gly
2020 2025 2030
Ala Asp Ser Leu Ala Ile Arg Leu His Val Ala Ala Leu Pro Pro Val
2035 2040 2045
Ile His Gln Glu Lys Leu Glu Asn Ile Ser Leu Pro Pro Gly Leu Ser
2050 2055 2060
Ile His Ile His Cys Thr Ala Lys Ala Ala Pro Leu Pro Ser Val Arg
2065 2070 2075 2080
Trp Val Leu Gly Asp Gly Thr Gln Ile Arg Pro Ser Gln Phe Leu His
2085 2090 2095
Gly Asn Leu Phe Val Phe Pro Asn Gly Thr Leu Tyr Ile Arg Asn Leu
2100 2105 2110
Ala Pro Lys Asp Ser Gly Arg Tyr Glu Cys Val Ala Ala Asn Leu Val
2115 2120 2125
Gly Ser Ala Arg Arg Thr Val Gln Leu Asn Val Gln Arg Ala Ala Ala
2130 2135 2140
Asn Ala Arg Ile Thr Gly Thr Ser Pro Arg Arg Thr Asp Val Arg Tyr
2145 2150 2155 2160
Gly Gly Thr Leu Lys Leu Asp Cys Ser Ala Ser Gly Asp Pro Trp Pro
2165 2170 2175
Arg Ile Leu Trp Arg Leu Pro Ser Lys Arg Met Ile Asp Ala Leu Phe
2180 2185 2190
Ser Phe Asp Ser Arg Ile Lys Val Phe Ala Asn Gly Thr Leu Val Val
2195 2200 2205
Lys Ser Val Thr Asp Lys Asp Ala Gly Asp Tyr Leu Cys Val Ala Arg
2210 2215 2220
Asn Lys Val Gly Asp Asp Tyr Val Val Leu Lys Val Asp Val Val Met
2225 2230 2235 2240
Lys Pro Ala Lys Ile Glu His Lys Glu Glu Asn Asp His Lys Val Phe
2245 2250 2255
Tyr Gly Gly Asp Leu Lys Val Asp Cys Val Ala Thr Gly Leu Pro Asn
2260 2265 2270
Pro Glu Ile Ser Trp Ser Leu Pro Asp Gly Ser Leu Val Asn Ser Phe
2275 2280 2285
Met Gln Ser Asp Asp Ser Gly Gly Arg Thr Lys Arg Tyr Val Val Phe
2290 2295 2300
Asn Asn Gly Thr Leu Tyr Phe Asn Glu Val Gly Met Arg Glu Glu Gly
2305 2310 2315 2320
Asp Tyr Thr Cys Phe Ala Glu Asn Gln Val Gly Lys Asp Glu Met Arg

2325 2330 2335
Val Arg Val Lys Val Val Thr Ala Pro Ala Thr Ile Arg Asn Lys Thr
2340 2345 2350
Tyr Leu Ala Val Gln Val Pro Tyr Gly Asp Val Val Thr Val Ala Cys
2355 2360 2365
Glu Ala Lys Gly Glu Pro Met Pro Lys Val Thr Trp Leu Ser Pro Thr
2370 2375 2380
Asn Lys Val Ile Pro Thr Ser Ser Glu Lys Tyr Gln Ile Tyr Gln Asp
2385 2390 2395 2400
Gly Thr Leu Leu Ile Gln Lys Ala Gln Arg Ser Asp Ser Gly Asn Tyr
2405 2410 2415
Thr Cys Leu Val Arg Asn Ser Ala Gly Glu Asp Arg Lys Thr Val Trp
2420 2425 2430
Ile His Val Asn Val Gln Pro Pro Lys Ile Asn Gly Asn Pro Asn Pro
2435 2440 2445
Ile Thr Thr Val Arg Glu Ile Ala Ala Gly Gly Ser Arg Lys Leu Ile
2450 2455 2460
Asp Cys Lys Ala Glu Gly Ile Pro Thr Pro Arg Val Leu Trp Ala Phe
2465 2470 2475 2480
Pro Glu Gly Val Val Leu Pro Ala Pro Tyr Tyr Gly Asn Arg Ile Thr
2485 2490 2495
Val His Gly Asn Gly Ser Leu Asp Ile Arg Ser Leu Arg Lys Ser Asp
2500 2505 2510
Ser Val Gln Leu Val Cys Met Ala Arg Asn Glu Gly Gly Glu Ala Arg
2515 2520 2525
Leu Ile Val Gln Leu Thr Val Leu Glu Pro Met Glu Lys Pro Ile Phe
2530 2535 2540
His Asp Pro Ile Ser Glu Lys Ile Thr Ala Met Ala Gly His Thr Ile
2545 2550 2555 2560
Ser Leu Asn Cys Ser Ala Ala Gly Thr Pro Thr Pro Ser Leu Val Trp
2565 2570 2575
Val Leu Pro Asn Gly Thr Asp Leu Gln Ser Gly Gln Gln Leu Gln Arg
2580 2585 2590
Phe Tyr His Lys Ala Asp Gly Met Leu His Ile Ser Gly Leu Ser Ser
2595 2600 2605
Val Asp Ala Gly Ala Tyr Arg Cys Val Ala Arg Asn Ala Ala Gly His
2610 2615 2620
Thr Glu Arg Leu Val Ser Leu Lys Val Gly Leu Lys Pro Glu Ala Asn
2625 2630 2635 2640
Lys Gln Tyr His Asn Leu Val Ser Ile Ile Asn Gly Glu Thr Leu Lys
2645 2650 2655
Leu Pro Cys Thr Pro Pro Gly Ala Gly Gln Gly Arg Phe Ser Trp Thr
2660 2665 2670
Leu Pro Asn Gly Met His Leu Glu Gly Pro Gln Thr Leu Gly Arg Val
2675 2680 2685
Ser Leu Leu Asp Asn Gly Thr Leu Thr Val Arg Glu Ala Ser Val Phe
2690 2695 2700
Asp Arg Gly Thr Tyr Val Cys Arg Met Glu Thr Glu Tyr Gly Pro Ser
2705 2710 2715 2720
Val Thr Ser Ile Pro Val Ile Val Ile Ala Tyr Pro Pro Arg Ile Thr
2725 2730 2735
Ser Glu Pro Thr Pro Val Ile Tyr Thr Arg Pro Gly Asn Thr Val Lys
2740 2745 2750
Leu Asn Cys Met Ala Met Gly Ile Pro Lys Ala Asp Ile Thr Trp Glu
2755 2760 2765
Leu Pro Asp Lys Ser His Leu Lys Ala Gly Val Gln Ala Arg Leu Tyr
2770 2775 2780
Gly Asn Arg Phe Leu His Pro Gln Gly Ser Leu Thr Ile Gln His Ala
2785 2790 2795 2800
Thr Gln Arg Asp Ala Gly Phe Tyr Lys Cys Met Ala Lys Asn Ile Leu
2805 2810 2815
Gly Ser Asp Ser Lys Thr Thr Tyr Ile His Val Phe
2820 2825

<210> 125
<211> 1464

<212> PRT
<213> Homo sapiens

<400> 125

```
Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu Leu Leu Ala Ala Thr
 1               5                  10                  15
Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
            20                  25                  30
Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
        35                  40                  45
Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
    50                  55                  60
Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
65                  70                  75                  80
Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
                85                  90                  95
Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
            100                 105                 110
Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro
        115                 120                 125
Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro
    130                 135                 140
Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala
145                 150                 155                 160
Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser
                165                 170                 175
Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro
            180                 185                 190
Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro
        195                 200                 205
Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly
    210                 215                 220
Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg
225                 230                 235                 240
Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro
                245                 250                 255
Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly
            260                 265                 270
Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu
        275                 280                 285
Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg
    290                 295                 300
Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly
305                 310                 315                 320
Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro
                325                 330                 335
Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys
            340                 345                 350
Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly
        355                 360                 365
Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro
    370                 375                 380
Ala Gly Asn Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Ala Asn
385                 390                 395                 400
Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly
                405                 410                 415
Pro Ser Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys Gly Asn
            420                 425                 430
Ser Gly Glu Pro Gly Ala Pro Gly Ser Lys Gly Asp Thr Gly Ala Lys
        435                 440                 445
Gly Glu Pro Gly Pro Val Gly Val Gln Gly Pro Pro Gly Pro Ala Gly
    450                 455                 460
Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu
465                 470                 475                 480
Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro
                485                 490                 495
Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly
```

500 505 510
Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg
515 520 525
Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro
530 535 540
Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly
545 550 555 560
Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln
565 570 575
Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro
580 585 590
Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly
595 600 605
Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro
610 615 620
Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro
625 630 635 640
Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly
645 650 655
Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro
660 665 670
Ser Gly Ala Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Val Gln
675 680 685
Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly
690 695 700
Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Ser
705 710 715 720
Gln Gly Ala Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala Ala
725 730 735
Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly Asp Ala Gly Pro Lys Gly
740 745 750
Ala Asp Gly Ser Pro Gly Lys Asp Gly Val Arg Gly Leu Thr Gly Pro
755 760 765
Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys Gly Glu Ser
770 775 780
Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg Gly Ala Pro Gly
785 790 795 800
Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly Pro
805 810 815
Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Pro Gly Asp Ala
820 825 830
Gly Ala Lys Gly Asp Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly
835 840 845
Pro Pro Gly Pro Ile Gly Asn Val Gly Ala Pro Gly Ala Lys Gly Ala
850 855 860
Arg Gly Ser Ala Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ala Ala
865 870 875 880
Gly Arg Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly
885 890 895
Pro Pro Gly Pro Ala Gly Lys Glu Gly Gly Lys Gly Pro Arg Gly Glu
900 905 910
Thr Gly Pro Ala Gly Arg Pro Gly Glu Val Gly Pro Pro Gly Pro Pro
915 920 925
Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly
930 935 940
Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly Gln Arg Gly Val
945 950 955 960
Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu Pro
965 970 975
Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Pro Ser Gly Ala Ser Gly
980 985 990
Glu Arg Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Leu Ala Gly Pro
995 1000 1005
Pro Gly Glu Ser Gly Arg Glu Gly Ala Pro Ala Ala Glu Gly Ser Pro
1010 1015 1020
Gly Arg Asp Gly Ser Pro Gly Ala Lys Gly Asp Arg Gly Glu Thr Gly
1025 1030 1035 1040

Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Pro
1045 1050 1055
Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Thr Gly Pro Ala
1060 1065 1070
Gly Pro Ala Gly Pro Val Gly Pro Val Gly Ala Arg Gly Pro Ala Gly
1075 1080 1085
Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Gln Gly Asp
1090 1095 1100
Arg Gly Ile Lys Gly His Arg Gly Phe Ser Gly Leu Gln Gly Pro Pro
1105 1110 1115 1120
Gly Pro Pro Gly Ser Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly
1125 1130 1135
Pro Ala Gly Pro Arg Gly Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys
1140 1145 1150
Asp Gly Leu Asn Gly Leu Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg
1155 1160 1165
Gly Arg Thr Gly Asp Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly
1170 1175 1180
Pro Pro Gly Pro Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe
1185 1190 1195 1200
Leu Pro Gln Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr
1205 1210 1215
Arg Ala Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp
1220 1225 1230
Thr Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro
1235 1240 1245
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met
1250 1255 1260
Cys His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln
1265 1270 1275 1280
Gly Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly
1285 1290 1295
Glu Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp
1300 1305 1310
Tyr Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu
1315 1320 1325
Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp
1330 1335 1340
Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr
1345 1350 1355 1360
Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr
1365 1370 1375
Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly
1380 1385 1390
Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr
1395 1400 1405
Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys
1410 1415 1420
Thr Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile
1425 1430 1435 1440
Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe
1445 1450 1455
Asp Val Gly Pro Val Cys Phe Leu
1460

<210> 126
<211> 308
<212> PRT
<213> Homo sapiens

<400> 126
Met Pro Gly Gln Glu Leu Arg Thr Val Asn Gly Ser Gln Met Leu Leu
1 5 10 15
Val Leu Leu Val Leu Ser Trp Leu Pro His Gly Gly Ala Leu Ser Leu
20 25 30
Ala Glu Ala Ser Arg Ala Ser Phe Pro Gly Pro Ser Glu Leu His Ser

```
        35                  40                  45
Glu Asp Ser Arg Phe Arg Glu Leu Arg Lys Arg Tyr Glu Asp Leu Leu
    50                  55                  60
Thr Arg Leu Arg Ala Asn Gln Ser Trp Glu Asp Ser Asn Thr Asp Leu
65                  70                  75                  80
Val Pro Ala Pro Ala Val Arg Ile Leu Thr Pro Glu Val Arg Leu Gly
                85                  90                  95
Ser Gly Gly His Leu His Leu Arg Ile Ser Arg Ala Ala Leu Pro Glu
            100                 105                 110
Gly Leu Pro Glu Ala Ser Arg Leu His Arg Ala Leu Phe Arg Leu Ser
        115                 120                 125
Pro Thr Ala Ser Arg Ser Trp Asp Val Thr Arg Pro Leu Arg Arg Gln
    130                 135                 140
Leu Ser Leu Ala Arg Pro Gln Ala Pro Ala Leu His Leu Arg Leu Ser
145                 150                 155                 160
Pro Pro Pro Ser Gln Ser Asp Gln Leu Leu Ala Glu Ser Ser Ser Ala
                165                 170                 175
Arg Pro Gln Leu Glu Leu His Leu Arg Pro Gln Ala Ala Arg Gly Arg
            180                 185                 190
Arg Arg Ala Arg Ala Arg Asn Gly Asp Asp Cys Pro Leu Gly Pro Gly
        195                 200                 205
Arg Cys Cys Arg Leu His Thr Val Arg Ala Ser Leu Glu Asp Leu Gly
    210                 215                 220
Trp Ala Asp Trp Val Leu Ser Pro Arg Glu Val Gln Val Thr Met Cys
225                 230                 235                 240
Ile Gly Ala Cys Pro Ser Gln Phe Arg Ala Ala Asn Met His Ala Gln
                245                 250                 255
Ile Lys Thr Ser Leu His Arg Leu Lys Pro Asp Thr Glu Pro Ala Pro
            260                 265                 270
Cys Cys Val Pro Ala Ser Tyr Asn Pro Met Val Leu Ile Gln Lys Thr
        275                 280                 285
Asp Thr Gly Val Ser Leu Gln Thr Tyr Asp Asp Leu Leu Ala Lys Asp
    290                 295                 300
Cys His Cys Ile
305
```

<210> 127
<211> 359
<212> PRT
<213> Homo sapiens

<400> 127

```
Met Pro Ala His Leu Leu Gln Asp Asp Ile Ser Ser Ser Tyr Thr Thr
 1               5                  10                  15
Thr Thr Thr Ile Thr Ala Pro Pro Ser Arg Val Leu Gln Asn Gly Gly
            20                  25                  30
Asp Lys Leu Glu Thr Met Pro Leu Tyr Leu Glu Asp Asp Ile Arg Pro
        35                  40                  45
Asp Ile Lys Asp Asp Ile Tyr Asp Pro Thr Tyr Lys Asp Lys Glu Gly
    50                  55                  60
Pro Ser Pro Lys Val Glu Tyr Val Trp Arg Asn Ile Ile Leu Met Ser
65                  70                  75                  80
Leu Leu His Leu Gly Ala Leu Tyr Gly Ile Thr Leu Ile Pro Thr Cys
                85                  90                  95
Lys Phe Tyr Thr Trp Leu Trp Gly Val Phe Tyr Tyr Phe Val Ser Ala
            100                 105                 110
Leu Gly Ile Thr Ala Gly Ala His Arg Leu Trp Ser His Arg Ser Tyr
        115                 120                 125
Lys Ala Arg Leu Pro Leu Arg Leu Phe Leu Ile Ile Ala Asn Thr Met
    130                 135                 140
Ala Phe Gln Asn Asp Val Tyr Glu Trp Ala Arg Asp His Arg Ala His
145                 150                 155                 160
His Lys Phe Ser Glu Thr His Ala Asp Pro His Asn Ser Arg Arg Gly
                165                 170                 175
Phe Phe Phe Ser His Val Gly Trp Leu Leu Val Arg Lys His Pro Ala
            180                 185                 190
```

```
Val Lys Glu Lys Gly Ser Thr Leu Asp Leu Ser Asp Leu Glu Ala Glu
        195                 200                 205
Lys Leu Val Met Phe Gln Arg Arg Tyr Tyr Lys Pro Gly Leu Leu Leu
    210                 215                 220
Met Cys Phe Ile Leu Pro Thr Leu Val Pro Trp Tyr Phe Trp Gly Glu
225                 230                 235                 240
Thr Phe Gln Asn Ser Val Phe Val Ala Thr Phe Leu Arg Tyr Ala Val
                245                 250                 255
Val Leu Asn Ala Thr Trp Leu Val Asn Ser Ala Ala His Leu Phe Gly
            260                 265                 270
Tyr Arg Pro Tyr Asp Lys Asn Ile Ser Pro Arg Glu Asn Ile Leu Val
        275                 280                 285
Ser Leu Gly Ala Val Gly Glu Gly Phe His Asn Tyr His His Ser Phe
    290                 295                 300
Pro Tyr Asp Tyr Ser Ala Ser Glu Tyr Arg Trp His Ile Asn Phe Thr
305                 310                 315                 320
Thr Phe Phe Ile Asp Cys Met Ala Ala Leu Gly Leu Ala Tyr Asp Arg
                325                 330                 335
Lys Lys Val Ser Lys Ala Ala Ile Leu Ala Arg Ile Lys Arg Thr Gly
            340                 345                 350
Asp Gly Asn Tyr Lys Ser Gly
        355
```

<210> 128
<211> 96
<212> PRT
<213> Homo sapiens

<400> 128

```
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 1               5                  10                  15
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
            20                  25                  30
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
        35                  40                  45
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
    50                  55                  60
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
65                  70                  75                  80
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
                85                  90                  95
```

<210> 129
<211> 518
<212> PRT
<213> Homo sapiens

<400> 129

```
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
 1               5                  10                  15
Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
            20                  25                  30
Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
        35                  40                  45
Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
    50                  55                  60
Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65                  70                  75                  80
Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
                85                  90                  95
Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
            100                 105                 110
Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
        115                 120                 125
Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
```

130 135 140
Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145 150 155 160
Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
165 170 175
Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
180 185 190
Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
195 200 205
Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
210 215 220
Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
225 230 235 240
Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
245 250 255
Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
260 265 270
Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
275 280 285
Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
290 295 300
Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305 310 315 320
Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
325 330 335
Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
340 345 350
Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
355 360 365
Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370 375 380
Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385 390 395 400
Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415
Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430
Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
435 440 445
Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460
Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
485 490 495
Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
500 505 510
Val Arg His Arg Trp Lys
515

<210> 130
<211> 423
<212> PRT
<213> Homo sapiens

<400> 130
Met Arg Ser Ser Gly Ala Asp Ala Gly Arg Cys Leu Val Thr Ala Arg
1 5 10 15
Ala Pro Gly Ser Val Pro Ala Ser Arg Glu Gly Ser Ala Gly Ser Arg
20 25 30
Gly Pro Gly Ala Arg Phe Pro Ala Arg Val Ser Ala Arg Gly Ser Ala
35 40 45
Pro Gly Pro Gly Leu Gly Gly Ala Gly Ala Leu Asp Pro Pro Ala Val
50 55 60
Val Ala Glu Ser Val Ser Ser Leu Thr Ile Ala Asp Ala Phe Ile Ala
65 70 75 80

Ala Gly Glu Ser Ser Ala Pro Thr Pro Pro Arg Pro Ala Leu Pro Arg
85 90 95
Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser Ala Asn Tyr Ser Lys Ala
100 105 110
Trp Lys Leu Asp Ala His Leu Cys Lys His Thr Gly Glu Arg Pro Phe
115 120 125
Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala Phe Ile Arg Asp Tyr His
130 135 140
Leu Ser Arg His Ile Leu Thr His Thr Gly Glu Lys Pro Phe Val Cys
145 150 155 160
Ala Ala Asn Gly Cys Asp Gln Lys Phe Asn Thr Lys Ser Asn Leu Lys
165 170 175
Lys His Phe Glu Arg Lys His Glu Asn Gln Gln Lys Gln Tyr Ile Cys
180 185 190
Ser Phe Glu Asp Cys Lys Lys Thr Phe Lys Lys His Gln Gln Leu Lys
195 200 205
Ile His Gln Cys Gln Asn Thr Asn Glu Pro Leu Phe Lys Cys Thr Gln
210 215 220
Glu Gly Cys Gly Lys His Phe Ala Ser Pro Ser Lys Leu Lys Arg His
225 230 235 240
Ala Lys Ala His Glu Gly Tyr Val Cys Gln Lys Gly Cys Ser Phe Val
245 250 255
Ala Lys Thr Trp Thr Glu Leu Leu Lys His Val Arg Glu Thr His Lys
260 265 270
Glu Glu Ile Leu Cys Glu Val Cys Arg Lys Thr Phe Lys Arg Lys Asp
275 280 285
Tyr Leu Lys Gln His Met Lys Thr His Ala Pro Glu Arg Asp Val Cys
290 295 300
Arg Cys Pro Arg Glu Gly Cys Gly Arg Thr Tyr Thr Thr Val Phe Asn
305 310 315 320
Leu Gln Ser His Ile Leu Ser Phe His Glu Glu Ser Arg Pro Phe Val
325 330 335
Cys Glu His Ala Gly Cys Gly Lys Thr Phe Ala Met Lys Gln Ser Leu
340 345 350
Thr Arg His Ala Val Val His Asp Pro Asp Lys Lys Lys Met Lys Leu
355 360 365
Lys Val Lys Lys Ser Arg Glu Lys Arg Glu Phe Gly Leu Ser Ser Gln
370 375 380
Trp Ile Tyr Pro Pro Lys Arg Lys Gln Gly Gln Gly Leu Ser Leu Cys
385 390 395 400
Gln Asn Gly Glu Ser Pro Asn Cys Val Glu Asp Lys Met Leu Ser Thr
405 410 415
Val Ala Val Leu Thr Leu Gly
420

<210> 131
<211> 677
<212> PRT
<213> Homo sapiens

<400> 131
Met Leu Ser Ser Thr Asp Phe Thr Phe Ala Ser Trp Glu Leu Val Val
1 5 10 15
Arg Val Asp His Pro Asn Glu Glu Gln Gln Lys Asp Val Thr Leu Arg
20 25 30
Val Ser Gly Asp Leu His Val Gly Gly Val Met Leu Lys Leu Val Glu
35 40 45
Gln Ile Asn Ile Ser Gln Asp Trp Ser Asp Phe Ala Leu Trp Trp Glu
50 55 60
Gln Lys His Cys Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr
65 70 75 80
Gly Val Gln Ala Asp Ala Lys Leu Leu Phe Thr Pro Gln His Lys Met
85 90 95
Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu Arg Val Ser
100 105 110
Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile Cys Lys Ile Leu

115 120 125
Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu Lys Pro Ser Gly Asp
130 135 140
Tyr Phe Lys Lys Lys Lys Lys Lys Asp Lys Asn Asn Lys Glu Pro Ile
145 150 155 160
Ile Glu Asp Ile Leu Asn Leu Glu Ser Ser Pro Thr Ala Ser Gly Ser
165 170 175
Ser Val Ser Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Ile Tyr Asp
180 185 190
Pro Ile Asn Gly Thr Pro Ala Ser Ser Thr Met Thr Trp Phe Ser Asp
195 200 205
Ser Pro Leu Thr Glu Gln Asn Cys Ser Ile Leu Ala Phe Ser Gln Pro
210 215 220
Pro Gln Ser Pro Glu Ala Leu Ala Asp Met Tyr Gln Pro Arg Ser Leu
225 230 235 240
Val Asp Lys Ala Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser Arg Ser
245 250 255
Leu Met Glu Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu Arg Phe
260 265 270
Lys Tyr Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala Val Arg
275 280 285
Ile Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu Glu Glu
290 295 300
Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu Gln Tyr
305 310 315 320
His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe Ala Gly
325 330 335
Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn Leu Glu Val
340 345 350
Thr Leu Glu Gly Gly Lys Ala Asp Ser Leu Leu Glu Asp Ile Thr Asp
355 360 365
Ile Pro Lys Leu Ala Asp Asn Leu Lys Leu Phe Arg Pro Lys Lys Leu
370 375 380
Leu Pro Lys Ala Phe Lys Gln Tyr Trp Phe Ile Phe Lys Asp Thr Ser
385 390 395 400
Ile Ala Tyr Phe Lys Asn Lys Glu Leu Glu Gln Gly Glu Pro Leu Glu
405 410 415
Lys Leu Asn Leu Arg Gly Cys Glu Val Val Pro Asp Val Asn Val Ala
420 425 430
Gly Arg Lys Phe Gly Ile Lys Leu Leu Ile Pro Val Ala Asp Gly Met
435 440 445
Asn Glu Met Tyr Leu Arg Cys Asp His Glu Asn Gln Tyr Ala Gln Trp
450 455 460
Met Ala Ala Cys Met Leu Ala Ser Lys Gly Lys Thr Met Ala Asp Ser
465 470 475 480
Ser Tyr Gln Pro Glu Val Leu Asn Ile Leu Ser Phe Leu Arg Met Lys
485 490 495
Asn Arg Asn Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn Met Asp
500 505 510
Met Asn Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Lys His Lys
515 520 525
Ser Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala
530 535 540
Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala Trp Gln
545 550 555 560
Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe Lys Gly
565 570 575
Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg Leu Ile Lys
580 585 590
Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp Arg Phe Thr Asn
595 600 605
Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg Gln Val Val Ile Glu
610 615 620
Phe Asp Gln Asn Val Phe Thr Ala Phe Thr Cys Leu Ser Ala Asp Cys
625 630 635 640
Lys Ile Val His Glu Tyr Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg
645 650 655

Ser Lys Asp Gln Asn Glu Thr Leu Asp Glu Asp Leu Phe His Lys Leu
660 665 670
Thr Gly Gly Gln Asp
675

<210> 132
<211> 836
<212> PRT
<213> Homo sapiens

<400> 132
Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
1 5 10 15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20 25 30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35 40 45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50 55 60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65 70 75 80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85 90 95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100 105 110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115 120 125
Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130 135 140
Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
145 150 155 160
Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
165 170 175
Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
180 185 190
Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys
195 200 205
Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His
210 215 220
Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe
225 230 235 240
Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr
245 250 255
Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe
260 265 270
Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
275 280 285
Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
290 295 300
Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
305 310 315 320
Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
325 330 335
Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
340 345 350
Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp
355 360 365
Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe
370 375 380
Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp
385 390 395 400
Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp
405 410 415
Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His
420 425 430
Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile

435 440 445
Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr
450 455 460
Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly
465 470 475 480
Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu
485 490 495
Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe
500 505 510
Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro
515 520 525
Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met
530 535 540
Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln
545 550 555 560
Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly
565 570 575
Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys
580 585 590
Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys
595 600 605
Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val
610 615 620
Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu
625 630 635 640
Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val
645 650 655
Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys
660 665 670
Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser
675 680 685
Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys
690 695 700
Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile
705 710 715 720
Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile
725 730 735
Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu
740 745 750
Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly
755 760 765
Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val
770 775 780
Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu
785 790 795 800
Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys
805 810 815
Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu
820 825 830
Gly Arg Ser Gln
835

<210> 133
<211> 303
<212> PRT
<213> Homo sapiens

<400> 133
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1 5 10 15
Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
20 25 30
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
35 40 45
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
50 55 60

Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
65 70 75 80
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
85 90 95
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
100 105 110
Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
115 120 125
Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
130 135 140
Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
145 150 155 160
Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
165 170 175
Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
180 185 190
Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
195 200 205
Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Phe Glu Lys Asn Tyr
210 215 220
Asn Met Tyr Ile Phe Pro Val His Trp Gln Phe Gly Gln Leu Asp Gln
225 230 235 240
His Pro Ile Asp Gly Tyr Leu Ser His Thr Glu Leu Ala Pro Leu Arg
245 250 255
Ala Pro Leu Ile Pro Met Glu His Cys Thr Thr Arg Phe Phe Glu Thr
260 265 270
Cys Asp Leu Asp Asn Asp Lys Tyr Ile Ala Leu Asp Glu Trp Ala Gly
275 280 285
Cys Phe Gly Ile Lys Gln Lys Asp Ile Asp Lys Asp Leu Val Ile
290 295 300

<210> 134
<211> 683
<212> PRT
<213> Homo sapiens

<400> 134
Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu Ala Leu
1 5 10 15
Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
20 25 30
Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45
Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60
Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80
Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95
Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110
Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125
Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140
Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160
Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
165 170 175
Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
180 185 190
Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
195 200 205
Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
210 215 220
Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr

225 230 235 240
Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
245 250 255
Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
260 265 270
Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
275 280 285
Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
290 295 300
Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
305 310 315 320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
325 330 335
Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
340 345 350
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
355 360 365
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
370 375 380
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
385 390 395 400
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
405 410 415
Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
420 425 430
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
435 440 445
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
450 455 460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
465 470 475 480
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
485 490 495
Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
500 505 510
Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
515 520 525
Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
530 535 540
Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
545 550 555 560
Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
565 570 575
Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
580 585 590
Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
595 600 605
Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
610 615 620
Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
625 630 635 640
Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
645 650 655
Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
660 665 670
Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
675 680

<210> 135
<211> 2355
<212> PRT
<213> Homo sapiens

<400> 135
Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
1 5 10 15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln
20 25 30
Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser
35 40 45
Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln
50 55 60
Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly
65 70 75 80
Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr
85 90 95
Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr
100 105 110
Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala
115 120 125
Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly
130 135 140
Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr
145 150 155 160
Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu
165 170 175
Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly
180 185 190
Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp
195 200 205
Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr
210 215 220
Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr
225 230 235 240
Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu
245 250 255
Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg
260 265 270
His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp
275 280 285
Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro
290 295 300
Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met
305 310 315 320
Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu
325 330 335
Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly
340 345 350
Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly
355 360 365
Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu
370 375 380
Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser Phe
385 390 395 400
Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn
405 410 415
Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr Thr
420 425 430
Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly Thr
435 440 445
Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala
450 455 460
Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile
465 470 475 480
Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys
485 490 495
Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser
500 505 510
Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn
515 520 525
Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr
530 535 540
Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln

545 550 555 560
Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp
565 570 575
Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg
580 585 590
Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser
595 600 605
Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn
610 615 620
Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys
625 630 635 640
Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu
645 650 655
Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys
660 665 670
Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly
675 680 685
His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr
690 695 700
Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro
705 710 715 720
Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe
725 730 735
Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val
740 745 750
Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu
755 760 765
Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg
770 775 780
Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser
785 790 795 800
Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp
805 810 815
Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser
820 825 830
Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser
835 840 845
Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser
850 855 860
Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile
865 870 875 880
Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln
885 890 895
Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp
900 905 910
Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr
915 920 925
Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val
930 935 940
Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr
945 950 955 960
Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys
965 970 975
Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln
980 985 990
Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn Glu
995 1000 1005
Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln Ile
1010 1015 1020
Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln Pro Arg
1025 1030 1035 1040
Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu Arg Asn Leu
1045 1050 1055
Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala Ile Lys Gly Asn
1060 1065 1070
Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr Thr Leu Gln Pro Gly
1075 1080 1085

Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val Thr Glu Thr Thr Ile Val
1090 1095 1100
Ile Thr Trp Thr Pro Ala Pro Arg Ile Gly Phe Lys Leu Gly Val Arg
1105 1110 1115 1120
Pro Ser Gln Gly Gly Glu Ala Pro Arg Glu Val Thr Ser Asp Ser Gly
1125 1130 1135
Ser Ile Val Val Ser Gly Leu Thr Pro Gly Val Glu Tyr Val Tyr Thr
1140 1145 1150
Ile Gln Val Leu Arg Asp Gly Gln Glu Arg Asp Ala Pro Ile Val Asn
1155 1160 1165
Lys Val Val Thr Pro Leu Ser Pro Pro Thr Asn Leu His Leu Glu Ala
1170 1175 1180
Asn Pro Asp Thr Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr Thr
1185 1190 1195 1200
Pro Asp Ile Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly Gln
1205 1210 1215
Gln Gly Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser Cys
1220 1225 1230
Thr Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val Tyr
1235 1240 1245
Thr Val Lys Asp Asp Lys Glu Ser Val Pro Ile Ser Asp Thr Ile Ile
1250 1255 1260
Pro Ala Val Pro Pro Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro
1265 1270 1275 1280
Asp Thr Met Arg Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr
1285 1290 1295
Asn Phe Leu Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala
1300 1305 1310
Glu Leu Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu
1315 1320 1325
Leu Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
1330 1335 1340
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp Ser
1345 1350 1355 1360
Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe Thr Val
1365 1370 1375
His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg Ile Arg His
1380 1385 1390
His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp Arg Val Pro His
1395 1400 1405
Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr Pro Gly Thr Glu Tyr
1410 1415 1420
Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu Glu Ser Pro Leu Leu
1425 1430 1435 1440
Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro Arg Asp Leu Glu Val
1445 1450 1455
Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala
1460 1465 1470
Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn
1475 1480 1485
Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr
1490 1495 1500
Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala
1505 1510 1515 1520
Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile
1525 1530 1535
Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln Met Gln Val Thr Asp
1540 1545 1550
Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu Pro Ser Ser Ser Pro
1555 1560 1565
Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys Asn Gly Pro Gly Pro
1570 1575 1580
Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr Glu Met Thr Ile Glu
1585 1590 1595 1600
Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser Val Tyr Ala Gln Asn
1605 1610 1615
Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr Ala Val Thr Asn Ile

1620 1625 1630
Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val Asp Val Asp Ser Ile
1635 1640 1645
Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg Val
1650 1655 1660
Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala Pro
1665 1670 1675 1680
Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly Ser
1685 1690 1695
Glu Tyr Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu Ser Gln
1700 1705 1710
Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro Thr Asp Leu
1715 1720 1725
Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro
1730 1735 1740
Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu
1745 1750 1755 1760
Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser
1765 1770 1775
Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val
1780 1785 1790
Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val
1795 1800 1805
Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp
1810 1815 1820
Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr
1825 1830 1835 1840
Ile Thr Gly Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro
1845 1850 1855
Ile Gln Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly
1860 1865 1870
Leu Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp
1875 1880 1885
Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp
1890 1895 1900
Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu
1905 1910 1915 1920
Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys
1925 1930 1935
Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg
1940 1945 1950
Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu
1955 1960 1965
Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro
1970 1975 1980
Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu Val Thr Leu
1985 1990 1995 2000
Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro Ser Thr
2005 2010 2015
Val Gln Lys Thr Pro Phe Val Thr His Pro Gly Tyr Asp Thr Gly Asn
2020 2025 2030
Gly Ile Gln Leu Pro Gly Thr Ser Gly Gln Gln Pro Ser Val Gly Gln
2035 2040 2045
Gln Met Ile Phe Glu Glu His Gly Phe Arg Arg Thr Thr Pro Pro Thr
2050 2055 2060
Thr Ala Thr Pro Ile Arg His Arg Pro Arg Pro Tyr Pro Pro Asn Val
2065 2070 2075 2080
Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile Ser Trp Ala Pro Phe Gln
2085 2090 2095
Asp Thr Ser Glu Tyr Ile Ile Ser Cys His Pro Val Gly Thr Asp Glu
2100 2105 2110
Glu Pro Leu Gln Phe Arg Val Pro Gly Thr Ser Thr Ser Ala Thr Leu
2115 2120 2125
Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn Ile Ile Val Glu Ala Leu
2130 2135 2140
Lys Asp Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly
2145 2150 2155 2160

Asn Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe
2165 2170 2175
Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg
2180 2185 2190
Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly
2195 2200 2205
Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly
2210 2215 2220
Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly
2225 2230 2235 2240
Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys
2245 2250 2255
Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His
2260 2265 2270
Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys
2275 2280 2285
Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
2290 2295 2300
Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn
2305 2310 2315 2320
Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys
2325 2330 2335
Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp
2340 2345 2350
Ser Arg Glu
2355

<210> 136
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 136
Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr
1 5 10 15
Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys
20 25 30
Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly
35 40 45
Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro
50 55 60
Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln
65 70 75 80
Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
85 90 95
Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly
100 105 110
Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
115 120 125
Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp
130 135 140
Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly
145 150 155 160
Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
165 170 175
Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
180 185 190
Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly
195 200 205
Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg
210 215 220
Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val
225 230 235 240
Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly
245 250 255
Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn

```
                260                 265                 270
Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
        275                 280                 285
Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
    290                 295                 300
Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
305                 310                 315                 320
Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
                325                 330                 335
Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly
            340                 345                 350
Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro
        355                 360                 365
Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
    370                 375                 380
Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
385                 390                 395                 400
Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val
                405                 410                 415
Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
            420                 425                 430
Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
        435                 440                 445
Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
    450                 455                 460
Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
465                 470                 475                 480
Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
                485                 490                 495
Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
            500                 505                 510
Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
        515                 520                 525
Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
    530                 535                 540
Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
545                 550                 555                 560
Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
                565                 570                 575
Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
            580                 585                 590
Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
        595                 600                 605
Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
    610                 615                 620
Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
625                 630                 635                 640
Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
                645                 650                 655
Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
            660                 665                 670
Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
        675                 680                 685
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
    690                 695                 700
Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
705                 710                 715                 720
Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
                725                 730                 735
Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
            740                 745                 750
Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
        755                 760                 765
Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
    770                 775                 780
Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
785                 790                 795                 800
```

Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
805 810 815
Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
820 825 830
Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
835 840 845
Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln
850 855 860
Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
865 870 875 880
Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
885 890 895
Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
900 905 910
Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly
915 920 925
Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His
930 935 940
Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
945 950 955 960
Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
965 970 975
Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala
980 985 990
Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys
995 1000 1005
Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly
1010 1015 1020
His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp
1025 1030 1035 1040
Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg Gly Pro Ala
1045 1050 1055
Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr Gly His Pro Gly
1060 1065 1070
Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln Gly His Gln Gly Pro
1075 1080 1085
Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser
1090 1095 1100
Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp Phe Tyr Arg Ala Asp
1105 1110 1115 1120
Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys Asp Tyr Glu Val Asp
1125 1130 1135
Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu Thr Leu Leu Thr Pro
1140 1145 1150
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Arg Leu
1155 1160 1165
Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp Ile Asp Pro Asn Gln
1170 1175 1180
Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys Asp Phe Ser Thr Gly
1185 1190 1195 1200
Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile Pro Ala Lys Asn Trp
1205 1210 1215
Tyr Arg Ser Ser Lys Asp Lys Lys His Val Trp Leu Gly Glu Thr Ile
1220 1225 1230
Asn Ala Gly Ser Gln Phe Glu Tyr Asn Val Glu Gly Val Thr Ser Lys
1235 1240 1245
Glu Met Ala Thr Gln Leu Ala Phe Met Arg Leu Leu Ala Asn Tyr Ala
1250 1255 1260
Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp
1265 1270 1275 1280
Glu Glu Thr Gly Asn Leu Lys Lys Ala Val Ile Leu Gln Gly Ser Asn
1285 1290 1295
Asp Val Glu Leu Val Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Val
1300 1305 1310
Leu Val Asp Gly Cys Ser Lys Lys Thr Asn Glu Trp Gly Lys Thr Ile
1315 1320 1325
Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg Leu Pro Phe Leu Asp Ile

1330 1335 1340
Ala Pro Leu Asp Ile Gly Gly Ala Asp His Glu Phe Phe Val Asp Ile
1345 1350 1355 1360
Gly Pro Val Cys Phe Lys
1365

<210> 137
<211> 105
<212> PRT
<213> Homo sapiens

<400> 137
Met Ala Lys Ile Ser Ser Pro Thr Glu Thr Glu Arg Cys Ile Glu Ser
1 5 10 15
Leu Ile Ala Val Phe Gln Lys Tyr Ala Gly Lys Asp Gly Tyr Asn Tyr
20 25 30
Thr Leu Ser Lys Thr Glu Phe Leu Ser Phe Met Asn Thr Glu Leu Ala
35 40 45
Ala Phe Thr Lys Asn Gln Lys Asp Pro Gly Val Leu Asp Arg Met Met
50 55 60
Lys Lys Leu Asp Thr Asn Ser Asp Gly Gln Leu Asp Phe Ser Glu Phe
65 70 75 80
Leu Asn Leu Ile Gly Gly Leu Ala Met Ala Cys His Asp Ser Phe Leu
85 90 95
Lys Ala Val Pro Ser Gln Lys Arg Thr
100 105

<210> 138
<211> 125
<212> PRT
<213> Homo sapiens

<400> 138
Met His Lys Glu Glu His Glu Val Ala Val Leu Gly Ala Pro Pro Ser
1 5 10 15
Thr Ile Leu Pro Arg Ser Thr Val Ile Asn Ile His Ser Glu Thr Ser
20 25 30
Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr Leu Phe Leu Asn
35 40 45
Trp Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser Val Lys Ser Arg
50 55 60
Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln Ala Tyr Ala Ser
65 70 75 80
Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu Gly Ile Leu Met
85 90 95
Thr Ile Gly Phe Ile Leu Leu Leu Val Phe Gly Ser Val Thr Val Tyr
100 105 110
His Ile Met Leu Gln Ile Ile Gln Glu Lys Arg Gly Tyr
115 120 125

<210> 139
<211> 163
<212> PRT
<213> Homo sapiens

<400> 139
Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe Gly
1 5 10 15
Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp Asn Gly
20 25 30
Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly Glu Asn Gly
35 40 45
Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys Gly Glu Phe Lys
50 55 60

Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp Gly Lys Thr Tyr His
65 70 75 80
Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu Gly Ala Ile Cys Ser Cys
85 90 95
Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys Asp Asn Cys Arg Arg
100 105 110
Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr Gly Gln Ser Tyr Asn
115 120 125
Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn Thr Asn Val Asn Cys
130 135 140
Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp
145 150 155 160
Ser Arg Glu

<210> 140
<211> 1466
<212> PRT
<213> Homo sapiens

<400> 140
Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
1 5 10 15
His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly Gly Cys
20 25 30
Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu
35 40 45
Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp
50 55 60
Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro
65 70 75 80
Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr
85 90 95
Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly
100 105 110
Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln
115 120 125
Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys
130 135 140
Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val
145 150 155 160
Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala
165 170 175
Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser Gly His Pro Gly
180 185 190
Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln
195 200 205
Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser
210 215 220
Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly
225 230 235 240
Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile
245 250 255
Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly Arg Asn
260 265 270
Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly
275 280 285
Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly Pro Arg Gly Ala
290 295 300
Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg
305 310 315 320
Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly
325 330 335
Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu
340 345 350
Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg

355 360 365
Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln Gly Pro Pro Gly
370 375 380
Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly Glu Met Gly Pro
385 390 395 400
Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala Arg Gly Pro Pro
405 410 415
Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly
420 425 430
Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu
435 440 445
Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala Lys Gly Glu Asp
450 455 460
Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly
465 470 475 480
Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro
485 490 495
Asn Gly Ile Pro Gly Glu Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro
500 505 510
Gly Pro Ala Gly Pro Arg Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly
515 520 525
Val Pro Gly Gly Pro Gly Met Arg Gly Met Pro Gly Ser Pro Gly Gly
530 535 540
Pro Gly Ser Asp Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser
545 550 555 560
Gly Arg Pro Gly Pro Pro Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly
565 570 575
Val Met Gly Phe Pro Gly Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys
580 585 590
Asn Gly Glu Arg Gly Gly Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro
595 600 605
Gly Lys Asn Gly Glu Thr Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly
610 615 620
Pro Gly Gly Asp Lys Gly Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu
625 630 635 640
Gln Gly Leu Pro Gly Thr Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro
645 650 655
Gly Glu Pro Gly Pro Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly
660 665 670
Gly Lys Gly Asp Ala Gly Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu
675 680 685
Ala Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu
690 695 700
Gly Gly Lys Gly Ala Ala Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly
705 710 715 720
Thr Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Gly Leu Gly Ser
725 730 735
Pro Gly Pro Lys Gly Asp Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp
740 745 750
Gly Val Pro Gly Lys Asp Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly
755 760 765
Pro Pro Gly Pro Ala Gly Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala
770 775 780
Pro Gly Leu Pro Gly Ile Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg
785 790 795 800
Gly Glu Thr Gly Pro Pro Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly
805 810 815
Gln Asn Gly Glu Pro Gly Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu
820 825 830
Lys Gly Glu Gly Gly Pro Pro Gly Val Ala Gly Pro Pro Gly Gly Ser
835 840 845
Gly Pro Ala Gly Pro Pro Gly Pro Gln Gly Val Lys Gly Glu Arg Gly
850 855 860
Ser Pro Gly Gly Pro Gly Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu
865 870 875 880
Pro Gly Pro Pro Gly Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser
885 890 895

Gly Ser Pro Gly Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly
900 905 910
Ala Pro Gly Ser Pro Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln
915 920 925
Pro Gly Glu Lys Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro
930 935 940
Gly Pro Leu Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly
945 950 955 960
Pro Pro Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly Val
965 970 975
Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly Glu Arg
980 985 990
Gly Pro Pro Gly Pro Gln Gly Leu Pro Gly Leu Ala Gly Thr Ala Gly
995 1000 1005
Glu Pro Gly Arg Asp Gly Asn Pro Gly Ser Asp Gly Leu Pro Gly Arg
1010 1015 1020
Asp Gly Ser Pro Gly Gly Lys Gly Asp Arg Gly Glu Asn Gly Ser Pro
1025 1030 1035 1040
Gly Ala Pro Gly Ala Pro Gly His Pro Gly Pro Pro Gly Pro Val Gly
1045 1050 1055
Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Ser Gly Pro Ala Gly Pro
1060 1065 1070
Ala Gly Ala Pro Gly Pro Ala Gly Ser Arg Gly Ala Pro Gly Pro Gln
1075 1080 1085
Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Arg Gly Ala Ala Gly
1090 1095 1100
Ile Lys Gly His Arg Gly Phe Pro Gly Asn Pro Gly Ala Pro Gly Ser
1105 1110 1115 1120
Pro Gly Pro Ala Gly Gln Gln Gly Ala Ile Gly Ser Pro Gly Pro Ala
1125 1130 1135
Gly Pro Arg Gly Pro Val Gly Pro Ser Gly Pro Pro Gly Lys Asp Gly
1140 1145 1150
Thr Ser Gly His Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Asn
1155 1160 1165
Arg Gly Glu Arg Gly Ser Glu Gly Ser Pro Gly His Pro Gly Gln Pro
1170 1175 1180
Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Pro Cys Cys Gly Gly Val
1185 1190 1195 1200
Gly Ala Ala Ala Ile Ala Gly Ile Gly Gly Glu Lys Ala Gly Gly Phe
1205 1210 1215
Ala Pro Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn Thr Asp
1220 1225 1230
Glu Ile Met Thr Ser Leu Lys Ser Val Asn Gly Gln Ile Glu Ser Leu
1235 1240 1245
Ile Ser Pro Asp Gly Ser Arg Lys Asn Pro Ala Arg Asn Cys Arg Asp
1250 1255 1260
Leu Lys Phe Cys His Pro Glu Leu Lys Ser Gly Glu Tyr Trp Val Asp
1265 1270 1275 1280
Pro Asn Gln Gly Cys Lys Leu Asp Ala Ile Lys Val Phe Cys Asn Met
1285 1290 1295
Glu Thr Gly Glu Thr Cys Ile Ser Ala Asn Pro Leu Asn Val Pro Arg
1300 1305 1310
Lys His Trp Trp Thr Asp Ser Ser Ala Glu Lys Lys His Val Trp Phe
1315 1320 1325
Gly Glu Ser Met Asp Gly Gly Phe Gln Phe Ser Tyr Gly Asn Pro Glu
1330 1335 1340
Leu Pro Glu Asp Val Leu Asp Val Gln Leu Ala Phe Leu Arg Leu Leu
1345 1350 1355 1360
Ser Ser Arg Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile
1365 1370 1375
Ala Tyr Met Asp Gln Ala Ser Gly Asn Val Lys Lys Ala Leu Lys Leu
1380 1385 1390
Met Gly Ser Asn Glu Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe
1395 1400 1405
Thr Tyr Thr Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp
1410 1415 1420
Ser Lys Thr Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro

1425 1430 1435 1440
Ile Val Asp Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu Phe
1445 1450 1455
Gly Val Asp Val Gly Pro Val Cys Phe Leu
1460 1465

<210> 141
<211> 180
<212> PRT
<213> Homo sapiens

<400> 141
Met Lys Ser Ile Tyr Phe Val Ala Gly Leu Phe Val Met Leu Val Gln
1 5 10 15
Gly Ser Trp Gln Arg Ser Leu Gln Asp Thr Glu Glu Lys Ser Arg Ser
20 25 30
Phe Ser Ala Ser Gln Ala Asp Pro Leu Ser Asp Pro Asp Gln Met Asn
35 40 45
Glu Asp Lys Arg His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys
50 55 60
Tyr Leu Asp Ser Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn
65 70 75 80
Thr Lys Arg Asn Arg Asn Asn Ile Ala Lys Arg His Asp Glu Phe Glu
85 90 95
Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu
100 105 110
Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
115 120 125
Arg Arg Asp Phe Pro Glu Glu Val Ala Ile Val Glu Glu Leu Gly Arg
130 135 140
Arg His Ala Asp Gly Ser Phe Ser Asp Glu Met Asn Thr Ile Leu Asp
145 150 155 160
Asn Leu Ala Ala Arg Asp Phe Ile Asn Trp Leu Ile Gln Thr Lys Ile
165 170 175
Thr Asp Arg Lys
180

<210> 142
<211> 1064
<212> PRT
<213> Homo sapiens

<400> 142
Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
1 5 10 15
Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
20 25 30
Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
35 40 45
Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
50 55 60
Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
65 70 75 80
Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
85 90 95
Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
100 105 110
Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
115 120 125
Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
130 135 140
Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
145 150 155 160
Cys Ser Ala Phe Arg Pro Phe Val Arg Asp Gly Arg Leu Gly Cys Thr
165 170 175

Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
180 185 190
Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
195 200 205
Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
210 215 220
Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
225 230 235 240
Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
245 250 255
Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
260 265 270
Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
275 280 285
Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
290 295 300
Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
305 310 315 320
Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
325 330 335
Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg
340 345 350
Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
355 360 365
Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
370 375 380
Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
385 390 395 400
Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys
405 410 415
Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
420 425 430
Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
435 440 445
Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
450 455 460
Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
465 470 475 480
Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
485 490 495
Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
500 505 510
Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
515 520 525
Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
530 535 540
Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
545 550 555 560
Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
565 570 575
Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
580 585 590
Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
595 600 605
Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
610 615 620
Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
625 630 635 640
Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
645 650 655
Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe
660 665 670
Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg
675 680 685
Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Gly Asn Thr Gln
690 695 700
Asp Glu Cys Ala Glu Tyr Gln Glu Gln Met Lys Asn Gly Arg Leu Ser

705 710 715 720
Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr
725 730 735
Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu
740 745 750
Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu
755 760 765
Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly
770 775 780
Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly
785 790 795 800
Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg
805 810 815
Glu Ala Ala Glu Lys Lys Lys Lys Glu Asp Glu Asp Arg Ser Asn Thr
820 825 830
Gly Glu Arg Ser Asn Thr Gly Glu Arg Ser Asn Asp Lys Glu Asp Leu
835 840 845
Cys Arg Glu Phe Arg Ser Met Gln Arg Asn Gly Lys Leu Ile Cys Thr
850 855 860
Arg Glu Asn Asn Pro Val Arg Gly Pro Tyr Gly Lys Met His Ile Asn
865 870 875 880
Lys Cys Ala Met Cys Gln Ser Ile Phe Asp Arg Glu Ala Asn Glu Arg
885 890 895
Lys Lys Lys Asp Glu Glu Lys Ser Ser Ser Lys Pro Ser Asn Asn Ala
900 905 910
Lys Asp Glu Cys Ser Glu Phe Arg Asn Tyr Ile Arg Asn Asn Glu Leu
915 920 925
Ile Cys Pro Arg Glu Asn Asp Pro Val His Gly Ala Asp Gly Lys Phe
930 935 940
Tyr Thr Asn Lys Cys Tyr Met Cys Arg Ala Val Phe Leu Thr Glu Ala
945 950 955 960
Leu Glu Arg Ala Lys Leu Gln Glu Lys Pro Ser His Val Arg Ala Ser
965 970 975
Gln Glu Glu Asp Ser Pro Asp Ser Phe Ser Ser Leu Asp Ser Glu Met
980 985 990
Cys Lys Asp Tyr Arg Val Leu Pro Arg Ile Gly Tyr Leu Cys Pro Lys
995 1000 1005
Asp Leu Lys Pro Val Cys Gly Asp Asp Gly Gln Thr Tyr Asn Asn Pro
1010 1015 1020
Cys Met Leu Cys His Glu Asn Leu Ile Arg Gln Thr Asn Thr His Ile
1025 1030 1035 1040
Arg Ser Thr Gly Lys Cys Glu Glu Ser Ser Thr Pro Gly Thr Thr Ala
1045 1050 1055
Ala Ser Met Pro Pro Ser Asp Glu
1060

<210> 143
<211> 967
<212> PRT
<213> Homo sapiens

<400> 143
Met Ala Lys Gly Phe Tyr Ile Ser Lys Ser Leu Gly Ile Leu Gly Ile
1 5 10 15
Leu Leu Gly Val Ala Ala Val Cys Thr Ile Ile Ala Leu Ser Val Val
20 25 30
Tyr Ser Gln Glu Lys Asn Lys Asn Ala Asn Ser Ser Pro Val Ala Ser
35 40 45
Thr Thr Pro Ser Ala Ser Ala Thr Thr Asn Pro Ala Ser Ala Thr Thr
50 55 60
Leu Asp Gln Ser Lys Ala Trp Asn Arg Tyr Arg Leu Pro Asn Thr Leu
65 70 75 80
Lys Pro Asp Ser Tyr Gln Val Thr Leu Arg Pro Tyr Leu Thr Pro Asn
85 90 95
Asp Arg Gly Leu Tyr Val Phe Lys Gly Ser Ser Thr Val Arg Phe Thr
100 105 110

Cys Lys Glu Ala Thr Asp Val Ile Ile Ile His Ser Lys Lys Leu Asn
115 120 125
Tyr Thr Leu Ser Gln Gly His Arg Val Val Leu Arg Gly Val Gly Gly
130 135 140
Ser Gln Pro Pro Asp Ile Asp Lys Thr Glu Leu Val Glu Pro Thr Glu
145 150 155 160
Tyr Leu Val Val His Leu Lys Gly Ser Leu Val Lys Asp Ser Gln Tyr
165 170 175
Glu Met Asp Ser Glu Phe Glu Gly Glu Leu Ala Asp Asp Leu Ala Gly
180 185 190
Phe Tyr Arg Ser Glu Tyr Met Glu Gly Asn Val Arg Lys Val Val Ala
195 200 205
Thr Thr Gln Met Gln Ala Ala Asp Ala Arg Lys Ser Phe Pro Cys Phe
210 215 220
Asp Glu Pro Ala Met Lys Ala Glu Phe Asn Ile Thr Leu Ile His Pro
225 230 235 240
Lys Asp Leu Thr Ala Leu Ser Asn Met Leu Pro Lys Gly Pro Ser Thr
245 250 255
Pro Leu Pro Glu Asp Pro Asn Trp Asn Val Thr Glu Phe His Thr Thr
260 265 270
Pro Lys Met Ser Thr Tyr Leu Leu Ala Phe Ile Val Ser Glu Phe Asp
275 280 285
Tyr Val Glu Lys Gln Ala Ser Asn Gly Val Leu Ile Arg Ile Trp Ala
290 295 300
Arg Pro Ser Ala Ile Ala Ala Gly His Gly Asp Tyr Ala Leu Asn Val
305 310 315 320
Thr Gly Pro Ile Leu Asn Phe Phe Ala Gly His Tyr Asp Thr Pro Tyr
325 330 335
Pro Leu Pro Lys Ser Asp Gln Ile Gly Leu Pro Asp Phe Asn Ala Gly
340 345 350
Ala Met Glu Asn Trp Gly Leu Val Thr Tyr Arg Glu Asn Ser Leu Leu
355 360 365
Phe Asp Pro Leu Ser Ser Ser Ser Ser Asn Lys Glu Arg Val Val Thr
370 375 380
Val Ile Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu Val Thr
385 390 395 400
Ile Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala Ser Tyr
405 410 415
Val Glu Tyr Leu Gly Ala Asp Tyr Ala Glu Pro Thr Trp Asn Leu Lys
420 425 430
Asp Leu Met Val Leu Asn Asp Val Tyr Arg Val Met Ala Val Asp Ala
435 440 445
Leu Ala Ser Ser His Pro Leu Ser Thr Pro Ala Ser Glu Ile Asn Thr
450 455 460
Pro Ala Gln Ile Ser Glu Leu Phe Asp Ala Ile Ser Tyr Ser Lys Gly
465 470 475 480
Ala Ser Val Leu Arg Met Leu Ser Ser Phe Leu Ser Glu Asp Val Phe
485 490 495
Lys Gln Gly Leu Ala Ser Tyr Leu His Thr Phe Ala Tyr Gln Asn Thr
500 505 510
Ile Tyr Leu Asn Leu Trp Asp His Leu Gln Glu Ala Val Asn Asn Arg
515 520 525
Ser Ile Gln Leu Pro Thr Thr Val Arg Asp Ile Met Asn Arg Trp Thr
530 535 540
Leu Gln Met Gly Phe Pro Val Ile Thr Val Asp Thr Ser Thr Gly Thr
545 550 555 560
Leu Ser Gln Glu His Phe Leu Leu Asp Pro Asp Ser Asn Val Thr Arg
565 570 575
Pro Ser Glu Phe Asn Tyr Val Trp Ile Val Pro Ile Thr Ser Ile Arg
580 585 590
Asp Gly Arg Gln Gln Gln Asp Tyr Trp Leu Ile Asp Val Arg Ala Gln
595 600 605
Asn Asp Leu Phe Ser Thr Ser Gly Asn Glu Trp Val Leu Leu Asn Leu
610 615 620
Asn Val Thr Gly Tyr Tyr Arg Val Asn Tyr Asp Glu Glu Asn Trp Arg
625 630 635 640
Lys Ile Gln Thr Gln Leu Gln Arg Asp His Ser Ala Ile Pro Val Ile

645 650 655
Asn Arg Ala Gln Ile Ile Asn Asp Ala Phe Asn Leu Ala Ser Ala His
660 665 670
Lys Val Pro Val Thr Leu Ala Leu Asn Asn Thr Leu Phe Leu Ile Glu
675 680 685
Glu Arg Gln Tyr Met Pro Trp Glu Ala Ala Leu Ser Ser Leu Ser Tyr
690 695 700
Phe Lys Leu Met Phe Asp Arg Ser Glu Val Tyr Gly Pro Met Lys Asn
705 710 715 720
Tyr Leu Lys Lys Gln Val Thr Pro Leu Phe Ile His Phe Arg Asn Asn
725 730 735
Thr Asn Asn Trp Arg Glu Ile Pro Glu Asn Leu Met Asp Gln Tyr Ser
740 745 750
Glu Val Asn Ala Ile Ser Thr Ala Cys Ser Asn Gly Val Pro Glu Cys
755 760 765
Glu Glu Met Val Ser Gly Leu Phe Lys Gln Trp Met Glu Asn Pro Asn
770 775 780
Asn Asn Pro Ile His Pro Asn Leu Arg Ser Thr Val Tyr Cys Asn Ala
785 790 795 800
Ile Ala Gln Gly Gly Glu Glu Glu Trp Asp Phe Ala Trp Glu Gln Phe
805 810 815
Arg Asn Ala Thr Leu Val Asn Glu Ala Asp Lys Leu Arg Ala Ala Leu
820 825 830
Ala Cys Ser Lys Glu Leu Trp Ile Leu Asn Arg Tyr Leu Ser Tyr Thr
835 840 845
Leu Asn Pro Asp Leu Ile Arg Lys Gln Asp Ala Thr Ser Thr Ile Ile
850 855 860
Ser Ile Thr Asn Asn Val Ile Gly Gln Gly Leu Val Trp Asp Phe Val
865 870 875 880
Gln Ser Asn Trp Lys Lys Leu Phe Asn Asp Tyr Gly Gly Gly Ser Phe
885 890 895
Ser Phe Ser Asn Leu Ile Gln Ala Val Thr Arg Arg Phe Ser Thr Glu
900 905 910
Tyr Glu Leu Gln Gln Leu Glu Gln Phe Lys Lys Asp Asn Glu Glu Thr
915 920 925
Gly Phe Gly Ser Gly Thr Arg Ala Leu Glu Gln Ala Leu Glu Lys Thr
930 935 940
Lys Ala Asn Ile Lys Trp Val Lys Glu Asn Lys Glu Val Val Leu Gln
945 950 955 960
Trp Phe Thr Glu Asn Ser Lys
965

<210> 144
<211> 261
<212> PRT
<213> Homo sapiens

<400> 144
Met Ser Gly Glu Ile Ala Met Cys Glu Pro Glu Phe Gly Asn Asp Lys
1 5 10 15
Ala Arg Glu Pro Ser Val Gly Gly Arg Trp Arg Val Ser Trp Tyr Glu
20 25 30
Arg Phe Val Gln Pro Cys Leu Val Glu Leu Leu Gly Ser Ala Leu Phe
35 40 45
Ile Phe Ile Gly Cys Leu Ser Val Ile Glu Asn Gly Thr Asp Thr Gly
50 55 60
Leu Leu Gln Pro Ala Leu Ala His Gly Leu Ala Leu Gly Leu Val Ile
65 70 75 80
Ala Thr Leu Gly Asn Ile Ser Gly Gly His Phe Asn Pro Ala Val Ser
85 90 95
Leu Ala Ala Met Leu Ile Gly Gly Leu Asn Leu Val Met Leu Leu Pro
100 105 110
Tyr Trp Val Ser Gln Leu Leu Gly Gly Met Leu Gly Ala Ala Leu Ala
115 120 125
Lys Val Val Ser Pro Glu Glu Arg Phe Trp Asn Ala Ser Gly Ala Ala
130 135 140

Phe Val Thr Val Gln Glu Gln Gly Gln Val Ala Gly Ala Leu Val Ala
145 150 155 160
Glu Ile Ile Leu Thr Thr Leu Leu Ala Leu Ala Val Cys Met Gly Ala
165 170 175
Ile Asn Glu Lys Thr Lys Gly Pro Leu Ala Pro Phe Ser Ile Gly Phe
180 185 190
Ala Val Thr Val Asp Ile Leu Ala Gly Gly Pro Val Ser Gly Gly Cys
195 200 205
Met Asn Pro Ala Arg Ala Phe Gly Pro Ala Val Val Ala Asn His Trp
210 215 220
Asn Phe His Trp Ile Tyr Trp Leu Gly Pro Leu Leu Ala Gly Leu Leu
225 230 235 240
Val Gly Leu Leu Ile Arg Cys Phe Ile Gly Asp Gly Lys Thr Arg Leu
245 250 255
Ile Leu Lys Ala Arg
260

<210> 145
<211> 112
<212> PRT
<213> Homo sapiens

<400> 145
Met Gly Cys Arg Ala Ala Ser Gly Leu Leu Pro Gly Val Ala Val Val
1 5 10 15
Leu Leu Leu Leu Leu Gln Ser Thr Gln Ser Val Tyr Ile Gln Tyr Gln
20 25 30
Gly Phe Arg Val Gln Leu Glu Ser Met Lys Lys Leu Ser Asp Leu Glu
35 40 45
Ala Gln Trp Ala Pro Ser Pro Arg Leu Gln Ala Gln Ser Leu Leu Pro
50 55 60
Ala Val Cys His His Pro Ala Leu Pro Gln Asp Leu Gln Pro Val Cys
65 70 75 80
Ala Ser Gln Glu Ala Ser Ser Ile Phe Lys Thr Leu Arg Thr Ile Ala
85 90 95
Asn Asp Asp Cys Glu Leu Cys Val Asn Val Ala Cys Thr Gly Cys Leu
100 105 110

<210> 146
<211> 917
<212> PRT
<213> Homo sapiens

<400> 146
Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu Leu
1 5 10 15
His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly Phe Glu
20 25 30
Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp Glu Lys Ile
35 40 45
Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser Thr Tyr Leu Phe
50 55 60
Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn Val Ser Ile Leu Ile
65 70 75 80
Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr Lys Arg Pro Lys His Glu
85 90 95
Asn His Lys His Ala Asp Val Ile Val Ala Pro Pro Thr Leu Pro Gly
100 105 110
Arg Asp Glu Pro Tyr Thr Lys Gln Phe Thr Glu Cys Gly Glu Lys Gly
115 120 125
Glu Tyr Ile His Phe Thr Pro Asp Leu Leu Leu Gly Lys Lys Gln Asn
130 135 140
Glu Tyr Gly Pro Pro Gly Lys Leu Phe Val His Glu Trp Ala His Leu
145 150 155 160
Arg Trp Gly Val Phe Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg

```
                 165                 170                 175
Ala Lys Ser Lys Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser
            180                 185                 190
Gly Arg Asn Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg
        195                 200                 205
Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln
    210                 215                 220
Phe Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met
225                 230                 235                 240
Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His Asn
                245                 250                 255
Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg Ser Thr
            260                 265                 270
Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr Ile Pro Met
        275                 280                 285
Val Thr Pro Pro Pro Pro Pro Val Phe Ser Leu Leu Lys Ile Arg Gln
    290                 295                 300
Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Gly Gly Lys
305                 310                 315                 320
Asp Arg Leu Asn Arg Met Asn Gln Ala Ala Lys His Phe Leu Leu Gln
                325                 330                 335
Thr Val Glu Asn Gly Ser Trp Val Gly Met Val His Phe Asp Ser Thr
            340                 345                 350
Ala Thr Ile Val Asn Lys Leu Ile Gln Ile Lys Ser Ser Asp Glu Arg
        355                 360                 365
Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr Pro Leu Gly Gly Thr Ser
    370                 375                 380
Ile Cys Ser Gly Ile Lys Tyr Ala Phe Gln Val Ile Gly Glu Leu His
385                 390                 395                 400
Ser Gln Leu Asp Gly Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp
                405                 410                 415
Asn Thr Ala Ser Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile
            420                 425                 430
Val His Phe Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu
        435                 440                 445
Met Ser Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala
    450                 455                 460
Gln Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn
465                 470                 475                 480
Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu Thr
                485                 490                 495
Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp Ser Thr
            500                 505                 510
Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser Leu Pro Pro
        515                 520                 525
Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met Glu Asn Phe Thr
    530                 535                 540
Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser Ile Pro Gly Thr Ala
545                 550                 555                 560
Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln Ala Lys Ala Asn Pro Glu
                565                 570                 575
Thr Leu Thr Ile Thr Val Thr Ser Arg Ala Ala Asn Ser Ser Val Pro
            580                 585                 590
Pro Ile Thr Val Asn Ala Lys Met Asn Lys Asp Val Asn Ser Phe Pro
        595                 600                 605
Ser Pro Met Ile Val Tyr Ala Glu Ile Leu Gln Gly Tyr Val Pro Val
    610                 615                 620
Leu Gly Ala Asn Val Thr Ala Phe Ile Glu Ser Gln Asn Gly His Thr
625                 630                 635                 640
Glu Val Leu Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys
                645                 650                 655
Asn Asp Gly Val Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly
            660                 665                 670
Arg Tyr Ser Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg
        675                 680                 685
Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp
    690                 695                 700
```

Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp
705 710 715 720
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly
725 730 735
Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln
740 745 750
Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp
755 760 765
Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly
770 775 780
Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu
785 790 795 800
Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser
805 810 815
Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn
820 825 830
Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile
835 840 845
Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr
850 855 860
Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr
865 870 875 880
Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser
885 890 895
Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile
900 905 910
Leu Ser Thr Thr Ile
915

<210> 147
<211> 437
<212> PRT
<213> Homo sapiens

<400> 147
Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu
1 5 10 15
Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln His Val
20 25 30
Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys Asn Thr Ser
35 40 45
Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met Leu Ile Glu Ser
50 55 60
Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly Cys Thr Glu Ala Lys
65 70 75 80
Asp Gln Glu Pro Arg Val Thr Glu His Arg Met Gly Pro Gly Leu Ser
85 90 95
Leu Ile Ser Tyr Thr Phe Val Cys Arg Gln Glu Asp Phe Cys Asn Asn
100 105 110
Leu Val Asn Ser Leu Pro Leu Trp Ala Pro Gln Pro Pro Ala Asp Pro
115 120 125
Gly Ser Leu Arg Cys Pro Val Cys Leu Ser Met Glu Gly Cys Leu Glu
130 135 140
Gly Thr Thr Glu Glu Ile Cys Pro Lys Gly Thr Thr His Cys Tyr Asp
145 150 155 160
Gly Leu Leu Arg Leu Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val
165 170 175
Gln Gly Cys Met Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln
180 185 190
Glu Ile Gly Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe
195 200 205
Leu Thr Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala
210 215 220
Gln Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
225 230 235 240
Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu Thr

245 250 255
Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala Gln Asn
260 265 270
Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val Leu Val Ala
275 280 285
Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn Ser Ala Ser Ser
290 295 300
Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln Ala Ala Pro Val Pro
305 310 315 320
Gly Asp Arg Gln Cys Pro Thr Cys Val Gln Pro Leu Gly Thr Cys Ser
325 330 335
Ser Gly Ser Pro Arg Met Thr Cys Pro Arg Gly Ala Thr His Cys Tyr
340 345 350
Asp Gly Tyr Ile His Leu Ser Gly Gly Gly Leu Ser Thr Lys Met Ser
355 360 365
Ile Gln Gly Cys Val Ala Gln Pro Ser Ser Phe Leu Leu Asn His Thr
370 375 380
Arg Gln Ile Gly Ile Phe Ser Ala Arg Glu Lys Arg Asp Val Gln Pro
385 390 395 400
Pro Ala Ser Gln His Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu
405 410 415
Thr Trp Gly Val Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val
420 425 430
Val Cys Pro Ser Cys
435

<210> 148
<211> 452
<212> PRT
<213> Homo sapiens

<400> 148
Met Leu Cys Gly Arg Pro Arg Ser Ser Ser Asp Asn Arg Asn Phe Leu
1 5 10 15
Arg Glu Arg Ala Gly Leu Ser Ser Ala Ala Val Gln Thr Arg Ile Gly
20 25 30
Asn Ser Ala Ala Ser Arg Arg Ser Pro Ala Ala Arg Pro Pro Val Pro
35 40 45
Ala Pro Pro Ala Leu Pro Arg Gly Arg Pro Gly Thr Glu Gly Ser Thr
50 55 60
Ser Leu Ser Ala Pro Ala Val Leu Val Val Ala Val Ala Val Val Val
65 70 75 80
Val Val Val Ser Ala Val Ala Trp Ala Met Ala Asn Tyr Ile His Val
85 90 95
Pro Pro Gly Ser Pro Glu Val Pro Lys Leu Asn Val Thr Val Gln Asp
100 105 110
Gln Glu Glu His Arg Cys Arg Glu Gly Ala Leu Ser Leu Leu Gln His
115 120 125
Leu Arg Pro His Trp Asp Pro Gln Glu Val Thr Leu Gln Leu Phe Thr
130 135 140
Asp Gly Ile Thr Asn Lys Leu Ile Gly Cys Tyr Val Gly Asn Thr Met
145 150 155 160
Glu Asp Val Val Leu Val Arg Ile Tyr Gly Asn Lys Thr Glu Leu Leu
165 170 175
Val Asp Arg Asp Glu Glu Val Lys Ser Phe Arg Val Leu Gln Ala His
180 185 190
Gly Cys Ala Pro Gln Leu Tyr Cys Thr Phe Asn Asn Gly Leu Cys Tyr
195 200 205
Glu Phe Ile Gln Gly Glu Ala Leu Asp Pro Lys His Val Cys Asn Pro
210 215 220
Ala Ile Phe Arg Leu Ile Ala Arg Gln Leu Ala Lys Ile His Ala Ile
225 230 235 240
His Ala His Asn Gly Trp Ile Pro Lys Ser Asn Leu Trp Leu Lys Met
245 250 255
Gly Lys Tyr Phe Ser Leu Ile Pro Thr Gly Phe Ala Asp Glu Asp Ile
260 265 270

```
Asn Lys Arg Phe Leu Ser Asp Ile Pro Ser Ser Gln Ile Leu Gln Glu
        275                 280                 285
Glu Met Thr Trp Met Lys Glu Ile Leu Ser Asn Leu Gly Ser Pro Val
    290                 295                 300
Val Leu Cys His Asn Asp Leu Leu Cys Lys Asn Ile Ile Tyr Asn Glu
305                 310                 315                 320
Lys Gln Gly Asp Val Gln Phe Ile Asp Tyr Glu Tyr Ser Gly Tyr Asn
                325                 330                 335
Tyr Leu Ala Tyr Asp Ile Gly Asn His Phe Asn Glu Phe Ala Gly Val
            340                 345                 350
Ser Asp Val Asp Tyr Ser Leu Tyr Pro Asp Arg Glu Leu Gln Ser Gln
        355                 360                 365
Trp Leu Arg Ala Tyr Leu Glu Ala Tyr Lys Glu Phe Lys Gly Phe Gly
    370                 375                 380
Thr Glu Val Thr Glu Lys Glu Val Glu Ile Leu Phe Ile Gln Val Asn
385                 390                 395                 400
Gln Phe Ala Leu Ala Ser His Phe Phe Trp Gly Leu Trp Ala Leu Ile
                405                 410                 415
Gln Ala Lys Tyr Ser Thr Ile Glu Phe Asp Phe Leu Gly Tyr Ala Ile
            420                 425                 430
Val Arg Phe Asn Gln Tyr Phe Lys Met Lys Pro Glu Val Thr Ala Leu
        435                 440                 445
Lys Val Pro Glu
    450
```

<210> 149
<211> 192
<212> PRT
<213> Homo sapiens

<400> 149

```
Met Gly Ser Leu Gly Ser Lys Asn Pro Gln Thr Lys Gln Ala Gln Val
 1               5                  10                  15
Leu Leu Leu Gly Leu Asp Ser Ala Gly Lys Ser Thr Leu Leu Tyr Lys
            20                  25                  30
Leu Lys Leu Ala Lys Asp Ile Thr Thr Ile Pro Thr Ile Gly Phe Asn
        35                  40                  45
Val Glu Met Ile Glu Leu Glu Arg Asn Leu Ser Leu Thr Val Trp Asp
    50                  55                  60
Val Gly Gly Gln Glu Lys Met Arg Thr Val Trp Gly Cys Tyr Cys Glu
65                  70                  75                  80
Asn Thr Asp Gly Leu Val Tyr Val Val Asp Ser Thr Asp Lys Gln Arg
                85                  90                  95
Leu Glu Glu Ser Gln Arg Gln Phe Glu His Ile Leu Lys Asn Glu His
            100                 105                 110
Ile Lys Asn Val Pro Val Val Leu Leu Ala Asn Lys Gln Asp Met Pro
        115                 120                 125
Gly Ala Leu Thr Ala Glu Asp Ile Thr Arg Met Phe Lys Val Lys Lys
    130                 135                 140
Leu Cys Ser Asp Arg Asn Trp Tyr Val Gln Pro Cys Cys Ala Leu Thr
145                 150                 155                 160
Gly Glu Gly Leu Ala Gln Gly Phe Arg Lys Leu Thr Gly Phe Val Lys
                165                 170                 175
Ser His Met Lys Ser Arg Gly Asp Thr Leu Ala Phe Phe Lys Gln Asn
            180                 185                 190
```

<210> 150
<211> 530
<212> PRT
<213> Homo sapiens

<400> 150

```
Met Ser Leu Lys Trp Thr Ser Val Phe Leu Leu Ile Gln Leu Ser Cys
 1               5                  10                  15
Tyr Phe Ser Ser Gly Ser Cys Gly Lys Val Leu Val Trp Pro Thr Glu
```

```
            20                  25                  30
Tyr Ser His Trp Ile Asn Met Lys Thr Ile Leu Glu Glu Leu Val Gln
        35                  40                  45
Arg Gly His Glu Val Thr Val Leu Thr Ser Ser Ala Ser Thr Leu Val
    50                  55                  60
Asn Ala Ser Lys Ser Ser Ala Ile Lys Leu Glu Val Tyr Pro Thr Ser
65                  70                  75                  80
Leu Thr Lys Asn Asp Leu Glu Asp Ser Leu Leu Lys Ile Leu Asp Arg
                85                  90                  95
Trp Ile Tyr Gly Val Ser Lys Asn Thr Phe Trp Ser Tyr Phe Ser Gln
            100                 105                 110
Leu Gln Glu Leu Cys Trp Glu Tyr Tyr Asp Tyr Ser Asn Lys Leu Cys
        115                 120                 125
Lys Asp Ala Val Leu Asn Lys Lys Leu Met Met Lys Leu Gln Glu Ser
    130                 135                 140
Lys Phe Asp Val Ile Leu Ala Asp Ala Leu Asn Pro Cys Gly Glu Leu
145                 150                 155                 160
Leu Ala Glu Leu Phe Asn Ile Pro Phe Leu Tyr Ser Leu Arg Phe Ser
                165                 170                 175
Val Gly Tyr Thr Phe Glu Lys Asn Gly Gly Gly Phe Leu Phe Pro Pro
            180                 185                 190
Ser Tyr Val Pro Val Val Met Ser Glu Leu Ser Asp Gln Met Ile Phe
        195                 200                 205
Met Glu Arg Ile Lys Asn Met Ile His Met Leu Tyr Phe Asp Phe Trp
    210                 215                 220
Phe Gln Ile Tyr Asp Leu Lys Lys Trp Asp Gln Phe Tyr Ser Glu Val
225                 230                 235                 240
Leu Gly Arg Pro Thr Thr Leu Phe Glu Thr Met Gly Lys Ala Glu Met
                245                 250                 255
Trp Leu Ile Arg Thr Tyr Trp Asp Phe Glu Phe Pro Arg Pro Phe Leu
            260                 265                 270
Pro Asn Val Asp Phe Val Gly Gly Leu His Cys Lys Pro Ala Lys Pro
        275                 280                 285
Leu Pro Lys Glu Met Glu Glu Phe Val Gln Ser Ser Gly Glu Asn Gly
    290                 295                 300
Ile Val Val Phe Ser Leu Gly Ser Met Ile Ser Asn Met Ser Glu Glu
305                 310                 315                 320
Ser Ala Asn Met Ile Ala Ser Ala Leu Ala Gln Ile Pro Gln Lys Val
                325                 330                 335
Leu Trp Arg Phe Asp Gly Lys Lys Pro Asn Thr Leu Gly Ser Asn Thr
            340                 345                 350
Arg Leu Tyr Lys Trp Leu Pro Gln Asn Asp Leu Leu Gly His Pro Lys
        355                 360                 365
Thr Lys Ala Phe Ile Thr His Gly Gly Thr Asn Gly Ile Tyr Glu Ala
    370                 375                 380
Ile Tyr His Gly Ile Pro Met Val Gly Ile Pro Leu Phe Ala Asp Gln
385                 390                 395                 400
His Asp Asn Ile Ala His Met Lys Ala Lys Gly Ala Ala Leu Ser Val
                405                 410                 415
Asp Ile Arg Thr Met Ser Ser Arg Asp Leu Leu Asn Ala Leu Lys Ser
            420                 425                 430
Val Ile Asn Asp Pro Val Tyr Lys Glu Asn Val Met Lys Leu Ser Arg
        435                 440                 445
Ile His His Asp Gln Pro Met Lys Pro Leu Asp Arg Ala Val Phe Trp
    450                 455                 460
Ile Glu Phe Val Met Arg His Lys Gly Ala Lys His Leu Arg Val Ala
465                 470                 475                 480
Ala His Asn Leu Thr Trp Ile Gln Tyr His Ser Leu Asp Val Ile Ala
                485                 490                 495
Phe Leu Leu Ala Cys Val Ala Thr Val Ile Phe Ile Ile Thr Lys Phe
            500                 505                 510
Cys Leu Phe Cys Phe Arg Lys Leu Ala Lys Thr Gly Lys Lys Lys Lys
        515                 520                 525
Arg Asp
    530
```

<210> 151
<211> 265
<212> PRT
<213> Homo sapiens

<400> 151
Met Gly Ser Pro Ser Ala Cys Pro Tyr Arg Val Cys Ile Pro Trp Gln
1 5 10 15
Gly Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Leu Pro Asn
20 25 30
Ser Ala Gln Thr Asn Ile Asp Val Val Pro Phe Asn Val Ala Glu Gly
35 40 45
Lys Glu Val Leu Leu Val Val His Asn Glu Ser Gln Asn Leu Tyr Gly
50 55 60
Tyr Asn Trp Tyr Lys Gly Glu Arg Val His Ala Asn Tyr Arg Ile Ile
65 70 75 80
Gly Tyr Val Lys Asn Ile Ser Gln Glu Asn Ala Pro Gly Pro Ala His
85 90 95
Asn Gly Arg Glu Thr Ile Tyr Pro Asn Gly Thr Leu Leu Ile Gln Asn
100 105 110
Val Thr His Asn Asp Ala Gly Phe Tyr Thr Leu His Val Ile Lys Glu
115 120 125
Asn Leu Val Asn Glu Glu Val Thr Arg Gln Phe Tyr Val Phe Ser Glu
130 135 140
Pro Pro Lys Pro Ser Ile Thr Ser Asn Asn Phe Asn Pro Val Glu Asn
145 150 155 160
Lys Asp Ile Val Val Leu Thr Cys Gln Pro Glu Thr Gln Asn Thr Thr
165 170 175
Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Leu Val Ser Pro Arg Leu
180 185 190
Leu Leu Ser Thr Asp Asn Arg Thr Leu Val Leu Leu Ser Ala Thr Lys
195 200 205
Asn Asp Ile Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Gly Ala
210 215 220
Ser Arg Ser Asp Pro Val Thr Leu Asn Val Arg Tyr Glu Ser Val Gln
225 230 235 240
Ala Ser Ser Pro Asp Leu Ser Ala Gly Thr Ala Val Ser Ile Met Ile
245 250 255
Gly Val Leu Ala Gly Met Ala Leu Ile
260 265

<210> 152
<211> 457
<212> PRT
<213> Homo sapiens

<400> 152
Met Arg Ser Ala Ala Val Leu Ala Leu Leu Leu Cys Ala Gly Gln Val
1 5 10 15
Thr Ala Leu Pro Val Asn Ser Pro Met Asn Lys Gly Asp Thr Glu Val
20 25 30
Met Lys Cys Ile Val Glu Val Ile Ser Asp Thr Leu Ser Lys Pro Ser
35 40 45
Pro Met Pro Val Ser Gln Glu Cys Phe Glu Thr Leu Arg Gly Asp Glu
50 55 60
Arg Ile Leu Ser Ile Leu Arg His Gln Asn Leu Leu Lys Glu Leu Gln
65 70 75 80
Asp Leu Ala Leu Gln Gly Ala Lys Glu Arg Ala His Gln Gln Lys Lys
85 90 95
His Ser Gly Phe Glu Asp Glu Leu Ser Glu Val Leu Glu Asn Gln Ser
100 105 110
Ser Gln Ala Glu Leu Lys Glu Ala Val Glu Glu Pro Ser Ser Lys Asp
115 120 125
Val Met Glu Lys Arg Glu Asp Ser Lys Glu Ala Glu Lys Ser Gly Glu
130 135 140
Ala Thr Asp Gly Ala Arg Pro Gln Ala Leu Pro Glu Pro Met Gln Glu

145 150 155 160
Ser Lys Ala Glu Gly Asn Asn Gln Ala Pro Gly Glu Glu Glu Glu Glu
165 170 175
Glu Glu Glu Ala Thr Asn Thr His Pro Pro Ala Ser Leu Pro Ser Gln
180 185 190
Lys Tyr Pro Gly Pro Gln Ala Glu Gly Asp Ser Glu Gly Leu Ser Gln
195 200 205
Gly Leu Val Asp Arg Glu Lys Gly Leu Ser Ala Glu Pro Gly Trp Gln
210 215 220
Ala Lys Arg Glu Glu Glu Glu Glu Glu Glu Glu Glu Ala Glu Ala Gly
225 230 235 240
Glu Glu Ala Val Pro Glu Glu Glu Gly Pro Thr Val Val Leu Asn Pro
245 250 255
His Pro Ser Leu Gly Tyr Lys Glu Ile Arg Lys Gly Glu Ser Arg Ser
260 265 270
Glu Ala Leu Ala Val Asp Gly Ala Gly Lys Pro Gly Ala Glu Glu Ala
275 280 285
Gln Asp Pro Glu Gly Lys Gly Glu Gln Glu His Ser Gln Gln Lys Glu
290 295 300
Glu Glu Glu Glu Met Ala Val Val Pro Gln Gly Leu Phe Arg Gly Gly
305 310 315 320
Lys Ser Gly Glu Leu Glu Gln Glu Glu Glu Arg Leu Ser Lys Glu Trp
325 330 335
Glu Asp Ser Lys Arg Trp Ser Lys Met Asp Gln Leu Ala Lys Glu Leu
340 345 350
Thr Ala Glu Lys Arg Leu Glu Gly Gln Glu Glu Glu Glu Asp Asn Arg
355 360 365
Asp Ser Ser Met Lys Leu Ser Phe Arg Ala Arg Ala Tyr Gly Phe Arg
370 375 380
Gly Pro Gly Pro Gln Leu Arg Arg Gly Trp Arg Pro Ser Ser Arg Glu
385 390 395 400
Asp Ser Leu Glu Ala Gly Leu Pro Leu Gln Val Arg Gly Tyr Pro Glu
405 410 415
Glu Lys Lys Glu Glu Glu Gly Ser Ala Asn Arg Arg Pro Glu Asp Gln
420 425 430
Glu Leu Glu Ser Leu Ser Ala Ile Glu Ala Glu Leu Glu Lys Val Ala
435 440 445
His Gln Leu Gln Ala Leu Arg Arg Gly
450 455

<210> 153
<211> 266
<212> PRT
<213> Homo sapiens

<400> 153
Met His Val Asn Gly Lys Val Ala Leu Val Thr Gly Ala Ala Gln Gly
1 5 10 15
Ile Gly Arg Ala Phe Ala Glu Ala Leu Leu Leu Lys Gly Ala Lys Val
20 25 30
Ala Leu Val Asp Trp Asn Leu Glu Ala Gly Val Gln Cys Lys Ala Ala
35 40 45
Leu His Glu Gln Phe Glu Pro Gln Lys Thr Leu Phe Ile Gln Cys Asp
50 55 60
Val Ala Asp Gln Gln Gln Leu Arg Asp Thr Phe Arg Lys Val Val Asp
65 70 75 80
His Phe Gly Arg Leu Asp Ile Leu Val Asn Asn Ala Gly Val Asn Asn
85 90 95
Glu Lys Asn Trp Glu Lys Thr Leu Gln Ile Asn Leu Val Ser Val Ile
100 105 110
Ser Gly Thr Tyr Leu Gly Leu Asp Tyr Met Ser Lys Gln Asn Gly Gly
115 120 125
Glu Gly Gly Ile Ile Ile Asn Met Ser Ser Leu Ala Gly Leu Met Pro
130 135 140
Val Ala Gln Gln Pro Val Tyr Cys Ala Ser Lys His Gly Ile Val Gly
145 150 155 160

Phe Thr Arg Ser Ala Ala Leu Ala Ala Asn Leu Met Asn Ser Gly Val
165 170 175
Arg Leu Asn Ala Ile Cys Pro Gly Phe Val Asn Thr Ala Ile Leu Glu
180 185 190
Ser Ile Glu Lys Glu Glu Asn Met Gly Gln Tyr Ile Glu Tyr Lys Asp
195 200 205
His Ile Lys Asp Met Ile Lys Tyr Tyr Gly Ile Leu Asp Pro Pro Leu
210 215 220
Ile Ala Asn Gly Leu Ile Thr Leu Ile Glu Asp Asp Ala Leu Asn Gly
225 230 235 240
Ala Ile Met Lys Ile Thr Thr Ser Lys Gly Ile His Phe Gln Asp Tyr
245 250 255
Asp Thr Thr Pro Phe Gln Ala Lys Thr Gln
260 265

<210> 154
<211> 181
<212> PRT
<213> Homo sapiens

<400> 154
Met Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile
1 5 10 15
Asn Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr
20 25 30
Ser Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile
35 40 45
Cys Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp
50 55 60
Gly His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro
65 70 75 80
Leu Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala
85 90 95
Leu Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile
100 105 110
Arg Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe
115 120 125
Lys Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln
130 135 140
Met Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val
145 150 155 160
Leu Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro
165 170 175
Thr Glu Gln Val Thr
180

<210> 155
<211> 312
<212> PRT
<213> Homo sapiens

<400> 155
Met Arg Met Leu Leu Ala Leu Leu Ala Leu Ser Ala Ala Arg Pro Ser
1 5 10 15
Ala Ser Ala Glu Ser His Trp Cys Tyr Glu Val Gln Ala Glu Ser Ser
20 25 30
Asn Tyr Pro Cys Leu Val Pro Val Lys Trp Gly Gly Asn Cys Gln Lys
35 40 45
Asp Arg Gln Ser Pro Ile Asn Ile Val Thr Thr Lys Ala Lys Val Asp
50 55 60
Lys Lys Leu Gly Arg Phe Phe Phe Ser Gly Tyr Asp Lys Lys Gln Thr
65 70 75 80
Trp Thr Val Gln Asn Asn Gly His Ser Val Met Met Leu Leu Glu Asn
85 90 95
Lys Ala Ser Ile Ser Gly Gly Gly Leu Pro Ala Pro Tyr Gln Ala Lys

100 105 110
Gln Leu His Leu His Trp Ser Asp Leu Pro Tyr Lys Gly Ser Glu His
115 120 125
Ser Leu Asp Gly Glu His Phe Ala Met Glu Met His Ile Val His Glu
130 135 140
Lys Glu Lys Gly Thr Ser Arg Asn Val Lys Glu Ala Gln Asp Pro Glu
145 150 155 160
Asp Glu Ile Ala Val Leu Ala Phe Leu Val Glu Ala Gly Thr Gln Val
165 170 175
Asn Glu Gly Phe Gln Pro Leu Val Glu Ala Leu Ser Asn Ile Pro Lys
180 185 190
Pro Glu Met Ser Thr Thr Met Ala Glu Ser Ser Leu Leu Asp Leu Leu
195 200 205
Pro Lys Glu Glu Lys Leu Arg His Tyr Phe Arg Tyr Leu Gly Ser Leu
210 215 220
Thr Thr Pro Thr Cys Asp Glu Lys Val Val Trp Thr Val Phe Arg Glu
225 230 235 240
Pro Ile Gln Leu His Arg Glu Gln Ile Leu Ala Phe Ser Gln Lys Leu
245 250 255
Tyr Tyr Asp Lys Glu Gln Thr Val Ser Met Lys Asp Asn Val Arg Pro
260 265 270
Leu Gln Gln Leu Gly Gln Arg Thr Val Ile Lys Ser Gly Ala Pro Gly
275 280 285
Arg Pro Leu Pro Trp Ala Leu Pro Ala Leu Leu Gly Pro Met Leu Ala
290 295 300
Cys Leu Leu Ala Gly Phe Leu Arg
305 310

<210> 156
<211> 398
<212> PRT
<213> Homo sapiens

<400> 156
Met Leu Arg Leu Tyr Val Leu Val Met Gly Val Ser Ala Phe Thr Leu
1 5 10 15
Gln Pro Ala Ala His Thr Gly Ala Ala Arg Ser Cys Arg Phe Arg Gly
20 25 30
Arg His Tyr Lys Arg Glu Phe Arg Leu Glu Gly Glu Pro Val Ala Leu
35 40 45
Arg Cys Pro Gln Val Pro Tyr Trp Leu Trp Ala Ser Val Ser Pro Arg
50 55 60
Ile Asn Leu Thr Trp His Lys Asn Asp Ser Ala Arg Thr Val Pro Gly
65 70 75 80
Glu Glu Glu Thr Arg Met Trp Ala Gln Asp Gly Ala Leu Trp Leu Leu
85 90 95
Pro Ala Leu Gln Glu Asp Ser Gly Thr Tyr Val Cys Thr Thr Arg Asn
100 105 110
Ala Ser Tyr Cys Asp Lys Met Ser Ile Glu Leu Arg Val Phe Glu Asn
115 120 125
Thr Asp Ala Phe Leu Pro Phe Ile Ser Tyr Pro Gln Ile Leu Thr Leu
130 135 140
Ser Thr Ser Gly Val Leu Val Cys Pro Asp Leu Ser Glu Phe Thr Arg
145 150 155 160
Asp Lys Thr Asp Val Lys Ile Gln Trp Tyr Lys Asp Ser Leu Leu Leu
165 170 175
Asp Lys Asp Asn Glu Lys Phe Leu Ser Val Arg Gly Thr Thr His Leu
180 185 190
Leu Val His Asp Val Ala Leu Glu Asp Ala Gly Tyr Tyr Arg Cys Val
195 200 205
Leu Thr Phe Ala His Glu Gly Gln Gln Tyr Asn Ile Thr Arg Ser Ile
210 215 220
Glu Leu Arg Ile Lys Lys Lys Lys Glu Glu Thr Ile Pro Val Ile Ile
225 230 235 240
Ser Pro Leu Lys Thr Ile Ser Ala Ser Leu Gly Ser Arg Leu Thr Ile
245 250 255

```
Pro Cys Lys Val Phe Leu Gly Thr Gly Thr Pro Leu Thr Thr Met Leu
            260                 265                 270
Trp Trp Thr Ala Asn Asp Thr His Ile Glu Ser Ala Tyr Pro Gly Gly
        275                 280                 285
Arg Val Thr Glu Gly Pro Arg Gln Glu Tyr Ser Glu Asn Asn Glu Asn
    290                 295                 300
Tyr Ile Glu Val Pro Leu Ile Phe Asp Pro Val Thr Arg Glu Asp Leu
305                 310                 315                 320
His Met Asp Phe Lys Cys Val Val His Asn Thr Leu Ser Phe Gln Thr
                325                 330                 335
Leu Arg Thr Thr Val Lys Glu Ala Ser Ser Thr Phe Ser Trp Gly Ile
            340                 345                 350
Val Leu Ala Pro Leu Ser Leu Ala Phe Leu Val Leu Gly Gly Ile Trp
        355                 360                 365
Met His Arg Arg Cys Lys His Arg Thr Gly Lys Ala Asp Gly Leu Thr
    370                 375                 380
Val Leu Trp Pro His His Gln Asp Phe Gln Ser Tyr Pro Lys
385                 390                 395
```

<210> 157
<211> 160
<212> PRT
<213> Homo sapiens

<400> 157

```
Met Glu Lys Phe Asn Thr Ile Ser Ala Ser Lys Cys Asn Lys Glu Thr
 1               5                  10                  15
Val Ala Met Lys Glu Lys Cys Lys Phe Gly Met Thr Ser Thr Ile Pro
            20                  25                  30
Ser Gly His Val Trp Arg Asn Thr Trp Asn Pro Val Ser Cys Ser Leu
        35                  40                  45
Ala Thr Val Lys Met Lys Glu Cys Leu Arg Gly Lys Leu Ile Tyr Leu
    50                  55                  60
Met Gly Asp Ser Thr Ile Arg Gln Trp Met Glu Tyr Phe Lys Ala Ser
65                  70                  75                  80
Ile Asn Thr Leu Lys Ser Val Asp Leu His Glu Ser Gly Lys Leu Gln
                85                  90                  95
His Gln Leu Ala Val Asp Leu Asp Arg Asn Ile Asn Ile Gln Trp Gln
            100                 105                 110
Lys Tyr Cys Tyr Pro Leu Ile Gly Ser Met Thr Tyr Ser Val Lys Glu
        115                 120                 125
Met Glu Tyr Leu Thr Arg Ala Ile Asp Arg Thr Gly Gly Glu Lys Lys
    130                 135                 140
Tyr Cys His Cys Tyr Phe Pro Gly Pro Ala Phe Gln Thr Leu Ser His
145                 150                 155                 160
```

<210> 158
<211> 267
<212> PRT
<213> Homo sapiens

<400> 158

```
Met Met Ser Ser Lys Pro Thr Ser His Ala Glu Val Asn Glu Thr Ile
 1               5                  10                  15
Pro Asn Pro Tyr Pro Pro Gly Ser Phe Met Ala Pro Gly Phe Gln Gln
            20                  25                  30
Pro Leu Gly Ser Ile Asn Leu Glu Asn Gln Ala Gln Gly Ala Gln Arg
        35                  40                  45
Ala Gln Pro Tyr Gly Ile Thr Ser Pro Gly Ile Phe Ala Ser Ser Gln
    50                  55                  60
Pro Gly Gln Gly Asn Ile Gln Met Ile Asn Pro Ser Val Gly Thr Ala
65                  70                  75                  80
Val Met Asn Phe Lys Glu Glu Ala Lys Ala Leu Gly Val Ile Gln Ile
                85                  90                  95
Met Val Gly Leu Met His Ile Gly Phe Gly Ile Val Leu Cys Leu Ile
```

100 105 110
Ser Phe Ser Phe Arg Glu Val Leu Gly Phe Ala Ser Thr Ala Val Ile
115 120 125
Gly Gly Tyr Pro Phe Trp Gly Gly Leu Ser Phe Ile Ile Ser Gly Ser
130 135 140
Leu Ser Val Ser Ala Ser Lys Glu Leu Ser Arg Cys Leu Val Lys Gly
145 150 155 160
Ser Leu Gly Met Asn Ile Val Ser Ser Ile Leu Ala Phe Ile Gly Val
165 170 175
Ile Leu Leu Leu Val Asp Met Cys Ile Asn Gly Val Ala Gly Gln Asp
180 185 190
Tyr Trp Ala Val Leu Ser Gly Lys Gly Ile Ser Ala Thr Leu Met Ile
195 200 205
Phe Ser Leu Leu Glu Phe Phe Val Ala Cys Ala Thr Ala His Phe Ala
210 215 220
Asn Gln Ala Asn Thr Thr Thr Asn Met Ser Val Leu Val Ile Pro Asn
225 230 235 240
Met Tyr Glu Ser Asn Pro Val Thr Pro Ala Ser Ser Ser Ala Pro Pro
245 250 255
Arg Cys Asn Asn Tyr Ser Ala Asn Ala Pro Lys
260 265

<210> 159
<211> 157
<212> PRT
<213> Homo sapiens

<400> 159
Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val
1 5 10 15
Ile Met Leu Phe Val Ser Thr Ile Ala Asn Val Trp Leu Val Ser Asn
20 25 30
Thr Val Asp Ala Ser Val Gly Leu Trp Lys Asn Cys Thr Asn Ile Ser
35 40 45
Cys Ser Asp Ser Leu Ser Tyr Ala Ser Glu Asp Ala Leu Lys Thr Val
50 55 60
Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Cys Val Ile Ala Leu Leu
65 70 75 80
Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe
85 90 95
Leu Ser Gly Ala Thr Thr Leu Val Cys Trp Leu Cys Ile Leu Val Gly
100 105 110
Val Ser Ile Tyr Thr Ser His Tyr Ala Asn Arg Asp Gly Thr Gln Tyr
115 120 125
His His Gly Tyr Ser Tyr Ile Leu Gly Trp Ile Cys Phe Cys Phe Ser
130 135 140
Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys
145 150 155

<210> 160
<211> 1035
<212> PRT
<213> Homo sapiens

<400> 160
Met Ser Thr Glu Asn Val Glu Gly Lys Pro Ser Asn Leu Gly Glu Arg
1 5 10 15
Gly Arg Ala Arg Ser Ser Thr Phe Leu Arg Val Val Gln Pro Met Phe
20 25 30
Asn His Ser Ile Phe Thr Ser Ala Val Ser Pro Ala Ala Glu Arg Ile
35 40 45
Arg Phe Ile Leu Gly Glu Glu Asp Asp Ser Pro Ala Pro Pro Gln Leu
50 55 60
Phe Thr Glu Leu Asp Glu Leu Leu Ala Val Asp Gly Gln Glu Met Glu
65 70 75 80

Trp Lys Glu Thr Ala Arg Trp Ile Lys Phe Glu Glu Lys Val Glu Gln
85 90 95
Gly Gly Glu Arg Trp Ser Lys Pro His Val Ala Thr Leu Ser Leu His
100 105 110
Ser Leu Phe Glu Leu Arg Thr Cys Met Glu Lys Gly Ser Ile Met Leu
115 120 125
Asp Arg Glu Ala Ser Ser Leu Pro Gln Leu Val Glu Met Ile Val Asp
130 135 140
His Gln Ile Glu Thr Gly Leu Leu Lys Pro Glu Leu Lys Asp Lys Val
145 150 155 160
Thr Tyr Thr Leu Leu Arg Lys His Arg His Gln Thr Lys Lys Ser Asn
165 170 175
Leu Arg Ser Leu Ala Asp Ile Gly Lys Thr Val Ser Ser Ala Ser Arg
180 185 190
Met Phe Thr Asn Pro Asp Asn Gly Ser Pro Ala Met Thr His Arg Asn
195 200 205
Leu Thr Ser Ser Ser Leu Asn Asp Ile Ser Asp Lys Pro Glu Lys Asp
210 215 220
Gln Leu Lys Asn Lys Phe Met Lys Lys Leu Pro Arg Asp Ala Glu Ala
225 230 235 240
Ser Asn Val Leu Val Gly Glu Val Asp Phe Leu Asp Thr Pro Phe Ile
245 250 255
Ala Phe Val Arg Leu Gln Gln Ala Val Met Leu Gly Ala Leu Thr Glu
260 265 270
Val Pro Val Pro Thr Arg Phe Leu Phe Ile Leu Leu Gly Pro Lys Gly
275 280 285
Lys Ala Lys Ser Tyr His Glu Ile Gly Arg Ala Ile Ala Thr Leu Met
290 295 300
Ser Asp Glu Val Phe His Asp Ile Ala Tyr Lys Ala Lys Asp Arg His
305 310 315 320
Asp Leu Ile Ala Gly Ile Asp Glu Phe Leu Asp Glu Val Ile Val Leu
325 330 335
Pro Pro Gly Glu Trp Asp Pro Ala Ile Arg Ile Glu Pro Pro Lys Ser
340 345 350
Leu Pro Ser Ser Asp Lys Arg Lys Asn Met Tyr Ser Gly Gly Glu Asn
355 360 365
Val Gln Met Asn Gly Asp Thr Pro His Asp Gly Gly His Gly Gly Gly
370 375 380
Gly His Gly Asp Cys Glu Glu Leu Gln Arg Thr Gly Arg Phe Cys Gly
385 390 395 400
Gly Leu Ile Lys Asp Ile Lys Arg Lys Ala Pro Phe Phe Ala Ser Asp
405 410 415
Phe Tyr Asp Ala Leu Asn Ile Gln Ala Leu Ser Ala Ile Leu Phe Ile
420 425 430
Tyr Leu Ala Thr Val Thr Asn Ala Ile Thr Phe Gly Gly Leu Leu Gly
435 440 445
Asp Ala Thr Asp Asn Met Gln Gly Val Leu Glu Ser Phe Leu Gly Thr
450 455 460
Ala Val Ser Gly Ala Ile Phe Cys Leu Phe Ala Gly Gln Pro Leu Thr
465 470 475 480
Ile Leu Ser Ser Thr Gly Pro Val Leu Val Phe Glu Arg Leu Leu Phe
485 490 495
Asn Phe Ser Lys Asp Asn Asn Phe Asp Tyr Leu Glu Phe Arg Leu Trp
500 505 510
Ile Gly Leu Trp Ser Ala Phe Leu Cys Leu Ile Leu Val Ala Thr Asp
515 520 525
Ala Ser Phe Leu Val Gln Tyr Phe Thr Arg Phe Thr Glu Glu Gly Phe
530 535 540
Ser Ser Leu Ile Ser Phe Ile Phe Ile Tyr Asp Ala Phe Lys Lys Met
545 550 555 560
Ile Lys Leu Ala Asp Tyr Tyr Pro Ile Asn Ser Asn Phe Lys Val Gly
565 570 575
Tyr Asn Thr Leu Phe Ser Cys Thr Cys Val Pro Pro Asp Pro Ala Asn
580 585 590
Ile Ser Ile Ser Asn Asp Thr Thr Leu Ala Pro Glu Tyr Leu Pro Thr
595 600 605
Met Ser Ser Thr Asp Met Tyr His Asn Thr Thr Phe Asp Trp Ala Phe

610 615 620
Leu Ser Lys Lys Glu Cys Ser Lys Tyr Gly Gly Asn Leu Val Gly Asn
625 630 635 640
Asn Cys Asn Phe Val Pro Asp Ile Thr Leu Met Ser Phe Ile Leu Phe
645 650 655
Leu Gly Thr Tyr Thr Ser Ser Met Ala Leu Lys Lys Phe Lys Thr Ser
660 665 670
Pro Tyr Phe Pro Thr Thr Ala Arg Lys Leu Ile Ser Asp Phe Ala Ile
675 680 685
Ile Leu Ser Ile Leu Ile Phe Cys Val Ile Asp Ala Leu Val Gly Val
690 695 700
Asp Thr Pro Lys Leu Ile Val Pro Ser Glu Phe Lys Pro Thr Ser Pro
705 710 715 720
Asn Arg Gly Trp Phe Val Pro Pro Phe Gly Glu Asn Pro Trp Trp Val
725 730 735
Cys Leu Ala Ala Ala Ile Pro Ala Leu Leu Val Thr Ile Leu Ile Phe
740 745 750
Met Asp Gln Gln Ile Thr Ala Val Ile Val Asn Arg Lys Glu His Lys
755 760 765
Leu Lys Lys Gly Ala Gly Tyr His Leu Asp Leu Phe Trp Val Ala Ile
770 775 780
Leu Met Val Ile Cys Ser Leu Met Ala Leu Pro Trp Tyr Val Ala Ala
785 790 795 800
Thr Val Ile Ser Ile Ala His Ile Asp Ser Leu Lys Met Glu Thr Glu
805 810 815
Thr Ser Ala Pro Gly Glu Gln Pro Lys Phe Leu Gly Val Arg Glu Gln
820 825 830
Arg Val Thr Gly Thr Leu Val Phe Ile Leu Thr Gly Leu Ser Val Phe
835 840 845
Met Ala Pro Ile Leu Lys Phe Ile Pro Met Pro Val Leu Tyr Gly Val
850 855 860
Phe Leu Tyr Met Gly Val Ala Ser Leu Asn Gly Val Gln Phe Met Asp
865 870 875 880
Arg Leu Lys Leu Leu Leu Met Pro Leu Lys His Gln Pro Asp Phe Ile
885 890 895
Tyr Leu Arg His Val Pro Leu Arg Arg Val His Leu Phe Thr Phe Leu
900 905 910
Gln Val Leu Cys Leu Ala Leu Leu Trp Ile Leu Lys Ser Thr Val Ala
915 920 925
Ala Ile Ile Phe Pro Val Met Ile Leu Ala Leu Val Ala Val Arg Lys
930 935 940
Gly Met Asp Tyr Leu Phe Ser Gln His Asp Leu Ser Phe Leu Asp Asp
945 950 955 960
Val Ile Pro Glu Lys Asp Lys Lys Lys Lys Glu Asp Glu Lys Lys Lys
965 970 975
Lys Lys Lys Lys Gly Ser Leu Asp Ser Asp Asn Asp Asp Ser Asp Cys
980 985 990
Pro Tyr Ser Glu Lys Val Pro Ser Ile Lys Ile Pro Met Asp Ile Met
995 1000 1005
Glu Gln Gln Pro Phe Leu Ser Asp Ser Lys Pro Ser Asp Arg Glu Arg
1010 1015 1020
Ser Pro Thr Phe Leu Glu Arg His Thr Ser Cys
1025 1030 1035

<210> 161
<211> 375
<212> PRT
<213> Homo sapiens

<400> 161
Met Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp
1 5 10 15
Glu Leu Lys Lys Pro Phe Ser Ile Glu Glu Val Glu Val Ala Pro Pro
20 25 30
Lys Ala His Glu Val Arg Ile Lys Met Val Ala Ala Gly Ile Cys Arg
35 40 45

```
Ser Asp Glu His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val
    50                  55                  60
Ile Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly
65                  70                  75                  80
Val Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro
                85                  90                  95
Gln Cys Gly Lys Cys Arg Ile Cys Lys Asn Pro Glu Ser Asn Tyr Cys
            100                 105                 110
Leu Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr
        115                 120                 125
Arg Arg Phe Thr Cys Ser Gly Lys Pro Ile His His Phe Val Gly Val
    130                 135                 140
Ser Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys
145                 150                 155                 160
Ile Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly
                165                 170                 175
Phe Ser Thr Gly Tyr Gly Ser Ala Val Lys Val Ala Lys Val Thr Pro
            180                 185                 190
Gly Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Val
        195                 200                 205
Val Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp
    210                 215                 220
Ile Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu
225                 230                 235                 240
Cys Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys
                245                 250                 255
Glu Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg
            260                 265                 270
Leu Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly
        275                 280                 285
Thr Ser Val Ile Val Gly Val Pro Pro Asp Ser Gln Asn Leu Ser Ile
    290                 295                 300
Asn Pro Met Leu Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Ile Phe
305                 310                 315                 320
Gly Gly Phe Lys Ser Lys Glu Ser Val Pro Lys Leu Val Ala Asp Phe
                325                 330                 335
Met Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr Asn Ile Leu Pro
            340                 345                 350
Phe Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu Arg Ser Gly Lys Ser
        355                 360                 365
Ile Arg Thr Val Leu Thr Phe
    370                 375


<210> 162
<211> 526
<212> PRT
<213> Homo sapiens

<400> 162
Met Gly His Leu Ser Ala Pro Leu His Arg Val Arg Val Pro Trp Gln
 1               5                  10                  15
Gly Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20                  25                  30
Thr Ala Gln Leu Thr Thr Glu Ser Met Pro Phe Asn Val Ala Glu Gly
        35                  40                  45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln Gln Leu Phe Gly
    50                  55                  60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Val
65                  70                  75                  80
Gly Tyr Ala Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Asn Ser
                85                  90                  95
Gly Arg Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val
            100                 105                 110
Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp
        115                 120                 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu
```

130 135 140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
145 150 155 160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
165 170 175
Leu Trp Trp Ile Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Leu Ser Val Thr Arg Asn
195 200 205
Asp Thr Gly Pro Tyr Glu Cys Glu Ile Gln Asn Pro Val Ser Ala Asn
210 215 220
Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly Pro Asp Thr Pro
225 230 235 240
Thr Ile Ser Pro Ser Asp Thr Tyr Tyr Arg Pro Gly Ala Asn Leu Ser
245 250 255
Leu Ser Cys Tyr Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Leu
260 265 270
Ile Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys His Ala Asn Asn Ser
290 295 300
Val Thr Gly Cys Asn Arg Thr Thr Val Lys Thr Ile Ile Val Thr Glu
305 310 315 320
Leu Ser Pro Val Val Ala Lys Pro Gln Ile Lys Ala Ser Lys Thr Thr
325 330 335
Val Thr Gly Asp Lys Asp Ser Val Asn Leu Thr Cys Ser Thr Asn Asp
340 345 350
Thr Gly Ile Ser Ile Arg Trp Phe Phe Lys Asn Gln Ser Leu Pro Ser
355 360 365
Ser Glu Arg Met Lys Leu Ser Gln Gly Asn Thr Thr Leu Ser Ile Asn
370 375 380
Pro Val Lys Arg Glu Asp Ala Gly Thr Tyr Trp Cys Glu Val Phe Asn
385 390 395 400
Pro Ile Ser Lys Asn Gln Ser Asp Pro Ile Met Leu Asn Val Asn Tyr
405 410 415
Asn Ala Leu Pro Gln Glu Asn Gly Leu Ser Pro Gly Ala Ile Ala Gly
420 425 430
Ile Val Ile Gly Val Val Ala Leu Val Ala Leu Ile Ala Val Ala Leu
435 440 445
Ala Cys Phe Leu His Phe Gly Lys Thr Gly Arg Ala Ser Asp Gln Arg
450 455 460
Asp Leu Thr Glu His Lys Pro Ser Val Ser Asn His Thr Gln Asp His
465 470 475 480
Ser Asn Asp Pro Pro Asn Lys Met Asn Glu Val Thr Tyr Ser Thr Leu
485 490 495
Asn Phe Glu Ala Gln Gln Pro Thr Gln Pro Thr Ser Ala Ser Pro Ser
500 505 510
Leu Thr Ala Thr Glu Ile Ile Tyr Ser Glu Val Lys Lys Gln
515 520 525

<210> 163
<211> 255
<212> PRT
<213> Homo sapiens

<400> 163
Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu Thr Ala Phe
1 5 10 15
Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Ser Ser Cys Phe
20 25 30
Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro Leu Cys Gly His
35 40 45
Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys Ile Lys Asn Met
50 55 60
Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu Leu Arg Ala Arg
65 70 75 80

Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu Tyr Pro Ala His
85 90 95
Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys Thr Ala Ile Gly
100 105 110
Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp Thr Gln Lys Leu
115 120 125
Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe Leu Glu Asn Leu
130 135 140
Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn Thr Gly Lys Val
145 150 155 160
Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly Gly Gln Thr Gln
165 170 175
Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp Val Gly Val Ala
180 185 190
Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu Ser Ser Tyr Trp
195 200 205
Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe Gln Cys Ser His
210 215 220
Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp Gly Arg Val Asp
225 230 235 240
Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr Leu Thr Ala
245 250 255

<210> 164
<211> 622
<212> PRT
<213> Homo sapiens

<400> 164
Met Pro Pro Gln Leu Gln Asn Gly Leu Asn Leu Ser Ala Lys Val Val
1 5 10 15
Gln Gly Ser Leu Asp Ser Leu Pro Gln Ala Val Arg Glu Phe Leu Glu
20 25 30
Asn Asn Ala Glu Leu Cys Gln Pro Asp His Ile His Ile Cys Asp Gly
35 40 45
Ser Glu Glu Glu Asn Gly Arg Leu Leu Gly Gln Met Glu Glu Glu Gly
50 55 60
Ile Leu Arg Arg Leu Lys Lys Tyr Asp Asn Cys Trp Leu Ala Leu Thr
65 70 75 80
Asp Pro Arg Asp Val Ala Arg Ile Glu Ser Lys Thr Val Ile Val Thr
85 90 95
Gln Glu Gln Arg Asp Thr Val Pro Ile Pro Lys Thr Gly Leu Ser Gln
100 105 110
Leu Gly Arg Trp Met Ser Glu Glu Asp Phe Glu Lys Ala Phe Asn Ala
115 120 125
Arg Phe Pro Gly Cys Met Lys Gly Arg Thr Met Tyr Val Ile Pro Phe
130 135 140
Ser Met Gly Pro Leu Gly Ser Pro Leu Ser Lys Ile Gly Ile Glu Leu
145 150 155 160
Thr Asp Ser Pro Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Met
165 170 175
Gly Thr Pro Val Leu Glu Ala Leu Gly Asp Gly Glu Phe Val Lys Cys
180 185 190
Leu His Ser Val Gly Cys Pro Leu Pro Leu Gln Lys Pro Leu Val Asn
195 200 205
Asn Trp Pro Cys Asn Pro Glu Leu Thr Leu Ile Ala His Leu Pro Asp
210 215 220
Arg Arg Glu Ile Ile Ser Phe Gly Ser Gly Tyr Gly Gly Asn Ser Leu
225 230 235 240
Leu Gly Lys Lys Cys Phe Ala Leu Arg Met Ala Ser Arg Leu Ala Glu
245 250 255
Glu Glu Gly Trp Leu Ala Glu His Met Leu Ile Leu Gly Ile Thr Asn
260 265 270
Pro Glu Gly Glu Lys Lys Tyr Leu Ala Ala Ala Phe Pro Ser Ala Cys
275 280 285
Gly Lys Thr Asn Leu Ala Met Met Asn Pro Ser Leu Pro Gly Trp Lys

290 295 300
Val Glu Cys Val Gly Asp Asp Ile Ala Trp Met Lys Phe Asp Ala Gln
305 310 315 320
Gly His Leu Arg Ala Ile Asn Pro Glu Asn Gly Phe Phe Gly Val Ala
325 330 335
Pro Gly Thr Ser Val Lys Thr Asn Pro Asn Ala Ile Lys Thr Ile Gln
340 345 350
Lys Asn Thr Ile Phe Thr Asn Val Ala Glu Thr Ser Asp Gly Gly Val
355 360 365
Tyr Trp Glu Gly Ile Asp Glu Pro Leu Ala Ser Gly Val Thr Ile Thr
370 375 380
Ser Trp Lys Asn Lys Glu Trp Ser Ser Glu Asp Gly Glu Pro Cys Ala
385 390 395 400
His Pro Asn Ser Arg Phe Cys Thr Pro Ala Ser Gln Cys Pro Ile Ile
405 410 415
Asp Ala Ala Trp Glu Ser Pro Glu Gly Val Pro Ile Glu Gly Ile Ile
420 425 430
Phe Gly Gly Arg Arg Pro Ala Gly Val Pro Leu Val Tyr Glu Ala Leu
435 440 445
Ser Trp Gln His Gly Val Phe Val Gly Ala Ala Met Arg Ser Glu Ala
450 455 460
Thr Ala Ala Ala Glu His Lys Gly Lys Ile Ile Met His Asp Pro Phe
465 470 475 480
Ala Met Arg Pro Phe Phe Gly Tyr Asn Phe Gly Lys Tyr Leu Ala His
485 490 495
Trp Leu Ser Met Ala Gln His Pro Ala Ala Lys Leu Pro Lys Ile Phe
500 505 510
His Val Asn Trp Phe Arg Lys Asp Lys Glu Gly Lys Phe Leu Trp Pro
515 520 525
Gly Phe Gly Glu Asn Ser Arg Val Leu Glu Trp Met Phe Asn Arg Ile
530 535 540
Asp Gly Lys Ala Ser Thr Asn Val Thr Pro Ile Gly Tyr Ile Pro Lys
545 550 555 560
Glu Asp Ala Leu Asn Leu Lys Gly Leu Gly His Ile Asn Met Met Glu
565 570 575
Leu Phe Ser Ile Ser Lys Glu Phe Trp Asp Lys Glu Val Glu Asp Ile
580 585 590
Glu Lys Tyr Leu Val Asp Gln Val Asn Ala Asp Leu Pro Cys Glu Ile
595 600 605
Glu Arg Glu Ile Leu Ala Leu Lys Gln Arg Ile Ser Gln Met
610 615 620

<210> 165
<211> 530
<212> PRT
<213> Homo sapiens

<400> 165
Met Ser Leu Lys Trp Met Ser Val Phe Leu Leu Met Gln Leu Ser Cys
1 5 10 15
Tyr Phe Ser Ser Gly Ser Cys Gly Lys Val Leu Val Trp Pro Thr Glu
20 25 30
Tyr Ser His Trp Ile Asn Met Lys Thr Ile Leu Glu Glu Leu Val Gln
35 40 45
Arg Gly His Glu Val Ile Val Leu Thr Ser Ser Ala Ser Ile Leu Val
50 55 60
Asn Ala Ser Lys Ser Ser Ala Ile Lys Leu Glu Val Tyr Pro Thr Ser
65 70 75 80
Leu Thr Lys Asn Asp Leu Glu Asp Phe Phe Met Lys Met Phe Asp Arg
85 90 95
Trp Thr Tyr Ser Ile Ser Lys Asn Thr Phe Trp Ser Tyr Phe Ser Gln
100 105 110
Leu Gln Glu Leu Cys Trp Glu Tyr Ser Asp Tyr Asn Ile Lys Leu Cys
115 120 125
Glu Asp Ala Val Leu Asn Lys Lys Leu Met Arg Lys Leu Gln Glu Ser
130 135 140

```
Lys Phe Asp Val Leu Leu Ala Asp Ala Val Asn Pro Cys Gly Glu Leu
145                 150                 155                 160
Leu Ala Glu Leu Leu Asn Ile Pro Phe Leu Tyr Ser Leu Arg Phe Ser
                165                 170                 175
Val Gly Tyr Thr Val Glu Lys Asn Gly Gly Gly Phe Leu Phe Pro Pro
            180                 185                 190
Ser Tyr Val Pro Val Val Met Ser Glu Leu Ser Asp Gln Met Ile Phe
        195                 200                 205
Met Glu Arg Ile Lys Asn Met Ile Tyr Met Leu Tyr Phe Asp Phe Trp
    210                 215                 220
Phe Gln Ala Tyr Asp Leu Lys Lys Trp Asp Gln Phe Tyr Ser Glu Val
225                 230                 235                 240
Leu Gly Arg Pro Thr Thr Leu Phe Glu Thr Met Gly Lys Ala Glu Met
                245                 250                 255
Trp Leu Ile Arg Thr Tyr Trp Asp Phe Glu Phe Pro Arg Pro Phe Leu
            260                 265                 270
Pro Asn Val Asp Phe Val Gly Gly Leu His Cys Lys Pro Ala Lys Pro
        275                 280                 285
Leu Pro Lys Glu Met Glu Glu Phe Val Gln Ser Ser Gly Glu Asn Gly
    290                 295                 300
Ile Val Val Phe Ser Leu Gly Ser Met Ile Ser Asn Met Ser Glu Glu
305                 310                 315                 320
Ser Ala Asn Met Ile Ala Ser Ala Leu Ala Gln Ile Pro Gln Lys Val
                325                 330                 335
Leu Trp Arg Phe Asp Gly Lys Lys Pro Asn Thr Leu Gly Ser Asn Thr
            340                 345                 350
Arg Leu Tyr Lys Trp Leu Pro Gln Asn Asp Leu Leu Gly His Pro Lys
        355                 360                 365
Thr Lys Ala Phe Ile Thr His Gly Gly Thr Asn Gly Ile Tyr Glu Ala
    370                 375                 380
Ile Tyr His Gly Ile Pro Met Val Gly Ile Pro Leu Phe Ala Asp Gln
385                 390                 395                 400
His Asp Asn Ile Ala His Met Lys Ala Lys Gly Ala Ala Leu Ser Val
                405                 410                 415
Asp Ile Arg Thr Met Ser Ser Arg Asp Leu Leu Asn Ala Leu Lys Ser
            420                 425                 430
Val Ile Asn Asp Pro Ile Tyr Lys Glu Asn Ile Met Lys Leu Ser Arg
        435                 440                 445
Ile His His Asp Gln Pro Val Lys Pro Leu Asp Arg Ala Val Phe Trp
    450                 455                 460
Ile Glu Phe Val Met Arg His Lys Gly Ala Lys His Leu Arg Val Ala
465                 470                 475                 480
Ala His Asn Leu Thr Trp Ile Gln Tyr His Ser Leu Asp Val Ile Ala
                485                 490                 495
Phe Leu Leu Ala Cys Val Ala Thr Met Ile Phe Met Ile Thr Lys Cys
            500                 505                 510
Cys Leu Phe Cys Phe Arg Lys Leu Ala Lys Thr Gly Lys Lys Lys Lys
        515                 520                 525
Arg Asp
    530
```

<210> 166
<211> 387
<212> PRT
<213> Homo sapiens

<400> 166

```
Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro
 1               5                  10                  15
Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly
            20                  25                  30
Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys
        35                  40                  45
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
    50                  55                  60
Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
```

65 70 75 80
Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
85 90 95
Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
100 105 110
Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys
115 120 125
Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln
130 135 140
Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
145 150 155 160
Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
165 170 175
Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
180 185 190
Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
195 200 205
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
210 215 220
Pro Met Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
225 230 235 240
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
245 250 255
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
260 265 270
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
275 280 285
Ala Glu Val Gln Glu Asp Tyr Gly Gln Asp Tyr Ile Leu Ala Gln Arg
290 295 300
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
305 310 315 320
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
325 330 335
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
340 345 350
Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
355 360 365
Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys
370 375 380
Lys Ala Thr
385

<210> 167
<211> 196
<212> PRT
<213> Homo sapiens

<400> 167
Met Gly Ser Arg Ser Ser His Ala Ala Val Ile Pro Asp Gly Asp Ser
1 5 10 15
Ile Arg Arg Glu Thr Gly Phe Ser Gln Ala Ser Leu Leu Arg Leu His
20 25 30
His Arg Phe Arg Ala Leu Asp Arg Asn Lys Lys Gly Tyr Leu Ser Arg
35 40 45
Met Asp Leu Gln Gln Ile Gly Ala Leu Ala Val Asn Pro Leu Gly Asp
50 55 60
Arg Ile Ile Glu Ser Phe Phe Pro Asp Gly Ser Gln Arg Val Asp Phe
65 70 75 80
Pro Gly Phe Val Arg Val Leu Ala His Phe Arg Pro Val Glu Asp Glu
85 90 95
Asp Thr Glu Thr Gln Asp Pro Lys Lys Pro Glu Pro Leu Asn Ser Arg
100 105 110
Arg Asn Lys Leu His Tyr Ala Phe Gln Leu Tyr Asp Leu Asp Arg Asp
115 120 125
Gly Lys Ile Ser Arg His Glu Met Leu Gln Val Leu Arg Leu Met Val
130 135 140

Gly Val Gln Val Thr Glu Glu Gln Leu Glu Asn Ile Ala Asp Arg Thr
145 150 155 160
Val Gln Glu Ala Asp Glu Asp Gly Asp Gly Ala Val Ser Phe Val Glu
165 170 175
Phe Thr Lys Ser Leu Glu Lys Met Asp Val Glu Gln Lys Met Ser Ile
180 185 190
Arg Ile Leu Lys
195

<210> 168
<211> 319
<212> PRT
<213> Homo sapiens

<400> 168
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu Trp
1 5 10 15
Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys Tyr Ile
20 25 30
Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala Ala Arg Thr
35 40 45
Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys Leu Thr Glu Ser
50 55 60
Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu Arg Leu Arg Thr Val
65 70 75 80
Leu Leu Asp Val Thr Asp Pro Glu Asn Val Lys Arg Thr Ala Gln Trp
85 90 95
Val Lys Asn Gln Val Gly Glu Lys Gly Leu Trp Gly Leu Ile Asn Asn
100 105 110
Ala Gly Val Pro Gly Val Leu Ala Pro Thr Asp Trp Leu Thr Leu Glu
115 120 125
Asp Tyr Arg Glu Pro Ile Glu Val Asn Leu Phe Gly Leu Ile Ser Val
130 135 140
Thr Leu Asn Met Leu Pro Leu Val Lys Lys Ala Gln Gly Arg Val Ile
145 150 155 160
Asn Val Ser Ser Val Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr
165 170 175
Thr Pro Ser Lys Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg
180 185 190
Asp Met Lys Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu
195 200 205
Phe Lys Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu
210 215 220
Ala Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
225 230 235 240
Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser Tyr
245 250 255
Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His Ala Leu
260 265 270
Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys Asp Ala Lys
275 280 285
Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala Leu Gln Asp Phe
290 295 300
Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn Pro Lys Ala Val
305 310 315

<210> 169
<211> 200
<212> PRT
<213> Homo sapiens

<400> 169
Met Gly Gln Glu Phe Ser Trp Glu Glu Ala Glu Ala Ala Gly Glu Ile
1 5 10 15
Asp Val Ala Glu Leu Gln Glu Trp Tyr Lys Lys Phe Val Met Glu Cys

```
            20                  25                  30
Pro Ser Gly Thr Leu Phe Met His Glu Phe Lys Arg Phe Phe Lys Val
        35                  40                  45
Thr Asp Asp Glu Glu Ala Ser Gln Tyr Val Glu Gly Met Phe Arg Ala
    50                  55                  60
Phe Asp Lys Asn Gly Asp Asn Thr Ile Asp Phe Leu Glu Tyr Val Ala
65                  70                  75                  80
Ala Leu Asn Leu Val Leu Arg Gly Thr Leu Glu His Lys Leu Lys Trp
                85                  90                  95
Thr Phe Lys Ile Tyr Asp Lys Asp Gly Asn Gly Cys Ile Asp Arg Leu
            100                 105                 110
Glu Leu Leu Asn Ile Val Glu Gly Ile Tyr Gln Leu Lys Lys Ala Cys
        115                 120                 125
Arg Arg Glu Leu Gln Thr Glu Gln Asp Gln Leu Leu Thr Pro Glu Glu
    130                 135                 140
Val Val Asp Arg Ile Phe Leu Leu Val Asp Glu Asn Gly Asp Gly Gln
145                 150                 155                 160
Leu Ser Leu Asn Glu Phe Val Glu Gly Ala Arg Arg Asp Lys Trp Val
                165                 170                 175
Met Lys Met Leu Gln Met Asp Met Asn Pro Ser Ser Trp Leu Ala Gln
            180                 185                 190
Gln Arg Arg Lys Ser Ala Met Phe
        195                 200


<210> 170
<211> 280
<212> PRT
<213> Homo sapiens

<400> 170
Met Ala Glu Lys Phe Asp Cys His Tyr Cys Arg Asp Pro Leu Gln Gly
 1                  5                  10                  15
Lys Lys Tyr Val Gln Lys Asp Gly His His Cys Cys Leu Lys Cys Phe
            20                  25                  30
Asp Lys Phe Cys Ala Asn Thr Cys Val Glu Cys Arg Lys Pro Ile Gly
        35                  40                  45
Ala Asp Ser Lys Glu Val His Tyr Lys Asn Arg Phe Trp His Asp Thr
    50                  55                  60
Cys Phe Arg Cys Ala Lys Cys Leu His Pro Leu Ala Asn Glu Thr Phe
65                  70                  75                  80
Val Ala Lys Asp Asn Lys Ile Leu Cys Asn Lys Cys Thr Thr Arg Glu
                85                  90                  95
Asp Ser Pro Lys Cys Lys Gly Cys Phe Lys Ala Ile Val Ala Gly Asp
            100                 105                 110
Gln Asn Val Glu Tyr Lys Gly Thr Val Trp His Lys Asp Cys Phe Thr
        115                 120                 125
Cys Ser Asn Cys Lys Gln Val Ile Gly Thr Gly Ser Phe Phe Pro Lys
    130                 135                 140
Gly Glu Asp Phe Tyr Cys Val Thr Cys His Glu Thr Lys Phe Ala Lys
145                 150                 155                 160
His Cys Val Lys Cys Asn Lys Ala Ile Thr Ser Gly Gly Ile Thr Tyr
                165                 170                 175
Gln Asp Gln Pro Trp His Ala Asp Cys Phe Val Cys Val Thr Cys Ser
            180                 185                 190
Lys Lys Leu Ala Gly Gln Arg Phe Thr Ala Val Glu Asp Gln Tyr Tyr
        195                 200                 205
Cys Val Asp Cys Tyr Lys Asn Phe Val Ala Lys Lys Cys Ala Gly Cys
    210                 215                 220
Lys Asn Pro Ile Thr Gly Phe Gly Lys Gly Ser Ser Val Val Ala Tyr
225                 230                 235                 240
Glu Gly Gln Ser Trp His Asp Tyr Cys Phe His Cys Lys Lys Cys Ser
                245                 250                 255
Val Asn Leu Ala Asn Lys Arg Phe Val Phe His Gln Glu Gln Val Tyr
            260                 265                 270
Cys Pro Asp Cys Ala Lys Lys Leu
        275                 280
```

<210> 171
<211> 470
<212> PRT
<213> Homo sapiens

<400> 171

```
Met Leu Arg Gly Ile Ser Gln Leu Pro Ala Val Ala Thr Met Ser Trp
 1               5                  10                  15
Val Leu Leu Pro Val Leu Trp Leu Ile Val Gln Thr Gln Ala Ile Ala
            20                  25                  30
Ile Lys Gln Thr Pro Glu Leu Thr Leu His Glu Ile Val Cys Pro Lys
        35                  40                  45
Lys Leu His Ile Leu His Lys Arg Glu Ile Lys Asn Asn Gln Thr Glu
    50                  55                  60
Lys His Gly Lys Glu Glu Arg Tyr Glu Pro Glu Val Gln Tyr Gln Met
65                  70                  75                  80
Ile Leu Asn Gly Glu Glu Ile Ile Leu Ser Leu Gln Lys Thr Lys His
                85                  90                  95
Leu Leu Gly Pro Asp Tyr Thr Glu Thr Leu Tyr Ser Pro Arg Gly Glu
            100                 105                 110
Glu Ile Thr Thr Lys Pro Glu Asn Met Glu His Cys Tyr Tyr Lys Gly
        115                 120                 125
Asn Ile Leu Asn Glu Lys Asn Ser Val Ala Ser Ile Ser Thr Cys Asp
    130                 135                 140
Gly Leu Arg Gly Tyr Phe Thr His His His Gln Arg Tyr Gln Ile Lys
145                 150                 155                 160
Pro Leu Lys Ser Thr Asp Glu Lys Glu His Ala Val Phe Thr Ser Asn
                165                 170                 175
Gln Glu Glu Gln Asp Pro Ala Asn His Thr Cys Gly Val Lys Ser Thr
            180                 185                 190
Asp Gly Lys Gln Gly Pro Ile Arg Ile Ser Arg Ser Leu Lys Ser Pro
        195                 200                 205
Glu Lys Glu Asp Phe Leu Arg Ala Gln Lys Tyr Ile Asp Leu Tyr Leu
    210                 215                 220
Val Leu Asp Asn Ala Phe Tyr Lys Asn Tyr Asn Glu Asn Leu Thr Leu
225                 230                 235                 240
Ile Arg Ser Phe Val Phe Asp Val Met Asn Leu Leu Asn Val Ile Tyr
                245                 250                 255
Asn Thr Ile Asp Val Gln Val Ala Leu Val Gly Met Glu Ile Trp Ser
            260                 265                 270
Asp Gly Asp Lys Ile Lys Val Val Pro Ser Ala Ser Thr Thr Phe Asp
        275                 280                 285
Asn Phe Leu Arg Trp His Ser Ser Asn Leu Gly Lys Lys Ile His Asp
    290                 295                 300
His Ala Gln Leu Leu Ser Gly Ile Ser Phe Asn Asn Arg Arg Val Gly
305                 310                 315                 320
Leu Ala Ala Ser Asn Ser Leu Cys Ser Pro Ser Ser Val Ala Val Ile
                325                 330                 335
Glu Ala Lys Lys Lys Asn Asn Val Ala Leu Val Gly Val Met Ser His
            340                 345                 350
Glu Leu Gly His Val Leu Gly Met Pro Asp Val Pro Phe Asn Thr Lys
        355                 360                 365
Cys Pro Ser Gly Ser Cys Val Met Asn Gln Tyr Leu Ser Ser Lys Phe
    370                 375                 380
Pro Lys Asp Phe Ser Thr Ser Cys Arg Ala His Phe Glu Arg Tyr Leu
385                 390                 395                 400
Leu Ser Gln Lys Pro Lys Cys Leu Leu Gln Ala Pro Ile Pro Thr Asn
                405                 410                 415
Ile Met Thr Thr Pro Val Cys Gly Asn His Leu Leu Glu Val Gly Glu
            420                 425                 430
Asp Cys Asp Cys Gly Ser Pro Lys Glu Cys Thr Asn Leu Cys Cys Glu
        435                 440                 445
Ala Leu Thr Cys Lys Leu Lys Pro Gly Thr Asp Cys Gly Gly Asp Ala
    450                 455                 460
Pro Asn His Thr Thr Glu
```

465 470

<210> 172
<211> 86
<212> PRT
<213> Homo sapiens

<400> 172
Met Ala Val Arg Gln Trp Val Ile Ala Leu Ala Leu Ala Ala Leu Leu
1 5 10 15
Val Val Asp Arg Glu Val Pro Val Ala Ala Gly Lys Leu Pro Phe Ser
20 25 30
Arg Met Pro Ile Cys Glu His Met Val Glu Ser Pro Thr Cys Ser Gln
35 40 45
Met Ser Asn Leu Val Cys Gly Thr Asp Gly Leu Thr Tyr Thr Asn Glu
50 55 60
Cys Gln Leu Cys Leu Ala Arg Ile Lys Thr Lys Gln Asp Ile Gln Ile
65 70 75 80
Met Lys Asp Gly Lys Cys
85

<210> 173
<211> 261
<212> PRT
<213> Homo sapiens

<400> 173
Met Ala Ser Pro Asp Trp Gly Tyr Asp Asp Lys Asn Gly Pro Glu Gln
1 5 10 15
Trp Ser Lys Leu Tyr Pro Ile Ala Asn Gly Asn Asn Gln Ser Pro Val
20 25 30
Asp Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro Ile
35 40 45
Ser Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val Gly
50 55 60
His Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val Leu
65 70 75 80
Lys Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His Phe
85 90 95
His Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp Gly
100 105 110
Val Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala Lys
115 120 125
Tyr Ser Ser Leu Ala Glu Ala Ala Ser Lys Ala Asp Gly Leu Ala Val
130 135 140
Ile Gly Val Leu Met Lys Val Gly Glu Ala Asn Pro Lys Leu Gln Lys
145 150 155 160
Val Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala Pro
165 170 175
Phe Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp Phe
180 185 190
Trp Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser Val
195 200 205
Thr Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln Leu
210 215 220
Ala Gln Phe Arg Ser Leu Leu Ser Asn Val Glu Gly Asp Asn Ala Val
225 230 235 240
Pro Met Gln His Asn Asn Arg Pro Thr Gln Pro Leu Lys Gly Arg Thr
245 250 255
Val Arg Ala Ser Phe
260

<210> 174
<211> 431

<212> PRT
<213> Homo sapiens

<400> 174
Met Thr Val Lys Thr Glu Ala Ala Lys Gly Thr Leu Thr Tyr Ser Arg
1 5 10 15
Met Arg Gly Met Val Ala Ile Leu Ile Ala Phe Met Lys Gln Arg Arg
20 25 30
Met Gly Leu Asn Asp Phe Ile Gln Lys Ile Ala Asn Asn Ser Tyr Ala
35 40 45
Cys Lys His Pro Glu Val Gln Ser Ile Leu Lys Ile Ser Gln Pro Gln
50 55 60
Glu Pro Glu Leu Met Asn Ala Asn Pro Ser Pro Pro Pro Ser Pro Ser
65 70 75 80
Gln Gln Ile Asn Leu Gly Pro Ser Ser Asn Pro His Ala Lys Pro Ser
85 90 95
Asp Phe His Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val
100 105 110
Leu Leu Ala Arg His Lys Ala Glu Glu Val Phe Tyr Ala Val Lys Val
115 120 125
Leu Gln Lys Lys Ala Ile Leu Lys Lys Lys Glu Glu Lys His Ile Met
130 135 140
Ser Glu Arg Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val
145 150 155 160
Gly Leu His Phe Ser Phe Gln Thr Ala Asp Lys Leu Tyr Phe Val Leu
165 170 175
Asp Tyr Ile Asn Gly Gly Glu Leu Phe Tyr His Leu Gln Arg Glu Arg
180 185 190
Cys Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser
195 200 205
Ala Leu Gly Tyr Leu His Ser Leu Asn Ile Val Tyr Arg Asp Leu Lys
210 215 220
Pro Glu Asn Ile Leu Leu Asp Ser Gln Gly His Ile Val Leu Thr Asp
225 230 235 240
Phe Gly Leu Cys Lys Glu Asn Ile Glu His Asn Ser Thr Thr Ser Thr
245 250 255
Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu His Lys Gln
260 265 270
Pro Tyr Asp Arg Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr
275 280 285
Glu Met Leu Tyr Gly Leu Pro Pro Phe Tyr Ser Arg Asn Thr Ala Glu
290 295 300
Met Tyr Asp Asn Ile Leu Asn Lys Pro Leu Gln Leu Lys Pro Asn Ile
305 310 315 320
Thr Asn Ser Ala Arg His Leu Leu Glu Gly Leu Leu Gln Lys Asp Arg
325 330 335
Thr Lys Arg Leu Gly Ala Lys Asp Asp Phe Met Glu Ile Lys Ser His
340 345 350
Val Phe Phe Ser Leu Ile Asn Trp Asp Asp Leu Ile Asn Lys Lys Ile
355 360 365
Thr Pro Pro Phe Asn Pro Asn Val Ser Gly Pro Asn Asp Leu Arg His
370 375 380
Phe Asp Pro Glu Phe Thr Glu Glu Pro Val Pro Asn Ser Ile Gly Lys
385 390 395 400
Ser Pro Asp Ser Val Leu Val Thr Ala Ser Val Lys Glu Ala Ala Glu
405 410 415
Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro Thr Asp Ser Phe Leu
420 425 430

<210> 175
<211> 381
<212> PRT
<213> Homo sapiens

<400> 175
Met Pro Phe Ser Asn Ser His Asn Ala Leu Lys Leu Arg Phe Pro Ala

```
 1               5                  10                  15
Glu Asp Glu Phe Pro Asp Leu Ser Ala His Asn Asn His Met Ala Lys
            20                  25                  30
Val Leu Thr Pro Glu Leu Tyr Ala Glu Leu Arg Ala Lys Ser Thr Pro
        35                  40                  45
Ser Gly Phe Thr Leu Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
    50                  55                  60
Gly His Pro Tyr Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
65                  70                  75                  80
Ser Tyr Glu Val Phe Lys Asp Leu Phe Asp Pro Ile Ile Glu Asp Arg
                85                  90                  95
His Gly Gly Tyr Lys Pro Ser Asp Glu His Lys Thr Asp Leu Asn Pro
            100                 105                 110
Asp Asn Leu Gln Gly Gly Asp Asp Leu Asp Pro Asn Tyr Val Leu Ser
        115                 120                 125
Ser Arg Val Arg Thr Gly Arg Ser Ile Arg Gly Phe Cys Leu Pro Pro
    130                 135                 140
His Cys Ser Arg Gly Glu Arg Arg Ala Ile Glu Lys Leu Ala Val Glu
145                 150                 155                 160
Ala Leu Ser Ser Leu Asp Gly Asp Leu Ala Gly Arg Tyr Tyr Ala Leu
                165                 170                 175
Lys Ser Met Thr Glu Ala Glu Gln Gln Gln Leu Ile Asp Asp His Phe
            180                 185                 190
Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ser Gly Met Ala
        195                 200                 205
Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Asp Asn Lys Thr
    210                 215                 220
Phe Leu Val Trp Val Asn Glu Glu Asp His Leu Arg Val Ile Ser Met
225                 230                 235                 240
Gln Lys Gly Gly Asn Met Lys Glu Val Phe Thr Arg Phe Cys Thr Gly
                245                 250                 255
Leu Thr Gln Ile Glu Thr Leu Phe Lys Ser Lys Asp Tyr Glu Phe Met
            260                 265                 270
Trp Asn Pro His Leu Gly Tyr Ile Leu Thr Cys Pro Ser Asn Leu Gly
        275                 280                 285
Thr Gly Leu Arg Ala Gly Val His Ile Lys Leu Pro Asn Leu Gly Lys
    290                 295                 300
His Glu Lys Phe Ser Glu Val Leu Lys Arg Leu Arg Leu Gln Lys Arg
305                 310                 315                 320
Gly Thr Gly Gly Val Asp Thr Ala Ala Val Gly Gly Val Phe Asp Val
                325                 330                 335
Ser Asn Ala Asp Arg Leu Gly Phe Ser Glu Val Glu Leu Val Gln Met
            340                 345                 350
Val Val Asp Gly Val Lys Leu Leu Ile Glu Met Glu Gln Arg Leu Glu
        355                 360                 365
Gln Gly Gln Ala Ile Asp Asp Leu Met Pro Ala Gln Lys
    370                 375                 380


<210> 176
<211> 739
<212> PRT
<213> Homo sapiens

<400> 176
Met Ser Ser Glu Ser Lys Glu Gln His Asn Val Ser Pro Arg Asp Ser
 1               5                  10                  15
Ala Glu Gly Asn Asp Ser Tyr Pro Ser Gly Ile His Leu Glu Leu Gln
            20                  25                  30
Arg Glu Ser Ser Thr Asp Phe Lys Gln Phe Glu Thr Asn Asp Gln Cys
        35                  40                  45
Arg Pro Tyr His Arg Ile Leu Ile Glu Arg Gln Glu Lys Ser Asp Thr
    50                  55                  60
Asn Phe Lys Glu Phe Val Ile Lys Lys Leu Gln Lys Asn Cys Gln Cys
65                  70                  75                  80
Ser Pro Ala Lys Ala Lys Asn Met Ile Leu Gly Phe Leu Pro Val Leu
                85                  90                  95
```

Gln Trp Leu Pro Lys Tyr Asp Leu Lys Lys Asn Ile Leu Gly Asp Val
100 105 110
Met Ser Gly Leu Ile Val Gly Ile Leu Leu Val Pro Gln Ser Ile Ala
115 120 125
Tyr Ser Leu Leu Ala Gly Gln Glu Pro Val Tyr Gly Leu Tyr Thr Ser
130 135 140
Phe Phe Ala Ser Ile Ile Tyr Phe Leu Leu Gly Thr Ser Arg His Ile
145 150 155 160
Ser Val Gly Ile Phe Gly Val Leu Cys Leu Met Ile Gly Glu Thr Val
165 170 175
Asp Arg Glu Leu Gln Lys Ala Gly Tyr Asp Asn Ala His Ser Ala Pro
180 185 190
Ser Leu Gly Met Val Ser Asn Gly Ser Thr Leu Leu Asn His Thr Ser
195 200 205
Asp Arg Ile Cys Asp Lys Ser Cys Tyr Ala Ile Met Val Gly Ser Thr
210 215 220
Val Thr Phe Ile Ala Gly Val Tyr Gln Val Ala Met Gly Phe Phe Gln
225 230 235 240
Val Gly Phe Val Ser Val Tyr Leu Ser Asp Ala Leu Leu Ser Gly Phe
245 250 255
Val Thr Gly Ala Ser Phe Thr Ile Leu Thr Ser Gln Ala Lys Tyr Leu
260 265 270
Leu Gly Leu Asn Leu Pro Arg Thr Asn Gly Val Gly Ser Leu Ile Thr
275 280 285
Thr Trp Ile His Val Phe Arg Asn Ile His Lys Thr Asn Leu Cys Asp
290 295 300
Leu Ile Thr Ser Leu Leu Cys Leu Leu Val Leu Leu Pro Thr Lys Glu
305 310 315 320
Leu Asn Glu His Phe Lys Ser Lys Leu Lys Ala Pro Ile Pro Ile Glu
325 330 335
Leu Val Val Val Val Ala Ala Thr Leu Ala Ser His Phe Gly Lys Leu
340 345 350
His Glu Asn Tyr Asn Ser Ser Ile Ala Gly His Ile Pro Thr Gly Phe
355 360 365
Met Pro Pro Lys Val Pro Glu Trp Asn Leu Ile Pro Ser Val Ala Val
370 375 380
Asp Ala Ile Ala Ile Ser Ile Ile Gly Phe Ala Ile Thr Val Ser Leu
385 390 395 400
Ser Glu Met Phe Ala Lys Lys His Gly Tyr Thr Val Lys Ala Asn Gln
405 410 415
Glu Met Tyr Ala Ile Gly Phe Cys Asn Ile Ile Pro Ser Phe Phe His
420 425 430
Cys Phe Thr Thr Ser Ala Ala Leu Ala Lys Thr Leu Val Lys Glu Ser
435 440 445
Thr Gly Cys His Thr Gln Leu Ser Gly Val Val Thr Ala Leu Val Leu
450 455 460
Leu Leu Val Leu Leu Val Ile Ala Pro Leu Phe Tyr Ser Leu Gln Lys
465 470 475 480
Ser Val Leu Gly Val Ile Thr Ile Val Asn Leu Arg Gly Ala Leu Arg
485 490 495
Lys Phe Arg Asp Leu Pro Lys Met Trp Ser Ile Ser Arg Met Asp Thr
500 505 510
Val Ile Trp Phe Val Thr Met Leu Ser Ser Ala Leu Leu Ser Thr Glu
515 520 525
Ile Gly Leu Leu Val Gly Val Cys Phe Ser Ile Phe Cys Val Ile Leu
530 535 540
Arg Thr Gln Lys Pro Lys Ser Ser Leu Leu Gly Leu Val Glu Glu Ser
545 550 555 560
Glu Val Phe Glu Ser Val Ser Ala Tyr Lys Asn Leu Gln Thr Lys Pro
565 570 575
Gly Ile Lys Ile Phe Arg Phe Val Ala Pro Leu Tyr Tyr Ile Asn Lys
580 585 590
Glu Cys Phe Lys Ser Ala Leu Tyr Lys Gln Thr Val Asn Pro Ile Leu
595 600 605
Ile Lys Val Ala Trp Lys Lys Ala Ala Lys Arg Lys Ile Lys Glu Lys
610 615 620
Val Val Thr Leu Gly Gly Ile Gln Asp Glu Met Ser Val Gln Leu Ser

625 630 635 640
His Asp Pro Leu Glu Leu His Thr Ile Val Ile Asp Cys Ser Ala Ile
645 650 655
Gln Phe Leu Asp Thr Ala Gly Ile His Thr Leu Lys Glu Val Arg Arg
660 665 670
Asp Tyr Glu Ala Ile Gly Ile Gln Val Leu Leu Ala Gln Cys Asn Pro
675 680 685
Thr Val Arg Asp Ser Leu Thr Asn Gly Glu Tyr Cys Lys Lys Glu Glu
690 695 700
Glu Asn Leu Leu Phe Tyr Ser Val Tyr Glu Ala Met Ala Phe Ala Glu
705 710 715 720
Val Ser Lys Asn Gln Lys Gly Val Cys Val Pro Asn Gly Leu Ser Leu
725 730 735
Ser Ser Asp

<210> 177
<211> 709
<212> PRT
<213> Homo sapiens

<400> 177
Met Ala Glu Val Glu Asp Gln Ala Ala Arg Asp Met Lys Arg Leu Glu
1 5 10 15
Glu Lys Asp Lys Glu Arg Lys Asn Val Lys Gly Ile Arg Asp Asp Ile
20 25 30
Glu Glu Glu Asp Asp Gln Glu Ala Tyr Phe Arg Tyr Met Ala Glu Asn
35 40 45
Pro Thr Ala Gly Val Val Gln Glu Glu Glu Glu Asp Asn Leu Glu Tyr
50 55 60
Asp Ser Asp Gly Asn Pro Ile Ala Pro Thr Lys Lys Ile Ile Asp Pro
65 70 75 80
Leu Pro Pro Ile Asp His Ser Glu Ile Asp Tyr Pro Pro Phe Glu Lys
85 90 95
Asn Phe Tyr Asn Glu His Glu Glu Ile Thr Asn Leu Thr Pro Gln Gln
100 105 110
Leu Ile Asp Leu Arg His Lys Leu Asn Leu Arg Val Ser Gly Ala Ala
115 120 125
Pro Pro Arg Pro Gly Ser Ser Phe Ala His Phe Gly Phe Asp Glu Gln
130 135 140
Leu Met His Gln Ile Arg Lys Ser Glu Tyr Thr Gln Pro Thr Pro Ile
145 150 155 160
Gln Cys Gln Gly Val Pro Val Ala Leu Ser Gly Arg Asp Met Ile Gly
165 170 175
Ile Ala Lys Thr Gly Ser Gly Lys Thr Ala Ala Phe Ile Trp Pro Met
180 185 190
Leu Ile His Ile Met Asp Gln Lys Glu Leu Glu Pro Gly Asp Gly Pro
195 200 205
Ile Ala Val Ile Val Cys Pro Thr Arg Glu Leu Cys Gln Gln Ile His
210 215 220
Ala Glu Cys Lys Arg Phe Gly Lys Ala Tyr Asn Leu Arg Ser Val Ala
225 230 235 240
Val Tyr Gly Gly Gly Ser Met Trp Glu Gln Ala Lys Ala Leu Gln Glu
245 250 255
Gly Ala Glu Ile Val Val Cys Thr Pro Gly Arg Leu Ile Asp His Val
260 265 270
Lys Lys Lys Ala Thr Asn Leu Gln Arg Val Ser Tyr Leu Val Phe Asp
275 280 285
Glu Ala Asp Arg Met Phe Asp Met Gly Phe Glu Tyr Gln Val Arg Ser
290 295 300
Ile Ala Ser His Val Arg Pro Asp Arg Gln Thr Leu Leu Phe Ser Ala
305 310 315 320
Thr Phe Arg Lys Lys Ile Glu Lys Leu Ala Arg Asp Ile Leu Ile Asp
325 330 335
Pro Ile Arg Val Val Gln Gly Asp Ile Gly Glu Ala Asn Glu Asp Val
340 345 350

Thr Gln Ile Val Glu Ile Leu His Ser Gly Pro Ser Lys Trp Asn Trp
355 360 365
Leu Thr Arg Arg Leu Val Glu Phe Thr Ser Ser Gly Ser Val Leu Leu
370 375 380
Phe Val Thr Lys Lys Ala Asn Ala Glu Glu Leu Ala Asn Asn Leu Lys
385 390 395 400
Gln Glu Gly His Asn Leu Gly Leu Leu His Gly Asp Met Asp Gln Ser
405 410 415
Glu Arg Asn Lys Val Ile Ser Asp Phe Lys Lys Lys Asp Ile Pro Val
420 425 430
Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Ser Ile
435 440 445
Lys Thr Val Ile Asn Tyr Asp Val Ala Arg Asp Ile Asp Thr His Thr
450 455 460
His Arg Ile Gly Arg Thr Gly Arg Ala Gly Glu Lys Gly Val Ala Tyr
465 470 475 480
Thr Leu Leu Thr Pro Lys Asp Ser Asn Phe Ala Gly Asp Leu Val Arg
485 490 495
Asn Leu Glu Gly Ala Asn Gln His Val Ser Lys Glu Leu Leu Asp Leu
500 505 510
Ala Met Gln Asn Ala Trp Phe Arg Lys Ser Arg Phe Lys Gly Gly Lys
515 520 525
Gly Lys Lys Leu Asn Ile Gly Gly Gly Gly Leu Gly Tyr Arg Glu Arg
530 535 540
Pro Gly Leu Gly Ser Glu Asn Met Asp Arg Gly Asn Asn Asn Val Met
545 550 555 560
Ser Asn Tyr Glu Ala Tyr Lys Pro Ser Thr Gly Ala Met Gly Asp Arg
565 570 575
Leu Thr Ala Met Lys Ala Ala Phe Gln Ser Gln Tyr Lys Ser His Phe
580 585 590
Val Ala Ala Ser Leu Ser Asn Gln Lys Ala Gly Ser Ser Ala Ala Gly
595 600 605
Ala Ser Gly Trp Thr Ser Ala Gly Ser Leu Asn Ser Val Pro Thr Asn
610 615 620
Ser Ala Gln Gln Gly His Asn Ser Pro Asp Ser Pro Val Thr Ser Ala
625 630 635 640
Ala Lys Gly Ile Pro Gly Phe Gly Asn Thr Gly Asn Ile Ser Gly Ala
645 650 655
Pro Val Thr Tyr Pro Ser Ala Gly Ala Gln Gly Val Asn Asn Thr Ala
660 665 670
Ser Gly Asn Asn Ser Arg Glu Gly Thr Gly Gly Ser Asn Gly Lys Arg
675 680 685
Glu Arg Tyr Thr Glu Asn Arg Gly Ser Ser Pro Ser Gln Ser Arg Arg
690 695 700
Asp Trp Gln Ser Ala
705

<210> 178
<211> 5178
<212> PRT
<213> Homo sapiens

<400> 178
Met Gly Leu Pro Leu Ala Arg Leu Ala Ala Val Cys Leu Ala Leu Ser
1 5 10 15
Leu Ala Gly Gly Ser Glu Leu Gln Thr Glu Gly Arg Thr Arg Tyr His
20 25 30
Gly Arg Asn Val Cys Ser Thr Trp Gly Asn Phe His Tyr Lys Thr Phe
35 40 45
Asp Gly Asp Val Phe Arg Phe Pro Gly Leu Cys Asp Tyr Asn Phe Ala
50 55 60
Ser Asp Cys Arg Gly Ser Tyr Lys Glu Phe Ala Val His Leu Lys Arg
65 70 75 80
Gly Pro Gly Gln Ala Glu Ala Pro Ala Gly Val Glu Ser Ile Leu Leu
85 90 95
Thr Ile Lys Asp Asp Thr Ile Tyr Leu Thr Arg His Leu Ala Val Leu

100 105 110
Asn Gly Ala Val Val Ser Thr Pro His Tyr Ser Pro Gly Leu Leu Ile
115 120 125
Glu Lys Ser Asp Ala Tyr Thr Lys Val Tyr Ser Arg Ala Gly Leu Thr
130 135 140
Leu Met Trp Asn Arg Glu Asp Ala Leu Met Leu Glu Leu Asp Thr Lys
145 150 155 160
Phe Arg Asn His Thr Cys Gly Leu Cys Gly Asp Tyr Asn Gly Leu Gln
165 170 175
Ser Tyr Ser Glu Phe Leu Ser Asp Gly Val Leu Phe Ser Pro Leu Glu
180 185 190
Phe Gly Asn Met Gln Lys Ile Asn Gln Pro Asp Val Val Cys Glu Asp
195 200 205
Pro Glu Glu Glu Val Ala Pro Ala Ser Cys Ser Glu His Arg Ala Glu
210 215 220
Cys Glu Arg Leu Leu Thr Ala Glu Ala Phe Ala Asp Cys Gln Asp Leu
225 230 235 240
Val Pro Leu Glu Pro Tyr Leu Arg Ala Cys Gln Gln Asp Arg Cys Arg
245 250 255
Cys Pro Gly Gly Asp Thr Cys Val Cys Ser Thr Val Ala Glu Phe Ser
260 265 270
Arg Gln Cys Ser His Ala Gly Gly Arg Pro Gly Asn Trp Arg Thr Ala
275 280 285
Thr Leu Cys Pro Lys Thr Cys Pro Gly Asn Leu Val Tyr Leu Glu Ser
290 295 300
Gly Ser Pro Cys Met Asp Thr Cys Ser His Leu Glu Val Ser Ser Leu
305 310 315 320
Cys Glu Glu His Arg Met Asp Gly Cys Phe Cys Pro Glu Gly Thr Val
325 330 335
Tyr Asp Asp Ile Gly Asp Ser Gly Cys Val Pro Val Ser Gln Cys His
340 345 350
Cys Arg Leu His Gly His Leu Tyr Thr Pro Gly Gln Glu Ile Thr Asn
355 360 365
Asp Cys Glu Gln Cys Val Cys Asn Ala Gly Arg Trp Val Cys Lys Asp
370 375 380
Leu Pro Cys Pro Gly Thr Cys Ala Leu Glu Gly Gly Ser His Ile Thr
385 390 395 400
Thr Phe Asp Gly Lys Thr Tyr Thr Phe His Gly Asp Cys Tyr Tyr Val
405 410 415
Leu Ala Lys Gly Asp His Asn Asp Ser Tyr Ala Leu Leu Gly Glu Leu
420 425 430
Ala Pro Cys Gly Ser Thr Asp Lys Gln Thr Cys Leu Lys Thr Val Val
435 440 445
Leu Leu Ala Asp Lys Lys Lys Asn Ala Val Val Phe Lys Ser Asp Gly
450 455 460
Ser Val Leu Leu Asn Gln Leu Gln Val Asn Leu Pro His Val Thr Ala
465 470 475 480
Ser Phe Ser Val Phe Arg Pro Ser Ser Tyr His Ile Met Val Ser Met
485 490 495
Ala Ile Gly Val Arg Leu Gln Val Gln Leu Ala Pro Val Met Gln Leu
500 505 510
Phe Val Thr Leu Asp Gln Ala Ser Gln Gly Gln Val Gln Gly Leu Cys
515 520 525
Gly Asn Phe Asn Gly Leu Glu Gly Asp Asp Phe Lys Thr Ala Ser Gly
530 535 540
Leu Val Glu Ala Thr Gly Ala Gly Phe Ala Asn Thr Trp Lys Ala Gln
545 550 555 560
Ser Thr Cys His Asp Lys Leu Asp Trp Leu Asp Asp Pro Cys Ser Leu
565 570 575
Asn Ile Glu Ser Ala Asn Tyr Ala Glu His Trp Cys Ser Leu Leu Lys
580 585 590
Lys Thr Glu Thr Pro Phe Gly Arg Cys His Ser Ala Val Asp Pro Ala
595 600 605
Glu Tyr Tyr Lys Arg Cys Lys Tyr Asp Thr Cys Asn Cys Gln Asn Asn
610 615 620
Glu Asp Cys Leu Cys Ala Ala Leu Ser Ser Tyr Ala Arg Ala Cys Thr
625 630 635 640

Ala Lys Gly Val Met Leu Trp Gly Trp Arg Glu His Val Cys Asn Lys
645 650 655
Asp Val Gly Ser Cys Pro Asn Ser Gln Val Phe Leu Tyr Asn Leu Thr
660 665 670
Thr Cys Gln Gln Thr Cys Arg Ser Leu Ser Glu Ala Asp Ser His Cys
675 680 685
Leu Glu Gly Phe Ala Pro Val Asp Gly Cys Gly Cys Pro Asp His Thr
690 695 700
Phe Leu Asp Glu Lys Gly Arg Cys Val Pro Leu Ala Lys Cys Ser Cys
705 710 715 720
Tyr His Arg Gly Leu Tyr Leu Glu Ala Gly Asp Val Val Val Arg Gln
725 730 735
Glu Glu Arg Cys Val Cys Arg Asp Gly Arg Leu His Cys Arg Gln Ile
740 745 750
Arg Leu Ile Gly Gln Ser Cys Thr Ala Pro Lys Ile His Met Asp Cys
755 760 765
Ser Asn Leu Thr Ala Leu Ala Thr Ser Lys Pro Arg Ala Leu Ser Cys
770 775 780
Gln Thr Leu Ala Ala Gly Tyr Tyr His Thr Glu Cys Val Ser Gly Cys
785 790 795 800
Val Cys Pro Asp Gly Leu Met Asp Asp Gly Arg Gly Gly Cys Val Val
805 810 815
Glu Lys Glu Cys Pro Cys Val His Asn Asn Asp Leu Tyr Ser Ser Gly
820 825 830
Ala Lys Ile Lys Val Asp Cys Asn Thr Cys Thr Cys Lys Arg Gly Arg
835 840 845
Trp Val Cys Thr Gln Ala Val Cys His Gly Thr Cys Ser Ile Tyr Gly
850 855 860
Ser Gly His Tyr Ile Thr Phe Asp Gly Lys Tyr Tyr Asp Phe Asp Gly
865 870 875 880
His Cys Ser Tyr Val Ala Val Gln Asp Tyr Cys Gly Gln Asn Ser Ser
885 890 895
Leu Gly Ser Phe Ser Ile Ile Thr Glu Asn Val Pro Cys Gly Thr Thr
900 905 910
Gly Val Thr Cys Ser Lys Ala Ile Lys Ile Phe Met Gly Arg Thr Glu
915 920 925
Leu Lys Leu Glu Asp Lys His Arg Val Val Ile Gln Arg Asp Glu Gly
930 935 940
His His Val Ala Tyr Thr Thr Arg Glu Val Gly Gln Tyr Leu Val Val
945 950 955 960
Glu Ser Ser Thr Gly Ile Ile Val Ile Trp Asp Lys Arg Thr Thr Val
965 970 975
Phe Ile Lys Leu Ala Pro Ser Tyr Lys Gly Thr Val Cys Gly Leu Cys
980 985 990
Gly Asn Phe Asp His Arg Ser Asn Asn Asp Phe Thr Thr Arg Asp His
995 1000 1005
Met Val Val Ser Ser Glu Leu Asp Phe Gly Asn Ser Trp Lys Glu Ala
1010 1015 1020
Pro Thr Cys Pro Asp Val Ser Thr Asn Pro Glu Pro Cys Ser Leu Asn
1025 1030 1035 1040
Pro His Arg Arg Ser Trp Ala Glu Lys Gln Cys Ser Ile Leu Lys Ser
1045 1050 1055
Ser Val Phe Ser Ile Cys His Ser Lys Val Asp Pro Lys Pro Phe Tyr
1060 1065 1070
Glu Ala Cys Val His Asp Ser Cys Ser Cys Asp Thr Gly Gly Asp Cys
1075 1080 1085
Glu Cys Phe Cys Ser Ala Val Ala Ser Tyr Ala Gln Glu Cys Thr Lys
1090 1095 1100
Glu Gly Ala Cys Val Phe Trp Arg Thr Pro Asp Leu Cys Pro Ile Phe
1105 1110 1115 1120
Cys Asp Tyr Tyr Asn Pro Pro His Glu Cys Glu Trp His Tyr Glu Pro
1125 1130 1135
Cys Gly Asn Arg Ser Phe Glu Thr Cys Arg Thr Ile Asn Gly Ile His
1140 1145 1150
Ser Asn Ile Ser Val Ser Tyr Leu Glu Gly Cys Tyr Pro Arg Cys Pro
1155 1160 1165
Lys Asp Arg Pro Ile Tyr Glu Glu Asp Leu Lys Lys Cys Val Thr Ala

1170 1175 1180
Asp Lys Cys Gly Cys Tyr Val Glu Asp Thr His Tyr Pro Pro Gly Ala
1185 1190 1195 1200
Ser Val Pro Thr Glu Glu Thr Cys Lys Ser Cys Val Cys Thr Asn Ser
1205 1210 1215
Ser Gln Val Val Cys Arg Pro Glu Glu Gly Lys Ile Leu Asn Gln Thr
1220 1225 1230
Gln Asp Gly Ala Phe Cys Tyr Trp Glu Ile Cys Gly Pro Asn Gly Thr
1235 1240 1245
Val Glu Lys His Phe Asn Ile Cys Ser Ile Thr Thr Arg Pro Ser Thr
1250 1255 1260
Leu Thr Thr Phe Thr Thr Ile Thr Leu Pro Thr Thr Pro Thr Ser Phe
1265 1270 1275 1280
Thr Thr Thr Thr Thr Thr Thr Thr Pro Thr Ser Ser Thr Val Leu Ser
1285 1290 1295
Thr Thr Pro Lys Leu Cys Cys Leu Trp Ser Asp Trp Ile Asn Glu Asp
1300 1305 1310
His Pro Ser Ser Gly Ser Asp Asp Gly Asp Arg Glu Pro Phe Asp Gly
1315 1320 1325
Val Cys Gly Ala Pro Glu Asp Ile Glu Cys Arg Ser Val Lys Asp Pro
1330 1335 1340
His Leu Ser Leu Glu Gln His Gly Gln Lys Val Gln Cys Asp Val Ser
1345 1350 1355 1360
Val Gly Phe Ile Cys Lys Asn Glu Asp Gln Phe Gly Asn Gly Pro Phe
1365 1370 1375
Gly Leu Cys Tyr Asp Tyr Lys Ile Arg Val Asn Cys Cys Trp Pro Met
1380 1385 1390
Asp Lys Cys Ile Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ser Pro
1395 1400 1405
Pro Pro Thr Thr Thr Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser Pro
1410 1415 1420
Pro Thr Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro
1425 1430 1435 1440
Pro Ile Thr Thr Thr Thr Thr Pro Leu Pro Thr Thr Thr Pro Ser Pro
1445 1450 1455
Pro Ile Ser Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro
1460 1465 1470
Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr
1475 1480 1485
Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Met
1490 1495 1500
Thr Thr Pro Ile Thr Pro Pro Ala Ser Thr Thr Thr Leu Pro Pro Thr
1505 1510 1515 1520
Thr Thr Pro Ser Pro Pro Thr Thr Thr Thr Thr Thr Pro Pro Pro Thr
1525 1530 1535
Thr Thr Pro Ser Pro Pro Thr Thr Thr Pro Ile Thr Pro Pro Thr Ser
1540 1545 1550
Thr Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr
1555 1560 1565
Thr Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr
1570 1575 1580
Thr Pro Ser Pro Pro Thr Ile Thr Thr Thr Thr Pro Pro Pro Thr Thr
1585 1590 1595 1600
Thr Pro Ser Pro Pro Thr Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr
1605 1610 1615
Thr Pro Ser Pro Pro Thr Thr Thr Pro Ile Thr Pro Pro Thr Ser Thr
1620 1625 1630
Thr Thr Leu Pro Pro Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr Thr
1635 1640 1645
Thr Thr Pro Pro Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Thr
1650 1655 1660
Pro Ser Pro Pro Ile Thr Thr Thr Thr Thr Pro Pro Pro Thr Thr Thr
1665 1670 1675 1680
Pro Ser Ser Pro Ile Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Met
1685 1690 1695
Thr Thr Pro Ser Pro Thr Thr Thr Pro Ser Ser Pro Ile Thr Thr Thr
1700 1705 1710

Thr Thr Pro Ser Ser Thr Thr Thr Pro Ser Pro Pro Pro Thr Thr Met
1715 1720 1725
Thr Thr Pro Ser Pro Thr Thr Thr Pro Ser Pro Pro Thr Thr Thr Met
1730 1735 1740
Thr Thr Leu Pro Pro Thr Thr Thr Ser Ser Pro Leu Thr Thr Thr Pro
1745 1750 1755 1760
Leu Pro Pro Ser Ile Thr Pro Pro Thr Phe Ser Pro Phe Ser Thr Thr
1765 1770 1775
Thr Pro Thr Thr Pro Cys Val Pro Leu Cys Asn Trp Thr Gly Trp Leu
1780 1785 1790
Asp Ser Gly Lys Pro Asn Phe His Lys Pro Gly Gly Asp Thr Glu Leu
1795 1800 1805
Ile Gly Asp Val Cys Gly Pro Gly Trp Ala Ala Asn Ile Ser Cys Arg
1810 1815 1820
Ala Thr Met Tyr Pro Asp Val Pro Ile Gly Gln Leu Gly Gln Thr Val
1825 1830 1835 1840
Val Cys Asp Val Ser Val Gly Leu Ile Cys Lys Asn Glu Asp Gln Lys
1845 1850 1855
Pro Gly Gly Val Ile Pro Met Ala Phe Cys Leu Asn Tyr Glu Ile Asn
1860 1865 1870
Val Gln Cys Cys Glu Cys Val Thr Gln Pro Thr Thr Met Thr Thr Thr
1875 1880 1885
Thr Thr Glu Asn Pro Thr Pro Pro Thr Thr Thr Pro Ile Thr Thr Thr
1890 1895 1900
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
1905 1910 1915 1920
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
1925 1930 1935
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
1940 1945 1950
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
1955 1960 1965
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
1970 1975 1980
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
1985 1990 1995 2000
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
2005 2010 2015
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
2020 2025 2030
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
2035 2040 2045
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
2050 2055 2060
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
2065 2070 2075 2080
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
2085 2090 2095
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
2100 2105 2110
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
2115 2120 2125
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
2130 2135 2140
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
2145 2150 2155 2160
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
2165 2170 2175
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
2180 2185 2190
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
2195 2200 2205
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
2210 2215 2220
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
2225 2230 2235 2240
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro

2245 2250 2255
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
2260 2265 2270
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
2275 2280 2285
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
2290 2295 2300
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
2305 2310 2315 2320
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
2325 2330 2335
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
2340 2345 2350
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
2355 2360 2365
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
2370 2375 2380
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
2385 2390 2395 2400
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
2405 2410 2415
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
2420 2425 2430
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
2435 2440 2445
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
2450 2455 2460
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
2465 2470 2475 2480
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
2485 2490 2495
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
2500 2505 2510
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
2515 2520 2525
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
2530 2535 2540
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
2545 2550 2555 2560
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
2565 2570 2575
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
2580 2585 2590
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
2595 2600 2605
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
2610 2615 2620
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
2625 2630 2635 2640
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
2645 2650 2655
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
2660 2665 2670
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
2675 2680 2685
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
2690 2695 2700
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
2705 2710 2715 2720
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
2725 2730 2735
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
2740 2745 2750
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
2755 2760 2765
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
2770 2775 2780

Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
2785 2790 2795 2800
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
2805 2810 2815
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
2820 2825 2830
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
2835 2840 2845
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
2850 2855 2860
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
2865 2870 2875 2880
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
2885 2890 2895
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
2900 2905 2910
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
2915 2920 2925
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
2930 2935 2940
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
2945 2950 2955 2960
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
2965 2970 2975
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
2980 2985 2990
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
2995 3000 3005
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
3010 3015 3020
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
3025 3030 3035 3040
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
3045 3050 3055
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
3060 3065 3070
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
3075 3080 3085
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
3090 3095 3100
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
3105 3110 3115 3120
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
3125 3130 3135
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
3140 3145 3150
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
3155 3160 3165
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
3170 3175 3180
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
3185 3190 3195 3200
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
3205 3210 3215
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
3220 3225 3230
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
3235 3240 3245
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
3250 3255 3260
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
3265 3270 3275 3280
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
3285 3290 3295
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
3300 3305 3310
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr

3315 3320 3325
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
3330 3335 3340
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
3345 3350 3355 3360
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
3365 3370 3375
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
3380 3385 3390
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
3395 3400 3405
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
3410 3415 3420
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
3425 3430 3435 3440
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
3445 3450 3455
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
3460 3465 3470
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
3475 3480 3485
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
3490 3495 3500
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
3505 3510 3515 3520
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
3525 3530 3535
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
3540 3545 3550
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
3555 3560 3565
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
3570 3575 3580
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
3585 3590 3595 3600
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
3605 3610 3615
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
3620 3625 3630
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
3635 3640 3645
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
3650 3655 3660
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
3665 3670 3675 3680
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
3685 3690 3695
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
3700 3705 3710
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
3715 3720 3725
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
3730 3735 3740
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
3745 3750 3755 3760
Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
3765 3770 3775
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
3780 3785 3790
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
3795 3800 3805
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
3810 3815 3820
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr
3825 3830 3835 3840
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile
3845 3850 3855

Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln
3860 3865 3870
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr
3875 3880 3885
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr
3890 3895 3900
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro
3905 3910 3915 3920
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr
3925 3930 3935
Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr
3940 3945 3950
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr
3955 3960 3965
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr
3970 3975 3980
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val
3985 3990 3995 4000
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro
4005 4010 4015
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr
4020 4025 4030
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro
4035 4040 4045
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr
4050 4055 4060
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr
4065 4070 4075 4080
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro
4085 4090 4095
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr
4100 4105 4110
Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr
4115 4120 4125
Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro
4130 4135 4140
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr
4145 4150 4155 4160
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr
4165 4170 4175
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly
4180 4185 4190
Thr Gln Thr Gly Pro Pro Thr His Thr Ser Thr Ala Pro Ile Ala Glu
4195 4200 4205
Leu Thr Thr Ser Asn Pro Pro Pro Glu Ser Ser Thr Pro Gln Thr Ser
4210 4215 4220
Arg Ser Thr Ser Ser Pro Leu Thr Glu Ser Thr Thr Leu Leu Ser Thr
4225 4230 4235 4240
Leu Pro Pro Ala Ile Glu Met Thr Ser Thr Ala Pro Pro Ser Thr Pro
4245 4250 4255
Thr Ala Pro Thr Thr Thr Ser Gly Gly His Thr Leu Ser Pro Pro Pro
4260 4265 4270
Ser Thr Thr Thr Ser Pro Pro Gly Thr Pro Thr Arg Gly Thr Thr Thr
4275 4280 4285
Gly Ser Ser Ser Ala Pro Thr Pro Ser Thr Val Gln Thr Thr Thr Thr
4290 4295 4300
Ser Ala Trp Thr Pro Thr Pro Thr Pro Leu Ser Thr Pro Ser Ile Ile
4305 4310 4315 4320
Arg Thr Thr Gly Leu Arg Pro Tyr Pro Ser Ser Val Leu Ile Cys Cys
4325 4330 4335
Val Leu Asn Asp Thr Tyr Tyr Ala Pro Gly Glu Glu Val Tyr Asn Gly
4340 4345 4350
Thr Tyr Gly Asp Thr Cys Tyr Phe Val Asn Cys Ser Leu Ser Cys Thr
4355 4360 4365
Leu Glu Phe Tyr Asn Trp Ser Cys Pro Ser Thr Pro Ser Pro Thr Pro
4370 4375 4380
Thr Pro Ser Lys Ser Thr Pro Thr Pro Ser Lys Pro Ser Ser Thr Pro

4385 4390 4395 4400
Ser Lys Pro Thr Pro Gly Thr Lys Pro Pro Glu Cys Pro Asp Phe Asp
4405 4410 4415
Pro Pro Arg Gln Glu Asn Glu Thr Trp Trp Leu Cys Asp Cys Phe Met
4420 4425 4430
Ala Thr Cys Lys Tyr Asn Asn Thr Val Glu Ile Val Lys Val Glu Cys
4435 4440 4445
Glu Pro Pro Pro Met Pro Thr Cys Ser Asn Gly Leu Gln Pro Val Arg
4450 4455 4460
Val Glu Asp Pro Asp Gly Cys Cys Trp His Trp Glu Cys Asp Cys Tyr
4465 4470 4475 4480
Cys Thr Gly Trp Gly Asp Pro His Tyr Val Thr Phe Asp Gly Leu Tyr
4485 4490 4495
Tyr Ser Tyr Gln Gly Asn Cys Thr Tyr Val Leu Val Glu Glu Ile Ser
4500 4505 4510
Pro Ser Val Asp Asn Phe Gly Val Tyr Ile Asp Asn Tyr His Cys Asp
4515 4520 4525
Pro Asn Asp Lys Val Ser Cys Pro Arg Thr Leu Ile Val Arg His Glu
4530 4535 4540
Thr Gln Glu Val Leu Ile Lys Thr Val His Met Met Pro Met Gln Val
4545 4550 4555 4560
Gln Val Gln Val Asn Arg Gln Ala Val Ala Leu Pro Tyr Lys Lys Tyr
4565 4570 4575
Gly Leu Glu Val Tyr Gln Ser Gly Ile Asn Tyr Val Val Asp Ile Pro
4580 4585 4590
Glu Leu Gly Val Leu Val Ser Tyr Asn Gly Leu Ser Phe Ser Val Arg
4595 4600 4605
Leu Pro Tyr His Arg Phe Gly Asn Asn Thr Lys Gly Gln Cys Gly Thr
4610 4615 4620
Cys Thr Asn Thr Thr Ser Asp Asp Cys Ile Leu Pro Ser Gly Glu Ile
4625 4630 4635 4640
Val Ser Asn Cys Glu Ala Ala Ala Asp Gln Trp Leu Val Asn Asp Pro
4645 4650 4655
Ser Lys Pro His Cys Pro His Ser Ser Ser Thr Thr Lys Arg Pro Ala
4660 4665 4670
Val Thr Val Pro Gly Gly Gly Lys Thr Thr Pro His Lys Asp Cys Thr
4675 4680 4685
Pro Ser Pro Leu Cys Gln Leu Ile Lys Asp Ser Leu Phe Ala Gln Cys
4690 4695 4700
His Ala Leu Val Pro Pro Gln His Tyr Tyr Asp Ala Cys Val Phe Asp
4705 4710 4715 4720
Ser Cys Phe Met Pro Gly Ser Ser Leu Glu Cys Ala Ser Leu Gln Ala
4725 4730 4735
Tyr Ala Ala Leu Cys Ala Gln Gln Asn Ile Cys Leu Asp Trp Arg Asn
4740 4745 4750
His Thr His Gly Ala Cys Leu Val Glu Cys Pro Ser His Arg Glu Tyr
4755 4760 4765
Gln Ala Cys Gly Pro Ala Glu Glu Pro Thr Cys Lys Ser Ser Ser Ser
4770 4775 4780
Gln Gln Asn Asn Thr Val Leu Val Glu Gly Cys Phe Cys Pro Glu Gly
4785 4790 4795 4800
Thr Met Asn Tyr Ala Pro Gly Phe Asp Val Cys Val Lys Thr Cys Gly
4805 4810 4815
Cys Val Gly Pro Asp Asn Val Pro Arg Glu Phe Gly Glu His Phe Glu
4820 4825 4830
Phe Asp Cys Lys Asn Cys Val Cys Leu Glu Gly Gly Ser Gly Ile Ile
4835 4840 4845
Cys Gln Pro Lys Arg Cys Ser Gln Lys Pro Val Thr His Cys Val Glu
4850 4855 4860
Asp Gly Thr Tyr Leu Ala Thr Glu Val Asn Pro Ala Asp Thr Cys Cys
4865 4870 4875 4880
Asn Ile Thr Val Cys Lys Cys Asn Thr Ser Leu Cys Lys Glu Lys Pro
4885 4890 4895
Ser Val Cys Pro Leu Gly Phe Glu Val Lys Ser Lys Met Val Pro Gly
4900 4905 4910
Arg Cys Cys Pro Phe Tyr Trp Cys Glu Ser Lys Gly Val Cys Val His
4915 4920 4925

Gly Asn Ala Glu Tyr Gln Pro Gly Ser Pro Val Tyr Ser Ser Lys Cys
4930 4935 4940
Gln Asp Cys Val Cys Thr Asp Lys Val Asp Asn Asn Thr Leu Leu Asn
4945 4950 4955 4960
Val Ile Ala Cys Thr His Val Pro Cys Asn Thr Ser Cys Ser Pro Gly
4965 4970 4975
Phe Glu Leu Met Glu Ala Pro Gly Glu Cys Cys Lys Lys Cys Glu Gln
4980 4985 4990
Thr His Cys Ile Ile Lys Arg Pro Asp Asn Gln His Val Ile Leu Lys
4995 5000 5005
Pro Gly Asp Phe Lys Ser Asp Pro Lys Asn Asn Cys Thr Phe Phe Ser
5010 5015 5020
Cys Val Lys Ile His Asn Gln Leu Ile Ser Ser Val Ser Asn Ile Thr
5025 5030 5035 5040
Cys Pro Asn Phe Asp Ala Ser Ile Cys Ile Pro Gly Ser Ile Thr Phe
5045 5050 5055
Met Pro Asn Gly Cys Cys Lys Thr Cys Thr Pro Arg Asn Glu Thr Arg
5060 5065 5070
Val Pro Cys Ser Thr Val Pro Val Thr Thr Glu Val Ser Tyr Ala Gly
5075 5080 5085
Cys Thr Lys Thr Val Leu Met Asn His Cys Ser Gly Ser Cys Gly Thr
5090 5095 5100
Phe Val Met Tyr Ser Ala Lys Ala Gln Ala Leu Asp His Ser Cys Ser
5105 5110 5115 5120
Cys Cys Lys Glu Glu Lys Thr Ser Gln Arg Glu Val Val Leu Ser Cys
5125 5130 5135
Pro Asn Gly Gly Ser Leu Thr His Thr Tyr Thr His Ile Glu Ser Cys
5140 5145 5150
Gln Cys Gln Asp Thr Val Cys Gly Leu Pro Thr Gly Thr Ser Arg Arg
5155 5160 5165
Ala Arg Arg Ser Pro Arg His Leu Gly Ser
5170 5175

<210> 179
<211> 508
<212> PRT
<213> Homo sapiens

<400> 179
Met Gln Arg Leu Leu Thr Pro Val Lys Arg Ile Leu Gln Leu Thr Arg
1 5 10 15
Ala Val Gln Glu Thr Ser Leu Thr Pro Ala Arg Leu Leu Pro Val Ala
20 25 30
His Gln Arg Phe Ser Thr Ala Ser Ala Val Pro Leu Ala Lys Thr Asp
35 40 45
Thr Trp Pro Lys Asp Val Gly Ile Leu Ala Leu Glu Val Tyr Phe Pro
50 55 60
Ala Gln Tyr Val Asp Gln Thr Asp Leu Glu Lys Tyr Asn Asn Val Glu
65 70 75 80
Ala Gly Lys Tyr Thr Val Gly Leu Gly Gln Thr Arg Met Gly Phe Cys
85 90 95
Ser Val Gln Glu Asp Ile Asn Ser Leu Cys Leu Thr Val Val Gln Arg
100 105 110
Leu Met Glu Arg Ile Gln Leu Pro Trp Asp Ser Val Gly Arg Leu Glu
115 120 125
Val Gly Thr Glu Thr Ile Ile Asp Lys Ser Lys Ala Val Lys Thr Val
130 135 140
Leu Met Glu Leu Phe Gln Asp Ser Gly Asn Thr Asp Ile Glu Gly Ile
145 150 155 160
Asp Thr Thr Asn Ala Cys Tyr Gly Gly Thr Ala Ser Leu Phe Asn Ala
165 170 175
Ala Asn Trp Met Glu Ser Ser Ser Trp Asp Gly Arg Tyr Ala Met Val
180 185 190
Val Cys Gly Asp Ile Ala Val Tyr Pro Ser Gly Asn Ala Arg Pro Thr
195 200 205
Gly Gly Ala Gly Ala Val Ala Met Leu Ile Gly Pro Lys Ala Pro Leu

210 215 220
Ala Leu Glu Arg Gly Leu Arg Gly Thr His Met Glu Asn Val Tyr Asp
225 230 235 240
Phe Tyr Lys Pro Asn Leu Ala Ser Glu Tyr Pro Ile Val Asp Gly Lys
245 250 255
Leu Ser Ile Gln Cys Tyr Leu Arg Ala Leu Asp Arg Cys Tyr Thr Ser
260 265 270
Tyr Arg Lys Lys Ile Gln Asn Gln Trp Lys Gln Ala Gly Ser Asp Arg
275 280 285
Pro Phe Thr Leu Asp Asp Leu Gln Tyr Met Ile Phe His Thr Pro Phe
290 295 300
Cys Lys Met Val Gln Lys Ser Leu Ala Arg Leu Met Phe Asn Asp Phe
305 310 315 320
Leu Ser Ala Ser Ser Asp Thr Gln Thr Ser Leu Tyr Lys Gly Leu Glu
325 330 335
Ala Phe Gly Gly Leu Lys Leu Glu Asp Thr Tyr Thr Asn Lys Asp Leu
340 345 350
Asp Lys Ala Leu Leu Lys Ala Ser Gln Asp Met Phe Asp Lys Lys Thr
355 360 365
Lys Ala Ser Leu Tyr Leu Ser Thr His Asn Gly Asn Met Tyr Thr Ser
370 375 380
Ser Leu Tyr Gly Cys Leu Ala Ser Leu Leu Ser His His Ser Ala Gln
385 390 395 400
Glu Leu Ala Gly Ser Arg Ile Gly Ala Phe Ser Tyr Gly Ser Gly Leu
405 410 415
Ala Ala Ser Phe Phe Ser Phe Arg Val Ser Gln Asp Ala Ala Pro Gly
420 425 430
Ser Pro Leu Asp Lys Leu Val Ser Ser Thr Ser Asp Leu Pro Lys Arg
435 440 445
Leu Ala Ser Arg Lys Cys Val Ser Pro Glu Glu Phe Thr Glu Ile Met
450 455 460
Asn Gln Arg Glu Gln Phe Tyr His Lys Val Asn Phe Ser Pro Pro Gly
465 470 475 480
Asp Thr Asn Ser Leu Phe Pro Gly Thr Trp Tyr Leu Glu Arg Val Asp
485 490 495
Glu Gln His Arg Arg Lys Tyr Ala Arg Arg Pro Val
500 505

<210> 180
<211> 914
<212> PRT
<213> Homo sapiens

<400> 180
Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu
1 5 10 15
Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Asn Gly Tyr
20 25 30
Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35 40 45
Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu
50 55 60
Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu
65 70 75 80
Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu
85 90 95
Glu Thr Tyr Lys Asn Ala Asp Val Leu Val Ala Glu Ser Thr Pro Pro
100 105 110
Gly Asn Asp Glu Pro Tyr Thr Glu Gln Met Gly Asn Cys Gly Glu Lys
115 120 125
Gly Glu Arg Ile His Leu Thr Pro Asp Phe Ile Ala Gly Lys Lys Leu
130 135 140
Ala Glu Tyr Gly Pro Gln Gly Lys Ala Phe Val His Glu Trp Ala His
145 150 155 160
Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Glu Lys Phe Tyr
165 170 175

Leu Ser Asn Gly Arg Ile Gln Ala Val Arg Cys Ser Ala Gly Ile Thr
180 185 190
Gly Thr Asn Val Val Lys Lys Cys Gln Gly Gly Ser Cys Tyr Thr Lys
195 200 205
Arg Cys Thr Phe Asn Lys Val Thr Gly Leu Tyr Glu Lys Gly Cys Glu
210 215 220
Phe Val Leu Gln Ser Arg Gln Thr Glu Lys Ala Ser Ile Met Phe Ala
225 230 235 240
Gln His Val Asp Ser Ile Val Glu Phe Cys Thr Glu Gln Asn His Asn
245 250 255
Lys Glu Ala Pro Asn Lys Gln Asn Gln Lys Cys Asn Leu Arg Ser Thr
260 265 270
Trp Glu Val Ile Arg Asp Ser Glu Asp Phe Lys Lys Thr Thr Pro Met
275 280 285
Thr Thr Gln Pro Pro Asn Pro Thr Phe Ser Leu Leu Gln Ile Gly Gln
290 295 300
Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ala Thr Gly
305 310 315 320
Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln
325 330 335
Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala
340 345 350
Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg
355 360 365
Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser
370 375 380
Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr
385 390 395 400
Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn
405 410 415
Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile
420 425 430
His Thr Val Ala Leu Gly Pro Ser Ala Ala Gln Glu Leu Glu Glu Leu
435 440 445
Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln
450 455 460
Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly
465 470 475 480
Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu
485 490 495
Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val
500 505 510
Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln
515 520 525
Ile Leu Leu Trp Asp Pro Ser Gly Gln Lys Gln Gly Gly Phe Val Val
530 535 540
Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys
545 550 555 560
Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr
565 570 575
Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr
580 585 590
Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu
595 600 605
Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala
610 615 620
Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu
625 630 635 640
Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
645 650 655
Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
660 665 670
Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
675 680 685
Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
690 695 700
Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp

705 710 715 720
Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
725 730 735
Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
740 745 750
Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
755 760 765
Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
770 775 780
Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785 790 795 800
Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
805 810 815
Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
820 825 830
Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
835 840 845
Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
850 855 860
Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865 870 875 880
Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
885 890 895
His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
900 905 910
Ile Ala

<210> 181
<211> 61
<212> PRT
<213> Homo sapiens

<400> 181
Met Asp Pro Asn Cys Ser Cys Ala Ala Gly Val Ser Cys Thr Cys Ala
1 5 10 15
Gly Ser Cys Lys Cys Lys Glu Cys Lys Cys Thr Ser Cys Lys Lys Ser
20 25 30
Cys Cys Ser Cys Cys Pro Val Gly Cys Ser Lys Cys Ala Gln Gly Cys
35 40 45
Val Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Asp
50 55 60

<210> 182
<211> 260
<212> PRT
<213> Homo sapiens

<400> 182
Met Ser His His Trp Gly Tyr Gly Lys His Asn Gly Pro Glu His Trp
1 5 10 15
His Lys Asp Phe Pro Ile Ala Lys Gly Glu Arg Gln Ser Pro Val Asp
20 25 30
Ile Asp Thr His Thr Ala Lys Tyr Asp Pro Ser Leu Lys Pro Leu Ser
35 40 45
Val Ser Tyr Asp Gln Ala Thr Ser Leu Arg Ile Leu Asn Asn Gly His
50 55 60
Ala Phe Asn Val Glu Phe Asp Asp Ser Gln Asp Lys Ala Val Leu Lys
65 70 75 80
Gly Gly Pro Leu Asp Gly Thr Tyr Arg Leu Ile Gln Phe His Phe His
85 90 95
Trp Gly Ser Leu Asp Gly Gln Gly Ser Glu His Thr Val Asp Lys Lys
100 105 110
Lys Tyr Ala Ala Glu Leu His Leu Val His Trp Asn Thr Lys Tyr Gly
115 120 125

Asp Phe Gly Lys Ala Val Gln Gln Pro Asp Gly Leu Ala Val Leu Gly
130 135 140
Ile Phe Leu Lys Val Gly Ser Ala Lys Pro Gly Leu Gln Lys Val Val
145 150 155 160
Asp Val Leu Asp Ser Ile Lys Thr Lys Gly Lys Ser Ala Asp Phe Thr
165 170 175
Asn Phe Asp Pro Arg Gly Leu Leu Pro Glu Ser Leu Asp Tyr Trp Thr
180 185 190
Tyr Pro Gly Ser Leu Thr Thr Pro Pro Leu Leu Glu Cys Val Thr Trp
195 200 205
Ile Val Leu Lys Glu Pro Ile Ser Val Ser Ser Glu Gln Val Leu Lys
210 215 220
Phe Arg Lys Leu Asn Phe Asn Gly Glu Gly Glu Pro Glu Glu Leu Met
225 230 235 240
Val Asp Asn Trp Arg Pro Ala Gln Pro Leu Lys Asn Arg Gln Ile Lys
245 250 255
Ala Ser Phe Lys
260

<210> 183
<211> 61
<212> PRT
<213> Homo sapiens

<400> 183
Met Asp Pro Asn Cys Ser Cys Glu Ala Gly Gly Ser Cys Ala Cys Ala
1 5 10 15
Gly Ser Cys Lys Cys Lys Lys Cys Lys Cys Thr Ser Cys Lys Lys Ser
20 25 30
Cys Cys Ser Cys Cys Pro Leu Gly Cys Ala Lys Cys Ala Gln Gly Cys
35 40 45
Ile Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Ala
50 55 60

<210> 184
<211> 61
<212> PRT
<213> Homo sapiens

<400> 184
Met Asp Pro Asn Cys Ser Cys Ala Ala Gly Val Ser Cys Thr Cys Ala
1 5 10 15
Ser Ser Cys Lys Cys Lys Glu Cys Lys Cys Thr Ser Cys Lys Lys Ser
20 25 30
Cys Cys Ser Cys Cys Pro Val Gly Cys Ala Lys Cys Ala Gln Gly Cys
35 40 45
Ile Cys Lys Gly Ala Ser Glu Lys Cys Ser Cys Cys Ala
50 55 60

<210> 185
<211> 167
<212> PRT
<213> Homo sapiens

<400> 185
Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly
1 5 10 15
Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Ser
20 25 30
Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro
35 40 45
Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu
50 55 60
Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn

65 70 75 80
Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln
85 90 95
Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr
100 105 110
Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe
115 120 125
Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly
130 135 140
Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr
145 150 155 160
Pro Thr Ser Cys Ser Arg Cys
165

<210> 186
<211> 61
<212> PRT
<213> Homo sapiens

<400> 186
Met Asp Pro Asn Cys Ser Cys Ser Pro Val Gly Ser Cys Ala Cys Ala
1 5 10 15
Gly Ser Cys Lys Cys Lys Glu Cys Lys Cys Thr Ser Cys Lys Lys Ser
20 25 30
Cys Cys Ser Cys Cys Pro Val Gly Cys Ala Lys Cys Ala Gln Gly Cys
35 40 45
Ile Cys Lys Gly Thr Ser Asp Lys Cys Ser Cys Cys Ala
50 55 60